

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:41; Search time 168.02 Seconds

(without alignments)
611.388 Million cell updates/sec

Title: US-09-771-382-4

Perfect score: 3019
Sequence: 1 MNKIRYINMSALNMAVAVS.....TAGSNRNGHGCASAVCYQM 594

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL_19:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.todent:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3019	100.0	594	2	Q930Y4
2	2931	97.1	594	2	Q93PI3
3	2927	97.0	594	2	Q93PS2
4	2874	95.2	594	2	Q93PH7
5	2863	94.8	598	2	Q93PT0
6	2861	94.8	598	2	Q93PT0
7	2855	94.6	598	2	Q93PS0
8	2852	94.5	598	2	Q93PS5
9	2806	92.9	600	2	Q93PS6
10	2790	92.4	590	2	Q93PS3
11	2762.5	91.5	599	2	Q93PS8
12	2758.5	91.4	591	2	Q93PS7
13	2751	91.1	592	16	Q93RI8
14	2739.5	90.7	591	2	Q93OFO
15	2739.5	90.7	591	2	Q93OY3
16	2736.5	90.6	599	2	Q93PS8

17	2718	90.0	598	2	Q93PR7	Q93PR7 neisseria m
18	2678	88.7	592	2	Q93PS9	Q93PS9 neisseria m
19	2655.5	88.0	595	2	Q93PH0	Q93PH0 neisseria m
20	2636	87.3	592	2	Q93OY2	Q93OY2 neisseria m
21	2606	86.3	600	2	Q93PS5	Q93PS5 neisseria m
22	2533	83.9	592	16	Q93OW4	Q93OW4 neisseria m
23	2527.5	83.7	589	2	Q93PI0	Q93PI0 neisseria m
24	2516.5	83.4	589	2	Q93OY1	Q93OY1 neisseria m
25	2444.5	81.0	526	2	Q93PS4	Q93PS4 neisseria m
26	2442.5	80.9	530	2	Q93PS1	Q93PS1 neisseria m
27	1328.5	44.0	2353	2	P71401	P71401 haemophilus
28	1030	34.1	1098	2	Q48152	Q48152 haemophilus
29	423	14.0	1299	16	Q9F3X6	Q9F3X6 pasteurella
30	398.5	13.2	2059	16	Q9PD50	Q9PD50 xyella fas
31	384.5	12.7	1190	16	Q9PC04	Q9PC04 xyella fas
32	384.5	12.7	2712	16	Q9F3X5	Q9F3X5 pasteurella
33	375.5	12.4	1107	2	Q9F2D8	Q9F2D8 salmoneila
34	263	8.7	1291	16	Q92X07	Q92X07 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98HJ2 rhizobium l
36	244	8.1	1039	2	Q9L6T7	Q9L6T7 escherichia
37	243	8.0	2276	2	Q93T76	Q93T76 staphylococ
38	239	7.9	1004	16	Q9PD53	Q9PD53 xyella fas
39	236	7.8	1039	2	Q9L6T8	Q9L6T8 escherichia
40	230	7.6	1040	2	Q9AL50	Q9AL50 shigella fl
41	228.5	7.6	1265	2	Q9FDAO	Q9FDAO xanthomonas
42	228.5	7.6	1557	2	Q9RNI2	Q9RNI2 haemophilus
43	224.5	7.4	989	2	Q9XD84	Q9XD84 escherichia
44	223	7.4	1213	16	Q98JH8	Q98JH8 rhizobium l
45	222	7.4	1018	16	Q9HW06	Q9HW06 pseudomonas

ALIGNMENTS

RESULT 1

Q930Y4 PRELIMINARY: PRT: 594 AA.

AC Q930Y4: 01-DEC-2001 (TREMBLrel. 19, Created)

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE NHHA OUTER MEMBRANE PROTEIN.

GN NHHA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxId=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EG327;

RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF157605; AAK68866.1; -

SQ SEQUENCE 594 AA: 62297 MW: 9DD48B043A8BA2 CRC64:

Query Match 100.0%; Score 3019; DB 2; Length 594;

Best Local Similarity 100.0%; Pred. No. 1.2e-118;

Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIRYINMSALNMAVAVSELTRNHTKRASATVAVATLTLFAVQASTDDDDLYLE 60

DB 1 MNKIRYINMSALNMAVAVSELTRNHTKRASATVAVATLTLFAVQASTDDDDLYLE 60

QY 61 PVORTAVVLSFRSDKEGTEKEVTEEDSNMGVYEDKKGVLTAGTITTKAGDNLIKONTNE 120

DB 61 PVORTAVVLSFRSDKEGTEKEVTEEDSNMGVYEDKKGVLTAGTITTKAGDNLIKONTNE 120

QY 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKVNITSDTKGLNPAKKTAEFTNGDTYVA 180

DB 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKVNITSDTKGLNPAKKTAEFTNGDTYVA 180

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QY 181 LKIGSTLTLDTLLNTGATNTVNDVTDDEKRRASAVKDVYNAGNNIKGVKPGTASDNV 240
    |||
Db 181 LKIGSTLTLDTLLNTGATNTVNDVTDDEKRRASAVKDVYNAGNNIKGVKPGTASDNV 240
QY 241 DFLVRYDVEFLSADTKTNTVNESKDKGKRTVEYIGAKTSVIREKDKLVTGDKGEND 300
    |||
Db 241 DFLVRYDVEFLSADTKTNTVNESKDKGKRTVEYIGAKTSVIREKDKLVTGDKGEND 300
QY 301 SSTDKGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFEYVTSCTNVPFASGKTTA 360
    |||
Db 301 SSTDKGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFEYVTSCTNVPFASGKTTA 360
QY 361 TVSKDDGNTITVMYDVNVDGALNVNQLONGSMNLDKRAVAGSSGKVISGNVSPSKGKME 420
    |||
Db 361 TVSKDDGNTITVMYDVNVDGALNVNQLONGSMNLDKRAVAGSSGKVISGNVSPSKGKME 420
QY 421 TVNINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSDDEGALNVGSKDANK 480
    |||
Db 421 TVNINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSDDEGALNVGSKDANK 480
QY 481 PVRITNVAPGVKEGDTVNVQOLKGYAQNMLNNHIDVNDGNARAGIAQAIATAGLVQAYLP 540
    |||
Db 481 PVRITNVAPGVKEGDTVNVQOLKGYAQNMLNNHIDVNDGNARAGIAQAIATAGLVQAYLP 540
QY 541 KSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGTASGNSRCHFGASASVGYOW 594
    |||
Db 541 KSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGTASGNSRCHFGASASVGYOW 594
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RESULT 2
Q9JP13 PRELIMINARY; PRT; 594 AA.

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AC Q9JP13;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OTHER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND B2232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteijn H.,
RA Moxon E.R., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -
DR EMBL: AF226369; AAF42518.1; -
SO SEQUENCE 594 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;
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Query Match 97.1%; Score 2931; DB 2; Length 594;
Best Local Similarity 97.1%; Pred. No. 5.6e-115;
Matches 577; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

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QY 1 MNKIRIIMNSALNMAWVAVSELTNRNHTKASATVATAVLATLTFATVQASTTDDDDLYLE 60
    |||
Db 1 MNKIRIIMNSALNMAWVAVSELTNRNHTKASATVATAVLATLTFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSRSDKEGKEVEYEDSNMGVYFDKKGVLTTAGTITLKAGDNLIKONTNE 120
    |||
Db 61 PVORTAVVLSRSDKEGKEVEYEDSNMGVYFDKKGVLTTAGTITLKAGDNLIKONTNE 120
QY 121 NTFNASSFTYSLKDLTDLTSVGETEKLSPFSANSNKVNITSDTKGLNFAKTAETNGDTTVH 180
    |||
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Db 121 NTFNASSFTYSLKDLTDLTSVGETEKLSPFSANSNKVNITSDTKGLNFAKTAETNGDTTVH 180
    |||
QY 181 LKIGSTLTLDTLLNTGATNTVNDVTDDEKRRASAVKDVYNAGNNIKGVKPGTASDNV 240
    |||
Db 181 LKIGSTLTLDTLLNTGATNTVNDVTDDEKRRASAVKDVYNAGNNIKGVKPGTASDNV 240
QY 241 DFLVRYDVEFLSADTKTNTVNESKDKGKRTVEYIGAKTSVIREKDKLVTGDKGEND 300
    |||
Db 241 DFLVRYDVEFLSADTKTNTVNESKDKGKRTVEYIGAKTSVIREKDKLVTGDKGEND 300
QY 301 SSTDKGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFEYVTSCTNVPFASGKTTA 360
    |||
Db 301 SSTDKGELVTAKEVIDAVNKAQMRKTTTANGOTGADKEFEYVTSCTNVPFASGKTTA 360
QY 361 TVSKDDGNTITVMYDVNVDGALNVNQLONGSMNLDKRAVAGSSGKVISGNVSPSKGKME 420
    |||
Db 361 TVSKDDGNTITVMYDVNVDGALNVNQLONGSMNLDKRAVAGSSGKVISGNVSPSKGKME 420
QY 421 TVNINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSDDEGALNVGSKDANK 480
    |||
Db 421 TVNINAGNNIETTRNGKNIDATSMTPOFSSVSLGAGADAPTLVSDDEGALNVGSKDANK 480
QY 481 PVRITNVAPGVKEGDTVNVQOLKGYAQNMLNNHIDVNDGNARAGIAQAIATAGLVQAYLP 540
    |||
Db 481 PVRITNVAPGVKEGDTVNVQOLKGYAQNMLNNHIDVNDGNARAGIAQAIATAGLVQAYLP 540
QY 541 KSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGTASGNSRCHFGASASVGYOW 594
    |||
Db 541 KSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGTASGNSRCHFGASASVGYOW 594
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RESULT 3
Q9JP52 PRELIMINARY; PRT; 594 AA.

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AC Q9JP52;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OTHER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG33;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteijn H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -
SO SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;
```

Query Match 97.0%; Score 2927; DB 2; Length 594;
Best Local Similarity 97.0%; Pred. No. 8.2e-115;
Matches 576; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

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QY 1 MNKIRIIMNSALNMAWVAVSELTNRNHTKASATVATAVLATLTFATVQASTTDDDDLYLE 60
    |||
Db 1 MNKIRIIMNSALNMAWVAVSELTNRNHTKASATVATAVLATLTFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSRSDKEGKEVEYEDSNMGVYFDKKGVLTTAGTITLKAGDNLIKONTNE 120
    |||
Db 61 PVORTAVVLSRSDKEGKEVEYEDSNMGVYFDKKGVLTTAGTITLKAGDNLIKONTNE 120
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QY 121 NTNASSFTYSLKKDLDTLTSVGEKLSFSAKSNKVNITSDTKLNFPAKKTAEFTNGDTYH 180
    |||||||
Db 121 NTNASSFTYSLKKDLDTLTSVGEKLSFSAKSNKVNITSDTKLNFPAKKTAEFTNGDTYH 180
QY 181 LNCIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKKVNLNAGNWKGVKPGTASDNV 240
    |||||||
Db 181 LNCIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKKVNLNAGNWKGVKPGTASDNV 240
QY 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEKDKLYTGKDKGEND 300
    |||||||
Db 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEKDKLYTGKDKGEND 300
QY 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGOTGADKFEFTVSGTNTVTFASGKTTA 360
    |||||||
Db 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGOTGADKFEFTVSGTNTVTFASGKTTA 360
QY 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKME 420
    |||||||
Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKME 420
QY 421 TVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVEGALNNGSKDANK 480
    |||||||
Db 421 TVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVEGALNNGSKDANK 480
QY 481 PVRTTVAAPGVKGDVTNVAOLKGVAONLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
    |||||||
Db 481 PVRTTVAAPGVKGDVTNVAOLKGVAONLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594
    |||||||
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594

RESULT 4
09JPH7 PRELIMINARY: PRT: 594 AA.
AC 09JPH7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE OUTFER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198; AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198;
RA Peak I.R., Strikhantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DDJ databases.
DR EMBL: AF2263368; AAF42517.1; -
DR EMBL: AF2263358; AAF42507.1; -
DR EMBL: AF157604; AAK68865.1; -
SQ SEQUENCE 594 AA: 62361 MW: 436BDDDED68263C5C CRC64;
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Query Match 95.2%; Score 2874; DB 2; Length 594;
Best local Similarity 95.6%; Pred. No. 1.3e-112;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIRIINWSALNAVAVSELTNRHHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
    |||||||
Db 1 MNKIRIINWSALNAVAVSELTNRHHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDKGTGEKEVTEDSNMGVYFDRKKGVLTAQITTLAKADNLKIKNTNE 120
    |||||||
Db 61 PVQRTAVVLSFRSDKGTGEKEVTEDSNMGVYFDRKKGVLTAQITTLAKADNLKIKNTNE 120
QY 121 NTNASSFTYSLKKDLDTLTSVGEKLSFSAKSNKVNITSDTKLNFPAKKTAEFTNGDTYH 180
    |||||||
Db 121 NTNASSFTYSLKKDLDTLTSVGEKLSFSAKSNKVNITSDTKLNFPAKKTAEFTNGDTYH 180
QY 181 LNCIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKKVNLNAGNWKGVKPGTASDNV 240
    |||||||
Db 181 LNCIGSTLDTLLNTGATNTVNDVYDDEKKRAASVKKVNLNAGNWKGVKPGTASDNV 240
QY 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEKDKLYTGKDKGEND 300
    |||||||
Db 241 DFRRTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEKDKLYTGKDKGEND 300
QY 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGOTGADKFEFTVSGTNTVTFASGKTTA 360
    |||||||
Db 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGOTGADKFEFTVSGTNTVTFASGKTTA 360
QY 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKME 420
    |||||||
Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKGKME 420
QY 421 TVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVEGALNNGSKDANK 480
    |||||||
Db 421 TVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVEGALNNGSKDANK 480
QY 481 PVRTTVAAPGVKGDVTNVAOLKGVAONLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
    |||||||
Db 481 PVRTTVAAPGVKGDVTNVAOLKGVAONLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594
    |||||||
Db 541 KSMMAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594

RESULT 5
09JPR9 PRELIMINARY: PRT: 598 AA.
AC 09JPR9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE OUTFER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF2263382; AAF42531.1; -
SQ SEQUENCE 598 AA: 62718 MW: 9095F8E31AD7C76D CRC64;
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Query Match 94.8%; Score 2863; DB 2; Length 598;
Best Local Similarity 95.0%; Pred. No. 3.8e-112;
Matches 568; Conservative 5; Mismatches 21; Indels 4; Gaps 1;

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OY 1 MNKIYRIIWNALNANWVAVSELTNRNHTKRASATVATATLLEFATVOASTTDDDDLYLE 60
    |||||||
DB 1 MNKIYRIIWNALNANWVAVSELTNRNHTKRASATVATATLLEFATVOANATDDDDLYLE 60
OY 61 PVORTAVVLSFRSDKEGEGEKEVEDSNMGVYFDKKGVLTAAGTTLKAGDNLIKQNTNE 120
    |||||||
DB 61 PVORTAVVLSFRSDKEGEGEKEVEDSNMGVYFDKKGVLTAAGTTLKAGDNLIKQNTNE 120
OY 121 NTNA-----SFTYSLKRLDTLTSVGTETKLSFSAANSKNVNTSPTKGLNFAKKAETNGD 176
    |||||||
DB 121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
OY 177 TTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVADVLANAGMNIKGVKPGTTA 236
    |||||||
DB 181 PTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVADVLANAGMNIKGVKPGTTA 240
OY 237 SDNDFEVRTYDVEFLSADTKTTTVNVESSKDNKRTVEYKIGAKTSVIEKDGKLVTKGDK 296
    |||||||
DB 241 SDNDFEVRTYDVEFLSADTKTTTVNVESSKDNKRTVEYKIGAKTSVIEKDGKLVTKGDK 300
OY 297 GENDSTDKGGLVYAKFVIDAVNKAQRMKTTPANQOTGADKEFEVTSCTNTTFFASGK 356
    |||||||
DB 301 DENGSSTDEGEGELVYAKFVIDAVNKAQRMKTTPANQOTGADKEFEVTSCTNTTFFASGK 360
OY 357 GTTATVSKDDGQNTVMDVNVGDLANVOQNSGMNLSKRAVAGSSKVTISGVNPSK 416
    |||||||
DB 361 GTTATVSKDDGQNTVMDVNVGDLANVOQNSGMNLSKRAVAGSSKVTISGVNPSK 420
OY 417 KMDFTVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGACADAPTLVSDDEGALNNGSK 476
    |||||||
DB 421 KMDFTVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGACADAPTLVSDDEGALNNGSK 480
OY 477 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHNDVNGNARAGIAQAIATAGLVQA 536
    |||||||
DB 481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHNDVNGNARAGIAQAIATAGLVQA 540
OY 537 YLPKGSMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 594
    |||||||
DB 541 YLPKGSMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598

RESULT 6
O9JPT0 PRELIMINARY; PRT; 598 AA.
AC O9JPT0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteilin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
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DR EMBL; AF226359; AAF42508.1; -
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EB3 CRC64;

Query Match 94.8%; Score 2861; DB 2; Length 598;
Best Local Similarity 94.8%; Pred. No. 4.6e-112;
Matches 567; Conservative 5; Mismatches 22; Indels 4; Gaps 1;

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OY 1 MNKIYRIIWNALNANWVAVSELTNRNHTKRASATVATATLLEFATVOASTTDDDDLYLE 60
    |||||||
DB 1 MNKIYRIIWNALNANWVAVSELTNRNHTKRASATVATATLLEFATVOANATDDDDLYLE 60
OY 61 PVORTAVVLSFRSDKEGEGEKEVEDSNMGVYFDKKGVLTAAGTTLKAGDNLIKQNTNE 120
    |||||||
DB 61 PVORTAVVLSFRSDKEGEGEKEVEDSNMGVYFDKKGVLTAAGTTLKAGDNLIKQNTNE 120
OY 121 NTNA-----SFTYSLKRLDTLTSVGTETKLSFSAANSKNVNTSPTKGLNFAKKAETNGD 176
    |||||||
DB 121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
OY 177 TTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVADVLANAGMNIKGVKPGTTA 236
    |||||||
DB 181 PTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVADVLANAGMNIKGVKPGTTA 240
OY 237 SDNDFEVRTYDVEFLSADTKTTTVNVESSKDNKRTVEYKIGAKTSVIEKDGKLVTKGDK 296
    |||||||
DB 241 SDNDFEVRTYDVEFLSADTKTTTVNVESSKDNKRTVEYKIGAKTSVIEKDGKLVTKGDK 300
OY 297 GENDSTDKGGLVYAKFVIDAVNKAQRMKTTPANQOTGADKEFEVTSCTNTTFFASGK 356
    |||||||
DB 301 GENDSTDKGGLVYAKFVIDAVNKAQRMKTTPANQOTGADKEFEVTSCTNTTFFASGK 360
OY 357 GTTATVSKDDGQNTVMDVNVGDLANVOQNSGMNLSKRAVAGSSKVTISGVNPSK 416
    |||||||
DB 361 GTTATVSKDDGQNTVMDVNVGDLANVOQNSGMNLSKRAVAGSSKVTISGVNPSK 420
OY 417 KMDFTVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGACADAPTLVSDDEGALNNGSK 476
    |||||||
DB 421 KMDFTVNINAGNNIEITRNGKNIDATSMTPQFSSVSLGACADAPTLVSDDEGALNNGSK 480
OY 477 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHNDVNGNARAGIAQAIATAGLVQA 536
    |||||||
DB 481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHNDVNGNARAGIAQAIATAGLVQA 540
OY 537 YLPKGSMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 594
    |||||||
DB 541 YLPKGSMAIGGTYRGAGYAIGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598

RESULT 7
O9JPS0 PRELIMINARY; PRT; 598 AA.
AC O9JPS0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tetteilin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
```


RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H15;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -;
DR EMBL: AF157607; AAK68868.1; -;
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 94.6%; Score 2855; DB 2; Length 598;
Best Local Similarity 94.6%; Pred. No. 8.2e-112;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANVAASELNRNHTKRASATVATATLTLFAATVQASTDDDDLYLE 60
DB 1 MNKIRIIMNSALNANVAASELNRNHTKRASATVATATLTLFAATVQASTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKGVLTAGTTTLKAGDNLIKONTNE 120
DB 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKGVLTAGTTTLKAGDNLIKONTNE 120
QY 121 NTNENNTDSEFFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTGLNFAKETAGTNGD 180
DB 121 NTNENNTDSEFFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTGLNFAKETAGTNGD 180
QY 177 TTVHLNGISGTLDTLNTGATTNVTNDVTDDEKRAASVKOVLANGMNKGVRPGTGA 236
DB 181 PTVHLNGISGTLDTLNTGATTNVTNDVTDDEKRAASVKOVLANGMNKGVRPGTGA 240
QY 237 SDNVDVFRITDYEFLSADTKTTTVNVESSKDNCKRTEVKGATSVYKEKDKGLVYTKDK 296
DB 241 SDNVDVFRITDYEFLSADTKTTTVNVESSKDNCKRTEVKGATSVYKEKDKGLVYTKDK 300
QY 297 GENDSSTDKEGELVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTVSGTVTFASGN 356
DB 301 GENDSSTDKEGELVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTVSGTVTFASGN 360
QY 357 GTTATVSKDDQGNITVYDVNVDALNVNOLQNSGMNLSKAAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDDQGNITVYDVNVDALNVNOLQNSGMNLSKAAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 476
DB 421 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 480
QY 477 DANKPVRTNVAVGKEGDTNVAOLKGVAQNINNHIDNVGNARAGIAQAIATAGIYQA 536
DB 481 DANKPVRTNVAVGKEGDTNVAOLKGVAQNINNHIDNVGNARAGIAQAIATAGIYQA 540
QY 537 YLPKGSMAIIGGTYRGEAGYALGYSISIDGMMIITKGTASGNSRGHFGASASVGYOW 594
DB 541 YLPKGSMAIIGGTYRGEAGYALGYSISIDGMMIITKGTASGNSRGHFGASASVGYOW 598

RESULT 8
ID 0930Y5 PRELIMINARY; PRT: 598 AA.
AC 0930Y5;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-B210;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157603; AAK68864.1; -;
SQ SEQUENCE 598 AA; 62687 MW; 18CEFF6410A15DF CRC64;

Query Match 94.5%; Score 2852; DB 2; Length 598;
Best Local Similarity 94.6%; Pred. No. 1.1e-111;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANVAASELNRNHTKRASATVATATLTLFAATVQASTDDDDLYLE 60
DB 1 MNKIRIIMNSALNANVAASELNRNHTKRASATVATATLTLFAATVQASTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKGVLTAGTTTLKAGDNLIKONTNE 120
DB 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKGVLTAGTTTLKAGDNLIKONTNE 120
QY 121 NTNENNTDSEFFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTGLNFAKETAGTNGD 180
DB 121 NTNENNTDSEFFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTGLNFAKETAGTNGD 180
QY 177 TTVHLNGISGTLDTLNTGATTNVTNDVTDDEKRAASVKOVLANGMNKGVRPGTGA 236
DB 181 PTVHLNGISGTLDTLNTGATTNVTNDVTDDEKRAASVKOVLANGMNKGVRPGTGA 240
QY 237 SDNVDVFRITDYEFLSADTKTTTVNVESSKDNCKRTEVKGATSVYKEKDKGLVYTKDK 296
DB 241 SDNVDVFRITDYEFLSADTKTTTVNVESSKDNCKRTEVKGATSVYKEKDKGLVYTKDK 300
QY 297 GENDSSTDKEGELVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTVSGTVTFASGN 356
DB 301 GENDSSTDKEGELVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEVTVSGTVTFASGN 360
QY 357 GTTATVSKDDQGNITVYDVNVDALNVNOLQNSGMNLSKAAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDDQGNITVYDVNVDALNVNOLQNSGMNLSKAAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 476
DB 421 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 480
QY 477 DANKPVRTNVAVGKEGDTNVAOLKGVAQNINNHIDNVGNARAGIAQAIATAGIYQA 536
DB 481 DANKPVRTNVAVGKEGDTNVAOLKGVAQNINNHIDNVGNARAGIAQAIATAGIYQA 540
QY 537 YLPKGSMAIIGGTYRGEAGYALGYSISIDGMMIITKGTASGNSRGHFGASASVGYOW 594
DB 541 YLPKGSMAIIGGTYRGEAGYALGYSISIDGMMIITKGTASGNSRGHFGASASVGYOW 598

RESULT 9
ID 09JPS6 PRELIMINARY; PRT: 600 AA.
AC 09JPS6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-E26;
RX MEDLINE=20175756; Pubmed=10710308;
RA Pizzella M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolotti E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; "-
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 92.9%; Score 2806; DB 2; Length 600;
Best Local Similarity 92.7%; Pred. No. 9.1e-110;
Matches 557; Conservative 14; Mismatches 22; Indels 8; Gaps 2;

OY 1 MKKIRIITNSALNMAVAVSELTNRHTRKASATVATLTLFAT-----VOASTTD 53
DB 1 MKKIRIITNSALNMAVAVSELTNRHTRKASATVATLTLFATVOASADN 60
OY 54 DDLELEPVRTAVVLSFRSDEKTEGEKVEDSDNMGVFDDKGVLTAGTITLKAGDNLK 113
DB 61 EEEELPEVVRTAPVLSFSDAEDEGEKEVENTNMGITFDKNGVYKAGTITLKAGDNLK 120
OY 114 IKONTNEMTASSFTYSLKKDLTDLTSVTEKLSFSANSKNVITSDTKGLNPAKKAET 173
DB 121 IKONTNEMTASSFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNPAKKAET 180
OY 174 NGDVTNHLNGISLTDLTLNLTGATNTVNDVTDDEKRAASVMDVNLNAGNITGVKRG 233
DB 181 NGDVTNHLNGISLTDLTLNLTGATNTVNDVTDDEKRAASVMDVNLNAGNITGVKRG 240
OY 234 TTASNDVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTEVKGAKTSVYKEKDKLVYG 293
DB 241 TTASNDVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTEVKGAKTSVYKEKDKLVYG 300
OY 294 KKGENDSSTDKBGLVYAKVIDAVNKAQWPAKTTTANGOTGQADKFEVTSSTNVTF 353
DB 301 KKGENDSSTDKBGLVYAKVIDAVNKAQWPAKTTTANGOTGQADKFEVTSSTNVTF 360
OY 354 SKGKTATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGVISGNVSP 413
DB 361 SKGKTATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGVISGNVSP 420
OY 414 SKGKDETVINAGNNEITRNKNIDTATSMTPQSSVSLGAGADAPTLVDEGALNV 473
DB 421 SKGKDETVINAGNNEITRNKNIDTATSMTPQSSVSLGAGADAPTLVDEGALNV 479
OY 474 GSKDANKPRTITNVAAPVKEGDTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGL 533
DB 480 GSKDANKPRTITNVAAPVKEGDTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGL 539
OY 534 VOAYLPKGSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRHFASASVGY 593
DB 540 VOAYLPKGSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRHFASASVGY 599
OY 594 W 594
DB 600 W 600

RESULT 10
O9JPS3 PRELIMINARY; PRT; 590 AA.
AC O9JPS3:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN-NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Commanducci M., Jennings G.T., Baldi L., Batoloni E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; "-
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 92.4%; Score 2790; DB 2; Length 590;
Best Local Similarity 93.5%; Pred. No. 4.1e-109;
Matches 557; Conservative 12; Mismatches 19; Indels 8; Gaps 3;

OY 1 MKKIRIITNSALNMAVAVSELTNRHTRKASATVATLTLFATVOASTDDDDLY-L 59
DB 1 MKKIRIITNSALNMAVAVSELTNRHTRKASATVATLTLFATVOANATDEDEEDL 60
OY 60 EEPVORTAVVLSFRSDEKTEGEKE-VTEDSNMGVYFDDKGVLTAGTITLKAGDNLKONT 118
DB 61 EPVQRTAVVLIYNSRKEGTEKEKEBNSDMAVYNEKGVLTAGTITLKAGDNLKIKO-- 118
OY 119 NENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVITSDTKGLNPAKKAETNGDTT 178
DB 119 ---NGTNEFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNPAKKAETAGCTTT 174
OY 179 VHLNGISLTDLTLNLTGATNTVNDVTDDEKRAASVMDVNLNAGNITGVKRGPTTASD 238
DB 175 VHLNGISLTDLTLNLTGATNTVNDVTDDEKRAASVMDVNLNAGNITGVKRGPTTASD 234
OY 239 NVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTEVKGAKTSVYKEKDKLVYKGE 298
DB 225 NVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTEVKGAKTSVYKEKDKLVYKGE 294
OY 299 NDSSTDKBGLVYAKVIDAVNKAQWPAKTTTANGOTGQADKFEVTSSTNVTFASGKT 358
DB 295 NDSSTDKBGLVYAKVIDAVNKAQWPAKTTTANGOTGQADKFEVTSSTNVTFASGKT 354
OY 359 TATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGVISGNVSPSKGM 418
DB 365 TATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGVISGNVSPSKGM 414
OY 419 DETVINAGNNEITRNKNIDTATSMTPQSSVSLGAGADAPTLVDEGALNVGSKDA 478
DB 415 DETVINAGNNEITRNKNIDTATSMTPQSSVSLGAGADAPTLVDEGALNVGSKDA 474
OY 479 NKPVRTITNVAAPVKEGDTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGVQAYL 538
DB 475 NKPVRTITNVAAPVKEGDTVNAQLKGYAQNLNHIDVNGNARAGIAQAIATAGVQAYL 534
OY 539 PEGSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRHFASASVGYOW 594
DB 535 PEGSMAIIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRHFASASVGYOW 590

RESULT 11
O9JPR8 PRELIMINARY; PRT; 599 AA.
AC O9JPR8:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]

NCBI_TaxID=487;
[1]
SEQUENCE FROM N.A.
RC STRAIN-NGH38;
MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -
DR EMBL: AF157608; AAK68869.1; -
SQ SEQUENCE 599 AA: 62844 MW: BBA16BFB53C1970C CRC64;

Query Match 91.5%; Score 2762.5; DB 2; Length 599;
Best Local Similarity 91.7%; Pred. No. 5.9e-108;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVATVATLLFATVQASTTD-DDDLVL 59
|||||
1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVATVATLLFATVQASTTD-DDDLVL 60
60 EPVORTAVVLSFRSDKEGTEGEKEVEDSDSNWGVYFDKKGVLTAGTITLKAGDNLIKQ--- 116
|||||
61 EPVRSALVLOFMDKEGNGENESTGNGSIYDHNHNTLHGATVTLKAGDNLIKQNTN 120
DB 117 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNG 175
|||||
121 KNTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNG 180
DB 176 DTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVDVNLNAGNINIGVPGTT 235
|||||
181 DTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVDVNLNAGNINIGVPGTT 240
DB 236 ASDNVDVRYTDTVEPLSADTKTTTVNVEKDKRTEVKGAKTSVIREKDKLVTGKD 295
|||||
241 ASDNVDVRYTDTVEPLSADTKTTTVNVEKDKRTEVKGAKTSVIREKDKLVTGKD 300
DB 296 KGENSDSTOKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGADKFEYVTSCTNVTFASG 355
|||||
301 KGENSDSTOKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGADKFEYVTSCTNVTFASG 360
DB 356 KGTATVSKDDOGNITVMTDVNVGDALNVNOLONGMNLDSKVAASGSGVVISGNVSPSK 415
|||||
361 KGTATVSKDDOGNITVMTDVNVGDALNVNOLONGMNLDSKVAASGSGVVISGNVSPSK 420
DB 416 GKDEFTVNNAGNIEITRNKNIDTATSMTPQSSVSLGAGADAPTLTSDVDEGALNVGS 475
|||||
421 GKDEFTVNNAGNIEITRNKNIDTATSMTPQSSVSLGAGADAPTLTSDVDEGALNVGS 480
DB 476 KDANKPVRTITNVAQVKEGDTNVNOLKGVNQLNNHIDNVGNARAGIAQAIATAGLVQ 535
|||||
481 KDANKPVRTITNVAQVKEGDTNVNOLKGVNQLNNHIDNVGNARAGIAQAIATAGLVQ 540
DB 536 AYLPKSMMAIGGCTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
|||||
541 AYLPKSMMAIGGCTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599

RESULT 12

09JPS7
ID 09JPS7 PRELIMINARY; PRT: 591 AA.
AC 09JPS7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -
SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91E1F CRC64;

Query Match 91.4%; Score 2758.5; DB 2; Length 591;
Best Local Similarity 92.3%; Pred. No. 8.5e-108;
Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVATVATLLFATVQASTTD---DDL 57
|||||
1 MNKIYRIIINNSALNANVAVSELTRNHTKRASATVATVATLLFATVQASTTD---DDL 60
58 YLEPVORTAVVLSFRSDKEGTEGEKE--VTEDSNMNGVYFDKKGVLTAGTITLKAGDNLIKQ 116
|||||
61 YLEPVORTAVVLSFRSDKEGTEGEKE--VTEDSNMNGVYFDKKGVLTAGTITLKAGDNLIKQ 120
DB 117 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNGD 176
|||||
121 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNGD 174
DB 177 TVVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVDVNLNAGNINIGVPGTTA 236
|||||
175 TVVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVDVNLNAGNINIGVPGTTA 234
DB 237 SDNVDVRYTDTVEPLSADTKTTTVNVEKDKRTEVKGAKTSVIREKDKLVTGKD 296
|||||
235 SDNVDVRYTDTVEPLSADTKTTTVNVEKDKRTEVKGAKTSVIREKDKLVTGKD 294
DB 297 GENDSDSTOKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGADKFEYVTSCTNVTFASG 356
|||||
295 GENDSDSTOKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGADKFEYVTSCTNVTFASG 354
DB 357 GTTATVSKDDOGNITVMTDVNVGDALNVNOLONGMNLDSKVAASGSGVVISGNVSPSK 416
|||||
355 GTTATVSKDDOGNITVMTDVNVGDALNVNOLONGMNLDSKVAASGSGVVISGNVSPSK 414
DB 417 KMEFTVNNAGNIEITRNKNIDTATSMTPQSSVSLGAGADAPTLTSDVDEGALNVGS 476
|||||
415 KMEFTVNNAGNIEITRNKNIDTATSMTPQSSVSLGAGADAPTLTSDVDEGALNVGS 473
DB 477 DANKPVRTITNVAQVKEGDTNVNOLKGVNQLNNHIDNVGNARAGIAQAIATAGLVQ 536
|||||
474 DANKPVRTITNVAQVKEGDTNVNOLKGVNQLNNHIDNVGNARAGIAQAIATAGLVQ 533
DB 537 YLPKSMMAIGGCTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
|||||
534 YLPKSMMAIGGCTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

RESULT	13		
09Jr18			
ID	09Jr18	PRELIMINARY:	PRT: 591 AA.
AC	09Jr18;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
D7	01-OCT-2000 (TrEMBLrel. 15, last sequence update)		
D7	01-DEC-2001 (TrEMBLrel. 19, last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).		
GN	GNA992 OR NMB0992 OR NHHA.		
OS	Neisseria meningitidis, and		
OS	Neisseria meningitidis (serogroup B).		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxId=487, 491;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-MC58 / SEROGROUP B, BZ169, B283, AND H44/76;		
RX	MEMLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Maignan V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Barcolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.";		
RL	Science 287:1816-1820(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-MC58 / SEROGROUP B;		
RX	MEMLINE=20175755; PubMed=10710307;		
RA	Tettein H., Saunders N.J., Heldelberg J., Jeffries A.C., Nelson K.E.,		
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,		
RA	Nelson M.C., Gwyn M.L., Deboy R., Peterson J.D., Hickey E.R.,		
RA	Hatt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T.D., Clecko A., Parsey D.S., Blair E., Ciltone H., Clark E.B.,		
RA	Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,		
RA	Gill J.J., Scarlato V., Maignan V., Pizza M., Grandi G., Sun L.,		
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;		
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain		
RT	MC58.";		
RL	Science 287:1809-1815(2000).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	SPECIES=N.meningitidis; STRAIN=PMC21;		
RA	Peak I.R., Srikanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis.";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF226375; AA042524.1; -		
DR	EMBL; AE002450; AA041395.1; -		
DR	EMBL; AF226367; AA042516.1; -		
DR	EMBL; AF226370; AA042519.1; -		
DR	EMBL; AF226374; AA042523.1; -		
DR	EMBL; AF157611; AAK68872.1; -		
DR	TIGR; NMB0992; -		
DR	Complete proteome.		
SO	SEQUENCE 591 AA; 62112 MW; 7C22F3CABE7F73BC6 CRC64;		

Query Match	91.4%	Score 2758.5	DB 16	Length 591
Best Local Similarity	92.3%	Pred. No. 8.5e-108		
Matches	552	Conservative 14	Mismatches 21	Indels 11
			Gaps 4	
QY	1	MNKTIRIINNSALNAAVAVSELTIRNHTKRASATVAAVATLTLFATVQASTD---DDDL	57	
				: :
DB	1	MNKYIRIINNSALNAAVAVSELTIRNHTKRASATVAAVATLTLFATVQASANNEEDBDL	60	
QY	58	YLEPVRQTAVALVSEFRSDKGTGEGE-VTEDSMMGVYEDKKGVTTAGTITLLKAGDNLIKQ	116	
DB	61	YLPVRQTAVALVNSDKGTGEGEVEENSDMAVYENEGVTLTAETLLKAGDNLIKQ	120	

OY	117	NTNENTAASTFYSYLKKDDLDLDSVGRKEKLSFSANSKRWITSDTGLNPAKTTAEI	117
OY	117	NTNENTAASTFYSYLKKDDLDLDSVGRKEKLSFSANSKRWITSDTGLNPAKTTAEI	117
Db	121	-----NQTNIETFLYKDKDLIDLDSVGRKEKLSFSANSKRWITSDTGLNPAKTTAEI	174
OY	177	TTVHLNGIGSLPTPLTLNTGATTVNTDNTVDDEKKRAAASVKKVVLNAGWIKGVKPGTTA	236
Db	175	TTVHLNGIGSLPTPLTLNTGATTVNTDNTVDDEKKRAAASVKKVVLNAGWIKGVKPGTTA	234
OY	237	SDNWDEFTVDTVEFLSADRTKTTTVNVEKSDNGKRETEVKGAKTSVKEKDKLVYGGDK	296
Db	235	SDNWDEFTVDTVEFLSADRTKTTTVNVEKSDNGKRETEVKGAKTSVKEKDKLVYGGDK	294
OY	297	GENDSSTPKGGGLYTAKEEYDAVNAKAGRMKTTTANQOTQOAPKEFTVSGTNTVTFASGK	356
Db	295	GENDSSTDEGEGGLYTAKEEYDAVNAKAGRMKTTTANQOTQOAPKEFTVSGTNTVTFASGK	354
OY	357	GTTATVSKDDGCGNTVWADVWAGALVYNOLONGSMNLDKAAVSSGKVIISGVNPSKG	416
Db	355	GTTATVSKDDGCGNTVWADVWAGALVYNOLONGSMNLDKAAVSSGKVIISGVNPSKG	414
OY	417	KMDETIVNINAGNNIEITPENGKNIDIATSMTPQFSSVSLGAGADAPTLVDEGALVYSGK	476
Db	415	KMDETIVNINAGNNIEITPENGKNIDIATSMTPQFSSVSLGAGADAPTLVSDGD-ALNVGSK	473
OY	477	DANKEVRTTNVAPGVKEGSDVTNVAQLKGVAONLNHNIDVNDGNARACIAIATAGLYOA	536
Db	474	KDNKEVRTTNVAPGVKEGSDVTNVAQLKGVAONLNHNIDVNDGNARACIAIATAGLYOA	533
OY	537	YLPGRSMAAIGGGYTRGEGAGTAIGSSISDGGNNITIGTASGNSRGHFGASASVGYOM	594
Db	534	YLPGRSMAAIGGGYTRGEGAGTAIGSSISDGGNNITIGTASGNSRGHFGASASVGYOM	591
RESULT 14			
O9AOF0 PRELIMINARY: PRT: 592 AA.			
AC	O9AOF0		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxId=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=MC58;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;		
RT	"Identification and characterisation of a gene encoding a novel outer-		
RL	membrane protein of Neisseria meningitidis.";		
SR	Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.		
SR	EMBL: AF125375; AAK09243.1; -		
SQ	SEQUENCE 592 AA: 62220 MW: 168966947381EFC5 CRC64:		

Query Match	91.1%	Score	2751	DB 2:	length	592;
Best Local Similarity	92.0%	Pred. No.	1.7e-107;			
Matches	551;	Conservative	13;	Mismatches	23;	Indels
						Gaps

QY	1	MNKRYRIINNSALNMAWVAVSELT	RNHTRKASATVATATLTLFATVQASTDD	---D	56
DB	1	MNKRYRIINNSALNMAWVAVSELT	RNHTRKASATVATATLTLFATVQASANNERRKRD		60
QY	57	LYLEPVQRTAVVLSPFSDEKGE	GEK-VIEDSWMGYEPFKKGYLTAGTITL	LAGDMLKTR	115
DB	61	LYLDPQQRIVAVVLIVNSDEK	GEKGEKVEENSMWAYFENEKGYLTARETTL	LAGDMLKTR	120
QY	116	QNTNEVNTNASFYLSLKQD	LTDLTSTGTEKLSPSANSNNVNTSDPKGLNFAKKTAE	TNG	175
DB	121	Q-----NCNTNPFYLSLKQD	LTDLTSTGTEKLSPSANSNNVNTSDPKGLNFAKKTAE	TNG	174

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QY 176 DTFVHLNGIGSLTDLTLNTGATNTVNDVDEDEKKRAASVADVLNAGNIGVPGTT 235
DB 175 DTFVHLNGIGSLTDLTLNTGATNTVNDVDEDEKKRAASVADVLNAGNIGVPGTT 234
QY 236 ASDNVDFVRYTDFEFLSADFTKTTTVNVEKSKNGKRTVEVIGAKTSVIREKDKLVTGKD 295
DB 235 ASDNVDFVRYTDFEFLSADFTKTTTVNVEKSKNGKRTVEVIGAKTSVIREKDKLVTGKD 294
QY 296 KGBNDSTDKGEGLYTAKKEVIDAVNKAQWRMTTANGOTGQADKFEYTSNGNTVFASG 355
DB 295 KGBNDSTDKGEGLYTAKKEVIDAVNKAQWRMTTANGOTGQADKFEYTSNGNTVFASG 354
QY 356 KGTATVSKDDOGNITVMTDVNVDALNVNOLNSGNNLSKAVAGSSGKVISGNVSPSK 415
DB 355 KGTATVSKDDOGNITVMTDVNVDALNVNOLNSGNNLSKAVAGSSGKVISGNVSPSK 414
QY 416 KGMDETVINAGNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 475
DB 415 KGMDETVINAGNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 473
QY 476 KQANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 535
DB 474 KQANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 533
QY 536 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 534 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 15
ID 0930Y3 PRELIMINARY: PRT: 591 AA.
AC 0930Y3:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RL membrane protein of Neisseria meningitidis.
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
SQ SEQUENCE 591 AA: 62048 MW: CDDC600798859C65 CRC64;

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Query Match          90.7%; Score 2739.5; DB 2; Length 591;
Best Local Similarity 91.8%; Pred. No. 5.3e-107;
Matches 549; Conserved 15; Mismatches 23; Indels 11; Gaps 4;

```

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QY 1 MKKIYIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFATVQASTD---DDDL 57
DB 1 MNEILRIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFATVQASANNEQEDDL 60
QY 58 YLEPVORTVAVLSFRSDKGTGEGKE-VTEDSNMGVYFEDKKGVLTACTITLKKAGDNLKIKO 116
DB 61 YLDPVLTAVAVLIVNSDKGTGEGKEVEKSDVAVYFNEKGVLTAREITLKKAGDNLKIKO 120
QY 117 NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVITSDTKGLNFAKTAFTNGD 176
DB 121 -----NGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKTAFTNGD 174
QY 177 TTVHLNGIGSLTDLTLNTGATNTVNDVDEDEKKRAASVADVLNAGNIGVPGTTA 236
DB 175 TTVHLNGIGSLTDLTLNTGATNTVNDVDEDEKKRAASVADVLNAGNIGVPGTTA 234
QY 237 SDNVDFVRYTDFEFLSADFTKTTTVNVEKSKNGKRTVEVIGAKTSVIREKDKLVTGKDK 296

```

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DB 235 SDNVDFVRYTDFEFLSADFTKTTTVNVEKSKNGKRTVEVIGAKTSVIREKDKLVTGKDK 294
QY 297 GENDSSTDKEGLVYAKKEVIDAVNKAQWRMTTANGOTGQADKFEYTSNGNTVFASG 356
DB 295 GENDSSTDKEGLVYAKKEVIDAVNKAQWRMTTANGOTGQADKFEYTSNGNTVFASG 354
QY 357 GTTATVSKDDOGNITVMTDVNVDALNVNOLNSGNNLSKAVAGSSGKVISGNVSPSK 416
DB 355 GTTATVSKDDOGNITVMTDVNVDALNVNOLNSGNNLSKAVAGSSGKVISGNVSPSK 414
QY 417 KMDETVINAGNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 476
DB 415 KMDETVINAGNIEITRNKNIDITATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 473
QY 477 DANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 536
DB 474 DANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 533
QY 537 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 534 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

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Search completed: July 3, 2002, 08:28:43
Job time: 1164 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:18 ; Search time 95.27 Seconds
(without alignments)
596.083 Million cell updates/sec

Title: US-09-771-382-5
Perfect score: 2999
Sequence: 1 MNEILRIIWSALNAWVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2984	99.5	591	2	G81133	adhesin NMB0992 [i
2	2445.5	81.5	592	2	A81888	probable surface f
3	600	20.0	298	2	I64138	adhesin homolog Hi
4	393	13.1	2059	2	D82671	surface protein XF
5	375	12.5	1107	2	AC0976	probable autotrans
6	372.5	12.4	1190	2	A82615	surface protein XF
7	368	12.3	1588	2	A86036	probable adhesin Z
8	368	12.3	1588	2	H91188	probable adhesin E
9	332.5	11.1	658	2	A01010	probable surface p
10	239.5	8.0	1004	2	C82672	surface-exposed ou
11	230.5	7.7	1536	2	A43855	high-molecular-we
12	228.5	7.6	1091	2	G64964	hypothetical prote
13	225	7.5	1477	2	B43855	high-molecular-we
14	219	7.3	1910	2	AF0394	probable adhesin h
15	216.5	7.2	2020	2	C48399	ABC-type transport
16	213.5	7.1	5291	2	F90696	hypothetical prote
17	212.5	7.1	4152	2	T31102	filamentous hemagg
18	212	7.1	1635	2	A10452	hemolysin [importe
19	211.5	7.1	4919	2	T31105	hypothetical prote
20	209	7.0	949	2	D90803	Aida-I adhesin-lik
21	209	7.0	1005	2	H85611	probable adhesin Z
22	209	7.0	2273	2	T09083	hemagglutinin/hemo
23	208.5	7.0	936	2	I40711	sapB protein - Cam
24	207.5	6.9	1109	2	A56143	surface-array prot
25	207.5	6.9	1577	2	A35140	hemolysin A precu
26	207	6.9	5188	2	B85547	probable RTX faml
27	203.5	6.8	1286	2	S28634	adhesin AIDA-I pre
28	202.5	6.8	1018	2	H83135	probable adhesin P
29	199	6.6	1325	2	A64905	ydek protein - Esc

30 199 6.6 1461 2 E90696 hypothetical prote
31 197 6.6 585 2 F90961 flagellin [importe
32 197 6.6 585 2 F85809 hypothetical prote
33 196.5 6.6 1487 2 AG2560 hypothetical prote
34 196.5 6.6 3013 2 AB0480 probable invasiv Y
35 196 6.5 3705 2 AD0123 probable autotrans
36 195 6.5 1461 2 A85547 hypothetical prote
37 194.5 6.5 1428 2 AC2224 hypothetical prote
38 193.5 6.5 4936 2 AH2515 hypothetical prote
39 192.5 6.4 3029 2 S76109 hypothetical prote
40 191.5 6.4 1343 2 D85724 hypothetical prote
41 191.5 6.4 1608 2 A28182 hemolysin A - Serr
42 191 6.4 2249 2 A41477 190K surface anti
43 190.5 6.4 1035 2 AD3203 autotransporter pr
44 190 6.3 1651 2 JC1340 outer membrane pro
45 189.5 6.3 1430 2 AF0351 probable autotrans

RESULT 1
G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlatti, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match 99.5%; Score 2984; DB 2; Length 591;
Best Local Similarity 99.5%; Pred. No. 3.9e-143;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNAWVVSSELTNRNHTKRASATVKAVLATLTLFATVQASANNEEQEDL 60
||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MNKIYRIIWSALNAWVVSSELTNRNHTKRASATVKAVLATLTLFATVQASANNEEQEDL 60
||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 YLDPVLRVTAVLVNSDKEGTGEKVEKVEENSDWAVFNEKGVLTAREITLKGADNLKIKQ 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 YLDPVQRTAVLVNSDKEGTGEKVEKVEENSDWAVFNEKGVLTAREITLKGADNLKIKQ 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 NGNFYTSLKKDLTDLTSGVTEKLSFANGKNYITSDTKGLNFAKETAGTGGTTFVHLN 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 NGNFYTSLKKDLTDLTSGVTEKLSFANGKNYITSDTKGLNFAKETAGTGGTTFVHLN 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 GIGSTLTDLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 GIGSTLTDLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 240
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 VRTYDVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDKGLVTGKDKGENGSS 300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 VRTYDVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDKGLVTGKDKGENGSS 300
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 301 TDEGEGLVTAKEVIDAVNKAGWEMKTTTANGOTGQADKFETVTSNTVTFASGKGTTATV 360
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 301 TDEGEGLVTAKEVIDAVNKAGWEMKTTTANGOTGQADKFETVTSNTVTFASGKGTTATV 360
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 361 SKDDQGNITVMYDVNVGDALNVNQLNSGWNLDSKAVAGSSGKVISGNSPKGMDETV 420

ALIGNMENTS

A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <STM>
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAP84338.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; B
Briñones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Cartaro, D.M.; Carrer, F
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.C. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1529

Query Match 13.1%; Score 393; DB 2; Length 2059;
Best Local Similarity 24.3%; Pred. No. 5.9e-12;
Matches 173; Conservative 93; Mismatches 216; Indels 230; Gaps 31;
QY 72 LIVNSDKECTGKEKVEENSDWAVFNE-KGVLTAARE-----ITLKAGDNLKIKONGT--- 123
DB 1386 VVINGGKISGVTAGTEETD---AVAFSQLKSISTADVGDTLTATGANGSKVAGSGTVDL 1443
QY 124 -----NFTYSLKDLTDL-----TSVGTCKLFSAN-----GNKVNTIS 157
DB 1444 KWTDCNLRISKSGSDNDVFNLSDELKESITVGTQDLKDKGVKSSNVLLDSNELVITS 1503
QY 158 DT-----KGLNFAKETA-----GTNGDTFVHLNGI-----GSTLDTLLNTGA--T 196
DB 1504 HSSTSVKTLANGSVNRTVNGDGVNIDVVVYNDLGLSVGGASLTSLGINAGSHKI 1563
QY 197 TNVT-----NDNVTDEKRAASVDVNLNAGNI-----KGVPKGTASDNVD----- 239
DB 1564 TNVTAGTEDTDVAFNSQLK---SVSEAVDKGWTLTATGANGSKVYSGGTVDLKNTDGNLA 1620
QY 240 ---FVRTDVTVEFLSADTK-----TTTVNVESKDNKGKTEVKIGAKTSVLEKDKGLV 289
DB 1621 ISKSGSDNDVFNLSKDFKVDVTAGNTVVNTDGVKVG---SDVSLGMLFTIANGPSVTA 1678
QY 290 TGKDRKEN-----GSSTDEGEGLVTAKEVIDAYNKAGWRMKTIT-----ANGQ 332
DB 1679 SGFNAGDKVISHVAVGMADTDVAVNSQLKQAVQSVTVKATRYISTNDGGTGGNVDGGA 1738
QY 333 TCGQ---ADKFEVITSGTNV-----TFASGKGTTA----- 358
DB 1739 TGSKAIAAGVGTQASGEAAAAGVSGAAASGKSTAGRNATIASADGSVALGDCAKDGGRG 1798
QY 359 -----TVS-----KDOGNITVVDVNVG--DALNVNOL-----QNSGWN 391
DB 1799 AESYTGKSGVQNNVTGTVSGDAAKGETRSISNVADAKEAMDVNLKOLDVAQAKSNLQ 1858
QY 392 LDS-----KAVAGSGKVISGNVSPSKGMDVTNIN 423
DB 1859 TDDMRHEINNIEDVFKITGDSASSVKGGVNAMAIGTNAAVSGTESVALGK---NTNVS 1915
QY 424 AGNNIEITRNKNIDIASTMTPOFSSVSLGAGADAPTLTSDGDALNVGSKDNKPKVRITN 483
DB 1916 ADNVAI--GNG-----SVADRANSVSVSGG-----GSER-----QVTN 1947
QY 484 VAPVKGEGDVTNVAOLKGAQNLRNINRVNCGNAR-----AGTAAIATAGLVQAYLPCKS 539
DB 1948 VAAGTADTDVAVNSQNLNGLITAKQYTDGMVGNLRRETSGGVAAAIATANLPQAYVQGRG 2007
QY 540 MMAIGGGTYRGEAGYAGYSSISDGGNWLIIKGTASGNSRGHFGASASVGYQW 591

DB 2008 MTSVGVSSYQGSATAVGVSAVSESCHWVFKFSGSANTRSHVGVGAGVGYQW 2059
RESULT 5
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:gl6504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB
Query Match 12.5%; Score 375; DB 2; Length 1107;
Best Local Similarity 21.1%; Pred. No. 2.1e-11;
Matches 176; Conservative 106; Mismatches 238; Indels 314; Gaps 31;
QY 9 WNSALNAWVWVSELTRNRHTKRASATVKATLAVLATLLFATVQASANNBEEQEDLYLDPVLT 68
DB 337 WNETNSF-----SASHGSSF-----TNKTNVAAGELSEESTDAVNGSOLFET 380
QY 69 VAVLIVNSDKETGKEKVEENSDWAVFNEKGVLTAREITLKAGDNLKIKONGT---NF 125
DB 381 -----NEKVDQNT-----TDIAANTTITONSTAIENL 408
QY 126 TYSLAKDLTDLTSVGTCKL-----SFSAN--GNKVNTISDTKGLNFAKETAING--- 173
DB 409 NTSVDINTSITGLTDNALLMDEDTGAFSANHGSGTSKITNVAAGALSSEDSDAVNGSOL 468
QY 174 -DTTVHLNIGISLTDLTLNLTGATTNVTNDVNTDDEKRAASVKDVLNAGNIKGVKPGT 232
DB 469 YETNKVKDONTSAIAD--INT-SITNLGTDALSWDDEGAFSASHCTSGTNKITNVAAGE 525
QY 233 TASDNVDFV---RTYDT-----VEFLSADTKTITVN-----VESKONGKTE 271
DB 526 IASDSTDAINGSOLVETNMLISQYNESISQLAGDTSYITENGTVGVKVIKRTNDNGLEQ 585
QY 272 VKIGAKTSVKEKDKGLVTGDKK-----GENGSSTDEG----- 304
DB 586 -----DAYATNGATAVGYDAVASGAGCALGALGNSSSSIEGSLAGSGTSNRAITTG 638
QY 305 -----EGLV-----TAKEVIDAVNKA---GNRMKTTTANGOTGQ----- 335
DB 639 IRETATSQVVGIVGNTDRELLGALSGLTGDGSTRQITNVADGSEAQAQAVTVRQLQNAI 698
QY 336 -----ADKFETVTSQNTVTFASGKGTTA---TVSKDDQG-----NITVMYDVNVGDAL 380
DB 699 GAVTTPTPKYHANSTEEDSLAVGTDLSLAMGAKTIVNADAGIGLNTLVMDAINGIAI 758
QY 381 NVN-----QLNSGNWLDK-----AVAGSGKVISGNVSPS 412
DB 759 GSNARANHANSIANGMSQTTTGAQTDYATAYNMDTPQNSVGEFSVSGEDGQRQITNVAAG 818
QY 413 KCKMDETIVNAG---NNIEITRNCKNI-----DIATSMTPQ 446
DB 819 SADTDA---VNVGQLKVTDAQVSRNTFQSTNLNTQVSNLDTRVTNIENGIGDIVITGSKT 875
QY 447 F-----SSVSLGAGADAP-----TSLVDGDALNVGSKDNKPKVRI 481

Db 1154 YROIIN-----VADGSEAHDAVT--VROLNAIGAIVATPTTKYFHANSTEEDSLAVGTD 1205
QY 271 EVKIGAKTSVIREK-----DGKLVTKGDKGE-----NGSSTDGEGL 307
Db 1206 SLAMGAKTIVNGDKGIGIGYGAYVDANALNGAIGSNAQVIHVNSTAINGSTTTTGAOT 1265
QY 308 VTAKEVIDAVNAGWRMKTITANGQ-----TGQADKEFTVTSCTNVTFSAGKGTATV 360
Db 1266 NVTAYNMDAPQNSVGEFSVGSADGQROIITNVAAGSAD-----TDAVNV--GOLKVTDAQV 1318
QY 361 SKDDQGNITVM-----YDVNVGDAL-----NVNQLNSGNWLDKAV 397
Db 1319 SONTQ--SITNLDNRVNTLDSRVNTNIENGICDIVTTGSTKYFKTNTDGVDSAAQKDSVAI 1377
QY 398 AGSSGKVISGNSPSKGM---DETVINAGNIEITRN---GKN-----IDIATSTMTPOF 447
Db 1378 GSGSIAAANDNSVALGTGVSATEENTISVGSSTNQRRITNVAAGKNATDAVNVAAQLKSSA 1437
QY 448 SSVSLGAGADAPTLSVDGDALNVGSKDNKPVRIITNVAPVKEGDVTNVAQLKGVAQ---- 504
Db 1438 GGVRYDTKADG---SIDYSNITLGG--GNGGTRISNVSGAVNNNDVNVYAAQLKQSVQETK 1493
QY 505 -----NLNNRIDVNDGNARAGIAQAATATAGLVQAYLPGKSMMAIGGTYRGEAGYAI 556
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIGGTYNGESAVAL 1553
QY 557 GYSSISDGGNWIITKTASGNSRGHFCASASVGYQW 591
Db 1554 GYSWVSANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 8
H91188
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R1MD)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-references: GB:BA000007; PIDN:BAB37903.1; PID:gl3363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs4480

Query Match 12.3%; Score 368; DB 2; Length 1588;
Best Local Similarity 23.3%; Pred. No. 7.6e-11;
Matches 162; Conservative 99; Mismatches 280; Indels 154; Gaps 25;
QY 31 SATVKTAVLATLLFATVQASANNEQEDLYLDPVLTVAVLVNSDKECTGEK-EKVVEE 89
Db 914 SAASDAINGSOLYTTNKYIDALGDAEVNADGTTAPTATYTIANAENYVNGDALDADD 973
QY 90 N-----SDWAVYFNEKGVLTAREITLKAGDNLK-----IKONGTNTFTYSLKKD 132
Db 974 NALLWDETANGAGAYNASHDKGASITVWANGSISEDSTDAVNGSQLNATNMIBQNTQ 1033
QY 133 LDTLSVGTKEKLSFANGKNV-ITSDTKGLNFAKETAGTNGDITVHLNGI----- 182
Db 1034 IINQLAGNTDATVIOENGAGINVRNTDDGLAFNDASAQGVGATAIGYNSVAKGDDSSVAI 1093
QY 183 -----GSTLTDLNLTGA--TTWNTDNV-----TDDEKKRAASVKD--- 217
Db 1094 GOGSYSDVTGIALGSSSVSRVIAKGRSDTSITENGVIYGYDTTDDGELLGALSIGDDGK 1153
QY 218 ---VLNAGNIGVKPGTASDNVDVFRVYDVFELSDTKITTVNVESKDNGK----KT 270

RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 11.1%; Score 332.5; DB 2; Length 658;
Best Local Similarity 24.3%; Pred. No. 1.5e-09;
Matches 155; Conservative 86; Mismatches 241; Indels 155; Gaps 29;
QY 27 TTRASTVVT-----AVLATLLFATVQAS-----ANNEQEDLYLDPVLTVAV----LIV 74
Db 105 TNLAPATISSTSDAVVGSQVLYLVQDGTTRYFHANSVNPNTDSLASC--LETTAVGPAVTV 162
QY 75 NSDK-EGTGEKEKV---EENSWMVYFNEK-----GVLTAR 106
Db 163 SGDNVGVGIGNTALVGAATGGTAIGFGTQVTAAGATAIGSAAQQAQALGAGAVTSQ 222
QY 107 EITLKAQDNKLKIQKQNTFTYSLKDLTDLTSVGTKEKLSFANGKNVNTISDTKGLNFAK 166
Db 223 ANSIALG--AASINTVCAQSSYSAYALTAQASVGEIGIG-TALGNR-KITGVAAG----- 274
QY 167 ETAGTNGDITVHLNGTSGTSLTDLTLLNTGATNTVN--DNVTDDEKKRAASVKDVLNAGWN 224
Db 275 -SASSDAVNVAAQLTAVGQDVQOQN-----TANITSLGRVTTIE---GSMASIANGG-G 322

QY 225 IKGVKPGTTASNDVFRVYDVEFLSADTKTTTVNVESKDNCKKT-----EVKIGAKT 278
Db 323 KYFHFANSTQPDV-----ASGTNSVAIGPASLASGNAALASGAGAIVG--D 368
QY 279 SVIKEKDGKLVTKDKGKENGSSDEGEGLVTAKEVIDAVNKAQWKMKTITTTANGQTQADK 338
Db 369 GAAASADGSAICGGSDNGRGVENIG-----KYSNASNTSSG----- 407
QY 339 FETVTSCTNVTAFASGRGTTATVSKDQGNITVMYDNGDALNVNQLNSGWNLDKSKAVA 398
Db 408 --TVSGNTAT-----GETRTVSNVADG-----LQATDAVNRLQD-----I 443
QY 399 GSSGKVIQNSVSPSKMDTVNINAGNIT--ETRNGKNIDI--ATSMTPQFSSVSLGAG 455
Db 444 AASIVVYNNVSLQNGTDCGMFQVNNSSGLAKPSATGASATGAGSVASGNNSTAFGSG 503
QY 456 ADAP-----TSLVSDGALNVGSKDNKPVRTNVPAGVKGEDVTNVAOLKGAQN 505
Db 504 AKATAANSALGANSADRANSVSGVGNR--QITNVPATQGTDAVNFDQLKSISNQ 561
QY 506 ----LNNRIDNVGNAR-----AGTAAIATAGLVQVLYLPGKSMMAIGGTYRGEAGY 554
Db 562 TNAYTNORYSELKQDLKQNSVLSAGTASAMSLTOPYTSGSSMTTIGAASRYGOSAL 621
QY 555 AIGYSSISDGGNIIKGTASGNSRGHFGASASVGYOW 591
Db 622 SLGVSSISDSGRVYSLQASSNTQDGFVGIGVGYOW 658

RESULT 10

C82672
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: G82672
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below

A:Accession: C82672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1004 <SIM>
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mencia, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, M.A.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1516

Query Match 8.0%; Score 239.5; DB 2; Length 1004;
Best Local Similarity 22.3%; Pred. No. 0.00012;
Matches 161; Conservative 97; Mismatches 277; Indels 193; Gaps 34;

QY 2 NEILRIIWNALNAWVYVSELTRNH-----TKRASATVKTAVLATLLFATVQASANNE 55
Db 4 NOIYKFWNLSLGSVASHMTNDGGSDVVLRHSGVNRSLVLAIGLALTSVTHQSVK 63
QY 56 QEDLDYLDPLVLTVA-VLIIVNSDKE-----GTGEKEKVEENSDWAV----- 95

Db 64 -----SPAWTASQVMVAHVDSQVNRADRIPTDGGSELMTMHWKFFPFGHNST 116
QY 96 --YFNEKGVLTAREITLKAGDNLKIKQNGTNYFTYSLKDLTDLTSVGTKEKLSANGKV 153
Db 117 IGYFSKAFAPNA-----IALGYNSSVTQSANN-CVALGSNST-VSGYNSVALGAGSMASEL 170
QY 154 NTSDDTKGLNFAKETAGTNGDDTTVHLNGIGSLTDLTLLTGATTNTVNDVTDEKRAA 213
Db 171 NVISVGGG-----DGVTPAVRRIRVNVG-----DGIGNDAVKNSQLDGVVTASVNDVAA 219
QY 214 SVKDLV-----NAGWNIKGVKPGCTTA--SDNVDFVRTYDVEF----- 249
Db 220 SVKTIALTNOVTGSSVASAGKKESTAIGSAQAVDN-----TVAFGGRAIANAVGA 271
QY 250 --LSADT-----KTTTVNVESKDNKTKTEYKIGAKTSV-----IKEKDGKLVTKGD 293
Db 272 SALGFDSHAKINSTVTGTSVSLG--QGGVSLGYNFVGBGSLGALGSLVLLQGV 330
QY 294 KGENG-----STDEGEGE--VTAKEVI-----DAVNKAQWKMKTITTTANGQ 332
Db 331 SVALGSGSMASEPNVSVSGDGLRGPVRRIRVNVGDGIGNNDVANKSOLDGVVTASVNDV 390
QY 333 TGOADKEFV--TSGTNVTFASCKGTAT--VSKDDOGNITVMYDNGDALNVNQLNSG 399
Db 391 VASVKNIACAIQITGSGVASVSGDSTAGASAAQAGDSIA-----LGARSRAAIGSSA 446
QY 390 WNLD-----SKAVAGSGKVISGNVSPSKGMDVTNINAGNNTIEITRNGKNIDIAT 442
Db 447 LGVDGHALGANSTALGQSTAISEGGTSLG---YNFVSGSATNGALGSN-----A 495
QY 443 MTPQFSSVSLGAGADAPTLVSV-----DGDALNVGSKDNKPVRTNVPAGVKGEDVTNVAQ 498
Db 496 IVSGVNSVALGAGSVASELNVISVGGDGVTPAVR-----RIVNVGDGIGNNDVANKSQ 550
QY 499 LKQVAQNLNN---RIDNVGNAR---AGTAAI---ATAGLVQVLYLPGKSMMAIG----- 544
Db 551 LDGVTASVNDVAASVKKIVGTITGSGVASAIGKSTATGASQAQVGDSSVALGTRATA 610
QY 545 -----GGTYRGEAGYAGYSSISDGGNIIK-----GTASGNSRGHFG 582
Db 611 NATGSSVLGVDSRARGINSTALGRQSNALGSGVSLGFLNSFVRQSGEHGVALGTDAVSG 670
QY 583 A-SASVGY 589
Db 671 KDSIALGY 678

RESULT 11

A43855
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae
C:Species: Haemophilus influenzae
C:Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: A43855
R:Barenkamp, S.J.; Leininger, E.
Infect. Immun. 60, 1302-1313, 1992
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable
detella pertussis.
A:Reference number: A43855; MUID:92192797
A:Accession: A43855
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1536 <BAR>
A:Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:89235, NCBI:89239)

Query Match 7.7%; Score 230.5; DB 2; Length 1536;
Best Local Similarity 22.3%; Pred. No. 0.00061;
Matches 133; Conservative 86; Mismatches 228; Indels 149; Gaps 26;
QY 40 ATLLFATVQASANNEEEDLDPLVLTVAVLIVNSDKEGTGEKEVEENSDWAVFNE 99

```

Db      778  SSURFTSGSTKGSIEKDLFLNATGGNITLLQV-----EGTOMI---G 820
Qy      100  KGVLTAREITKAGDNLIKQNGTFTYSLKKDLTDLTFSVTEKLSFSAANGKNVITS- 158
Db      821  KGIVAKKNITFEFG-----NITFSRKAVTEIEG---NVTINNANVTIGSDF 866
Qy      159  ---TKGLNFAKE-----TAGTN-----GDTVHLNGIGSTLTDLLLNTGAT-TNVTN 201
Db      867  DNHQKPLTIKKDVIINSGMLTAGGINVIAGNLTAVESNANFKATNTFNVNGLFDNKG 926
Qy      202  DNYTDDKKRAASAKVDLWAGNNIKGVKPGGTASDNVDFVRYDTVEFLSADTKTTTVN 261
Db      927  SNIS--IAKGGARFXDIDS---KNLSITNSSS-----TYRTISGNITNKGDLNI 974
Qy      262  ESKDNCKTEVKIGAKTSVKEKKDLVTGDK-----GENGSTDEGEGLVTA 310
Db      975  TNE--GSDTFEMQIGGDVS---OKEGNLTISDDKINITKQITIKAGVDGENSDS- 1022
Qy      311  KEVIDAVNKAQWRMKTTTANGQTQGADEFVTSCTNVTFAAGKGTATVSKDDOGNITV 370
Db      1023  ----DATNANLTIKT-----KELKITDOLNI---SGENKAEITAKD--GSDLT 1062
Qy      371  MYDVNVGDALNV-----NOLQNGWNLDKSAVAGSSGKVISGNSPKGKMDFTVINAG 425
Db      1063  IGNTNSADGNTAKKVTFNQVKDSKISADGHKVTLHKSIVETSGSNNTDSSD----- 1114
Qy      426  NNTETRNCKNDIATSWTPQPSVSYSLGAGADAPTLSDVDGDLNVGSKDNKVPRTNVA 485
Db      1115  NNAGLTIDAKNTVNNNIIP-SHKAVSISATSGEITTKT-GTTINATTGNVEITAGTGSIL 1172
Qy      486  PGVK--EGDVTNVAQLKGVAQNLNRIDNVGNRAGIAQAIATAGLVQAVLPCKSMMAI 543
Db      1173  GGISSGSGVTLTATGALA-----VSNISGNTVTVTANGSALTTLAGSTIKGTESVTT 1226
Qy      544  G-----GGTYRGEAGYAIGYSSISDGGNWIK-----GTASGNS 577
Db      1227  SSQSGDIGGTISGGTVFVKATESLTQTSNSIKATTGEANVTSATGTIGGTISGNT 1282

RESULT 12
G64964
hypothetical protein b2000 - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
R:Accession: G64964
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
A:Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64964
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1091 <BLAT>
A:Cross-references: GB:AE000291; GB:U00096; NID:q1788298; PIDN:AC75061.1;
A:Experimental source: strain K-12, substrain MG1655
C:Keywords: nucleotide binding; P-loop
F:683-690/Region: nucleotide-binding motif A (P-loop)

```

```

Query Match          7.6%; Score 228.5; DB 2; Length 1091;
Best Local Similarity 23.6%; Pred. No. 0.0005;
Matches 147; Conservative 69; Mismatches 203; Indels 203; Gaps 36;

Qy 1 MNEILRIWNSALNAAVVVSELTNRHTRKASATYKTTAVLATLLFATVOASANNEEQEEDL 60
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 57 LNTCYRLVWNHMTGAFVYVASELARARGKRGVAVALSAAVTSLPVLAA-----DI 107

Qy 61 YLDPVLRTVAVLIVNSDKEGTGEKEKVEENSDDWAVYNEKGVLTAREITLKAGNLKLI-- 118
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 108 VWHP-----GE-----TVNGGTLANHDNQVTFG 130

```

Qy	119	KQNCTNTFTYSLKDDLLDLSVSGTEKLFSFANGKNVITSDTGLNPAKETAGTGDTTVH	178
		: :	:
Db	131	TTNMTISTLGEPDNEANTGQQWQGDTANKTTVTSG--GLQ-RVNPGGSVDSTVIS	187
		: :	:
Qy	179	LNGIGSFL---TDTLINTC-----ATTNVINDVNTDDEKKRAASVKDLNAGNNI	225
		: : :	:
Db	188	AGG-GQSLOGRAVVNTLNGGEQMHEGAATGTVINDK-----GMQV	228
		:	:
Qy	226	KGVPKPQTASNDVFRT-----YDTVEFLSADTKTTTTNVNESKDNGKKTETVIG	275
		: :	:
Db	229	--VKPGETVATDV-VNTGAEGGPDAENGDTGGQVRGDVAVRTIN----KNGRQIVRABG	280
		: :	:
Qy	276	-AKTSVTKEKDGKLVTCGRKKGNGSSUDE-----GEGLV-----TAKEVIDAVNKAGRWM-	324
		: :	:
Db	281	TANITTY-----YAGGDQTHGHALDITPLNGGYOVHHGGTASTDV--VNSDGMQIQIK	331
		: :	:
Qy	325	-----KTTTAGOTGOADKFETVTSCTNYTFASG-----KGTATVSCKDOG-NIIVMVDV	374
		: :	:
Db	332	NGGVAGNTTYN-QKGRU-QVDAGGTATNVTLKGGALVTSTAATV-----GINRLGAFSV	385
		: :	:
Qy	375	NVGDALVNQLONGSWNLDSKAVAGSSGKVISGNVSPSKCMDETNIINAGNNIEITRG	434
		: :	:
Db	386	VEGKADNV-YLENGG-RLD-----VLTCHTATN-----TRVDGGGTLDV-RNG	425
		: :	:
Qy	435	KNIDIATSMPQPQSFSSVSLGAGADAPTLSVDGDALNYGSKDNPKPVRIITNPAPGVKEGDVT	494
		: :	:
Db	426	-----GTATT-----VSMGNGG---VILLADSGAAVSSTRSDGK-----AFIGGGQAD	465
		: :	:
Qy	495	NVAOLKVAONLNRRIDNVGNRNARAGIAQAIAITAGLVQAYLPKKSMMATGGGTGYRGEAGY	554
		: : :	:
Db	466	ALMLEKGSSEFLN-----AGDATDdT-----VNGGLETFARGET	499
		: :	:
Qy	555	AIGYSISSDGGNWLIKIKTASN	576
		: :	:
Db	500	LAGPTTLNNGAILTSLGKTVNN	521
		: :	:
RESULT 13			
B43855			
high-molecular-weight surface-exposed protein - Haemophilus influenzae			
C:	Species: Haemophilus influenzae		
C:	Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1999		
C:	Accession: B43855		
R:	Barenkamp, S.J.; Leininger, E.		
I:	Infect. Immun. 60, 1302-1313, 1992		
A:	Title: Cloning, expression, and DNA sequence analysis of genes encoding detella pertussis.		
A:	Reference number: A43855; PMID:92192797		
A:	Accession: B43855		
A:	Status: preliminary		
A:	Molecule type: DNA		
A:	Residues: 1-1477 <BAR>		
A:	Note: sequence inconsistent with the nucleotide translation		
A:	Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBIP:89240)		

Query Match	7.5%	Score 225;	DB 2;	Length 1477;
Best Local Similarity	22.6%;	Pred. NO. 0.0011;		
Matches 139: Conservative	93: Mismatches	230: Indels	152: Gaps	30:

Qy	11	SALNAWYVVSSELNRHIT --- KRASATVKTAVALTLFATVQASANNEQEEDLYLDPVLV	67
		: :	
Db	821	NAINSTYNISILIGNVNVLGGQSSSI - TGNITIEKAAVNTEANNPQQNI - RDRVIK	878
Qy	68	TVAVLINSOKEGTGEKEKYEENSMAVFNEKGVLTAREITL --- KAGDNLIKIQNGTN	124
		: :	
Db	879	-LGSLLVGSLSTGENADI ----- KGNITISATFCKTRDTLNITGNFTN	925
Qy	125	FTYSLLKDLTDLSVCPEKLFSANGKNYNTSDTK - ----- GLAFKET	168
		: :	
Db	926	-NGFAEINIQO ---- GVVKLVGNTNOGDNLNITTHAKRNORSIIIGNKKSGLNI - - - -	976
Qy	169	AGTNGDPTVHLHGISTGSTPLTDTLLNTGATTNVT - - - - - NDNYTDE	208

Db 977 TDSNDAEIOIGNISQKEGNLTSSDKINITKQITIKKIDGEDSSSDATSANLT-1K 1035
QY 209 KKAASVQDLNAGWNKVGKPGTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNKG 268
Db 1036 TKEKLTEDLSISGFN---KAEITAKDGRDLTIGNSDNGSNGAEAKTVTFN-----NVK 1086
QY 269 KTEVKIGAKTSVKEKDKGLVTKGDKGSGSSSTDEGEL-VTAKEVIDAYNKAAGRMMKT 327
Db 1087 DSKISADGHNWTL---NSKVKTSSSGRESNDSNDTGLTITAKNV---EVNKDITSUKTV 1141
QY 328 TANGOTQADKFFETVSGTNTWTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLN 387
Db 1142 NIT-----ASEKVTTTAGSTINATNGKASITTKTGDISGTIS-----GNTVSVSA-- 1186
QY 388 SGWNLDSKAVAGSGKVISSG--NVSPSKGKMDFTVNINAGNTEITRNGKNIDTATSMTP 445
Db 1187 ---TVDTLTTSGSKIEAKSGEANVTATGTIGGTI---SGNTVNTVANAGDLTVG----- 1235
QY 446 QFSSVSLGAGADAPTLSDVDGAL--NVGSKDNKPVRTITNVAPGVKEDVTNVAQLKGVA 503
Db 1236 --NGAEINATEGAATLATNTLTTEAGSS-----ITST-----KGQVDLLAQNGSIA 1281
QY 504 QNLNRRIDNVGDNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYRGEAGYAISSYSSD 563
Db 1282 GSIN--AANVTLN-----TTG-----TLTTVAGSDIKATSG-----TLVIN 1315
QY 564 GGNWIKGTASGNS 577
Db 1316 AKDAKMGDASGDS 1329

RESULT 14

AF0394
Probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0394
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Status: preliminary
A:Accession: AF0394
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175
C:Genetics:
A:Gene: hmwA

Query Match 7.3%; Score 219; DB 2; Length 1910;
Best Local Similarity 20.5%; Pred. No. 0.0031;
Matches 148; Conservative 92; Mismatches 255; Indels 228; Gaps 28;

QY 14 NAWVVSELTEHHTKRASATVKTAVALTLFPATVQ-----ASAA 51
Db 998 NATITANNISMN-----GNITANDAVLMTNTFLTAKGDIKTDLTSPTKGLFRNGGWTAA 953
QY 52 NNEEQEEDLYDPLVRLTAVVLIVNSDEGTGKEKEVEENSDWVYFNEKGVLTAETLTK 111
Db 954 NN-----ILLVANS--TSSGETVKINASS-----NKNMITAGKDISII 990
QY 112 AG-----DNLIKONGNFYYSUKKDLTDTSVGTTEKLSFANGKNVNIISDT 159
Db 991 AGNSKTATGPNINIERVNIETNNGFT-----TNGITSTWLSGVNVVSANG--VDITSNS 1042
QY 160 KGLNFAKETACTGDTTVHLNGIGSTLTDTLTNGATTNTVNDVNDDEKKRAASVDV- 218
Db 1043 TG-----TGGIVLDNTNLTTVGD-----INT-IVTNSSGKGIWIKSNSTLNSNKDIT 1089

QY 219 ---LNAAGWNKGV--KPGTTASDNVDFVRYDTVEFLSADTKTTTNNVESKDNKGKTEVK 273
Db 1090 LVGVSAQN-EGVIOGSSDASN-----NISAQGNITLIGKMGNGSGQSHLIN 1137
QY 274 IG--AKTSVKEKDKGLVTKGDKGSGSSSTDEGELVTAKEVIDAYNKAAGRMMKTFTA-- 329
Db 1138 LGNVSLTS-----SGRNIDINGSSAGTGDVYFTNVVELNATAGNVSIIYAEKTTALS 1187
QY 330 -----NGOTGQADKFFETVSGTNTWTFASGKGTATVSKDDQGNITV----- 370
Db 1188 TSLNAVLSLGGNNSIKRAQNGWLICKAFNTTQAGAGIGFRANSSLSVDGNIILKGETEGVGA 1247
QY 371 -----MYDVNVDGALNVNQLNSGWNLDKAVAG----- 399
Db 1248 TRKGIDFYGANTLNIILKGSQSLGKGAQDTAGGNGISYTSLSAKLTVNNGSLKMEGR 1307
QY 400 -----SSGKVISGNVSPSKGKMD----- 417
Db 1308 STSGTGINFPPSSNNTLVFNGDGTLLKGSVAGTGAISGVVNNSTGPMTEIGISTDGAG 1367
QY 418 -----ETVNIAGN---NIEITRNGKNIDIA-TSMTPOFSSVSLGA--GADAPT 460
Db 1368 VHLFSAEHRIDRINVTCSSSTHAEGLRISGNAIVDTTLTKGSINGSGVKIDSLPGSSVVT 1427
QY 461 LSVGDGALNVGSKDNKPVRTITNVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGDNARAG 520
Db 1428 RSVLDNATLNGSSSGKGVETTSIDINGIHSSINGTTGTGTGIGIDIGEN-SNVTGTSEAD 1486
QY 521 --TAQATATAGL-VQAYLPCKSMMAIGGGTYRGEAGYAISS-ISPQGNWIKGTASGN 576
Db 1487 LLILQGVATTGTGTGIKLNGNNDLSNTSLNSSAVDGIALDITGLANQGNVILNGTASGS 1546
QY 577 SRG 579
Db 1547 GIG 1549

RESULT 15

C48399
ABC-type transport protein ydBA.2 - Escherichia coli
C:Species: Escherichia coli
C:Date: 19-Nov-1993 #sequence_revision 16-Oct-1998 #text_change 08-Oct-1999
C:Accession: C48399; D64891; H64891
R:Moszer, I.; Glaser, P.; Danchin, A.
Biochimie 73, 1361-1374, 1991
A:Title: Multiple IS insertion sequences near the replication terminus in Escherichia coli
A:Reference number: A48399; MUID:92190338
A:Accession: C48399
A:Molecule type: DNA
A:Residues: 464-2020 <MOS>
A:Cross-references: GB:D85081; NID:g3041754
A:Experimental source: strain K-12
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:88089, NCBI:88090)
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A:Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: D64891
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-839, 'LDLPLYFOTSVIT', <BLAL>
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g17876
A:Experimental source: strain K-12, substrain MGL655
A:Accession: H64891
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 'M', 915-2020 <BLA2>
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876
A:Experimental source: strain K-12, substrain MGL655
C:Genetics:
A:Gene: ydBA_2

A:Start codon: GTG

Query Match 7.2%; Score 216.5; DB 2; Length 2020;
Best Local Similarity 23.4%; Pred. No. 0.0044;
Matches 165; Conservative 78; Mismatches 238; Indels 225; Gaps 38;

QY 33 TVKTAVALTLFATVQ-----ASANNEEQEEDLY-LDPVLRVAVLVIVNSDKEGTGE 83
Db 151 TEKTLIRSVFTYENADGTISLQSNRKKATINLWQIDEANNTVALEGVSDAG----- 206
QY 84 KEKVEENSDWAVYFNEKGVLTAREITLKAGDNLIKQNGTNTFTYSLKKOILDTLSVGT- 142
Db 207 -----TKWQYNHGELVIT-----GDNATVNNNG-----KTTVDGKDSGTGEI 244
QY 143 -----KLSFSANGKNVITSDT-----KG-----LNFAK 166
Db 245 NGNNGKVIQDGLDVSGGGHGDITGDSATVDNKGTMVTDPESMGIOIDGDKAIVNNEG 304
QY 167 ETAGTNGDITVHLNG-----IGSTLTDTLTNTGATNTVNDNVTDDEKKRAASVKDVL 219
Db 305 ESTITNGGTGTOINGDDATANNNGKTTVDGKDSGTGEINGNCKVIOD-----GDLVDS 358
QY 220 NAGWNIGKVPKPTASDNVDVRYDYVEF-LSADTKTTTVNVVESKD-----NG 267
Db 359 GCGHGI-DITGDSATVDNKGTMVTDPESIGIQVDGDAQVNVNNEGESAITNGGTGTOING 417
QY 268 KTEVKIGAKTSVIKEKDKLVTKGD-KGENG-----SSTDEG 304
Db 418 DDATANNGKTTV-----DGKDSGTGEIAGNNGKVIQDGLDVSGGGHGDITGDSATVDN 473
QY 305 EGLVTAKE-----VIDA-----VNKAGWRMKTITANGOTGOADKFEFTVSGTNVTFASGK 354
Db 474 KGTMTVDPESIGIQIDGDAQVNVNNEG---ESTITNGGTG-----TQINGNDAT-ANNS 523
QY 355 GTTATVSKDD-----QGNITVMYDVNVGDALNV-----NOLQNSGWN--LDSK-----AVA 398
Db 524 GKTTVDGKDSGTGKTAGNIGI---VNLDGSLTVTGGAHGVENIGDNGTVNNKGDIVVSDT 580
QY 399 GSSGKVISGNVSPSKGMDETVNIAGNIEITRNKNIDTIATSM-TPQPS----- 448
Db 581 GSGVLINGEGATVSNITGDVNVNS-NEATGFSITNSGKVSAGSMQVDFSTGVDLNGNN 639
QY 449 -SVSLGA-----GADAPTLSDVDALNV---GSKKDNKPVRTNVA-----PGV----- 488
Db 640 NSVTLAAKDLKVVGQKATGINVSGDANTVNTGNVLVDKDKTADNAAEYFFDFPSVGINVY 699
QY 489 -KEGDVTNVAQLKGVAQN-LNNRIDNV-DGNARAGIAQAIAATAGLV-----Q 532
Db 700 GSDNNVTLDGKLTWSDSEVTSRQSNLFDGSAE-----KTSGLVIVIGDGNVNNMNGGL 752
QY 533 AYLPGSKMMAIGGTYRGAGYAI-----GYSSISDGGNWIIG 571
Db 753 ELIGEKNALADGSQVTSRLRTGYSYTSVIVVSGESSVYLNAGDITISG 798

Search completed: July 3, 2002, 08:12:25
Job time: 447 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:30:02 ; Search time 48.34 Seconds

(without alignments)
473.381 Million cell updates/sec

Title: US-09-771-382-5

Perfect score: 2999

Sequence: 1 MNEILRIIWNLSALNAWVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	228.5	7.6	1039	1 AG43_ECOLI	P39180 escherichia
2	216.5	7.2	2003	1 YDBA_ECOLI	P33666 escherichia
3	207.5	6.9	1577	1 HLYA_PROMI	P16466 proteus mir
4	203.5	6.8	1286	1 AIDA_ECOLI	Q03155 escherichia
5	199	6.6	1325	1 YDBK_ECOLI	P32051 escherichia
6	196	6.5	1654	1 OMPB_RICRI	Q53047 r outer mem
7	191.5	6.4	1608	1 HLYA_SERMA	P15320 serratia ma
8	191	6.4	2249	1 OMPA_RICRI	P15921 rickettsia
9	189.5	6.3	1953	1 BIGA_SALTY	P25927 salmonella
10	186.5	6.2	1655	1 OMPB_RICCN	Q9kka3 r outer mem
11	185	6.2	1645	1 OMPB_RICTV	P96989 r outer mem
12	183.5	6.1	928	1 HXA2_HAEIN	P43354 haemophilus
13	183	6.1	1007	1 Y741_CHLMU	Q9Pjt6 chlamydia m
14	181	6.0	917	1 HXA3_HAEIN	P52143 escherichia
15	180.5	6.0	1569	1 YFJA_ECOLI	P05653 r outer mem
16	180	6.0	1656	1 OMPB_RICUA	P43555 haemophilus
17	180	6.0	2334	1 WAPA_BACSU	O07833 bacillus su
18	178.5	6.0	933	1 SLAP_CAMPE	P35827 campylobact
19	176	5.9	1861	1 APU_THETU	P38536 t amylolupl
20	175.5	5.9	1567	1 ICEN_XANCT	P18127 xanthomonas
21	174	5.8	918	1 YWJB_CAEEL	P34487 caenorhabdi
22	172.5	5.8	2021	1 OMPA_RICCN	O52657 rickettsia
23	167	5.6	1643	1 OMPB_RICPR	Q53020 r outer mem
24	166	5.5	1025	1 SLAP_CAUCR	P35828 caulobacter
25	164.5	5.5	444	1 SLAP_LACAC	P35829 lactobacill
26	164.5	5.5	1148	1 ICEK_PSEEX	O30611 pseudomonas
27	164.5	5.5	1300	1 120K_RICRI	P14914 rickettsia
28	163	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
29	160.5	5.4	954	1 FLEY_CAUCR	P15345 caulobacter
30	159.5	5.3	642	1 FLID_CAMUE	Q9phw6 campylobact
31	159	5.3	671	1 ALYS_ENTFA	P37710 enterococcu
32	159	5.3	928	1 PM10_CHLPN	Q9rb65 chlamydia p
33	159	5.3	1694	1 IGA0_HAEIN	P44969 haemophilus

34 159 5.3 1702 1 IGA2_HAEIN P45384 haemophilus
35 158 5.3 497 1 FLIC_ECOLI P04949 escherichia
36 157.5 5.3 1153 1 PVDB_PLANK P50493 plasmidium
37 157 5.2 1196 1 ICEV_PSEEX O33479 pseudomonas
38 156.5 5.2 817 1 YG4A_YEAST P46949 saccharomyc
39 156.5 5.2 1637 1 MRSP_STAAU P80544 staphylococ
40 155.5 5.2 1076 1 NUP1_YEAST P06062 saccharomyc
41 155 5.2 1200 1 ICEN_PSEY P06260 pseudomonas
42 155 5.2 1848 1 CBPA_CLOCL P38058 clostridium
43 154.5 5.2 507 1 FLIC_SALON Q06974 salmonella
44 154.5 5.2 948 1 HP1L_DEIRA P58867 deinococcus
45 154 5.1 1288 1 VACA_HELPJ Q9ZKw5 helicobacte

ALIGNMENTS

RESULT 1
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT: 1039 AA.
AC P39180: P76360: P75614: P97241: Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizumoto H., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RX Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded

Db 364 KETDIDNRWFSWKYDTEKEIOQIGSQIDAQKNNATLTATKGDVTLDAAKINAGNNLA 423
QY 118 IKONGTNTFYSLKDLTSLVSG-TEKLSFSAANGKVNITS-----DTKGLNFA 165
Db 424 INAN-----KDIHNGLVEKSENGSENGNRNHTSRLESWSNSHQTTETLKAS 471
QY 166 KETAG-----TNGDTTVHLN-----GIGSTLTDLL---NT 193
Db 472 ELTAGDGLDLAGOCSITAOAKLHANENLVNAKDINLNQKNTNDKTVTDHNVWGGI 531
QY 194 GATTNVTNDN-----VTDDEKRAASVKDVLNAGWNIG-----VKPGTTASDNVD 239
Db 532 GCGONKNNNOQOVSHATQLTADQLLADNNVNITGSOVKGNQGAFFV--TTQGDVVI 589
QY 240 FVRTYDTEFLSAD-----TKTTVTNVESKDKGKTEVKIGAKTSVIKEKD-----GKL 288
Db 590 DNALSETISKIDERTGTAFNITKSSHKNETKOTSTGSELISDAQLTVVSGNDVNVIGSL 649
QY 289 VTGDK-----GE-NGSST-----DEGEGLVT-----AKEVIDAVNKAQWRMKTITANG 331
Db 650 IKSADKLGISLGDINVKSAQVTKIDDEKTSLAITCHAKEVEDKQYSAGFHITHTNKN 709
QY 332 OTQADKFETVTSNTVFASGKGTATVS--KDDGNIITVYDVNVGDALNQLONGS 389
Db 710 TSTETEQA NSTISGANVDLOANKDVTFAGSDLKTAGNASITGD-NVAFVSTENKKQTD- 767
QY 390 WNLDSKAVAGSSKVISGNVSPKSGKMDETVNNAGNNEITRN-GKNIDDIATSMTPQFS 448
Db 768 -NTDTTISGGFS---YTGGVYDKVGSRADFOYD-KQHTQTEVTNRGSGQTEVAGDLTITAN 822
QY 449 SVSLGAGA-----DAPTLSDVDGALNVGSKKD-----NKPV 479
Db 823 KDLLEHGAASHVBRQVQESCENTIOHLAVNDSESKT---DSLNVGIDVGVNLDVSGYTKPV 880
QY 480 R-----ITNVAPGVKEGDTNVNAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVQA 533
Db 881 KKAIEDGVNTKPG-NNTDLTKKTARDAIANLAN-LSNLE-TPNVGVEVGK-----930
QY 534 YLPKSKMAATGGTYRGEAGYATGYSISDG 564
Db 931 -----GGGSQSQSTDSQAVSTISNAG 951

RESULT 4
AIDA_ECOLI
ID AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC Q03155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aidA-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG Plasmid p186.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -I- FUNCTION: THIS IS AN ADHESIN PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -I- SUBCELLULAR LOCATION: Outer membrane.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X65022; CA446156.1; -
KW PIR; S28634; S28634.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP 5 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 6.8%; Score 203.5; DB 1; Length 1286;

Best Local Similarity 21.4%; Pred. No. 0.0063;

Matches 146; Conservative 92; Mismatches 274; Indels 171; Gaps 30;

QY 1 MNEILRIINLSALNANWVSELTNRH-----TKRASATVKTA--VLATLLFATVOASA 51
Db 1 MNKAYSIIINSHSRQAVIVASELARGHGFVLAKNTLLVAVVSTIGNAFVAVNISGTVSSGG 60
QY 52 NNEEQEEDLYL-----DPVLRVAVLIIV-----SDKEGT-GEKEKVEEN 90
Db 61 TVSSGETQIVYSGRGSNATVNSGGTQIVNNGKTTATTVNSSGSONVGTSGATISTIVN 120
QY 91 SDNAVYFNEKGLVLTAREIT-----LKAGDNLKIKQNGTNTFTYSLK-KDLTDLTLSVGT 141
Db 121 SGGIQRVSSGGVASATNLSCGAQNIYNLGHASNTVIFSGGNQTIIFSGGIDTSDNISGGQ 180
QY 142 EKLSFSAANGKVNITSDTKGLNFAKETAGTDTTTLN-----GIGSTLTDLLNTG 194
Db 181 QRV--SSGGVASTNTINSSG---AONILSEGAISTHISGGNQYISAGANATETIVNSG 235
QY 195 ATTNVTNDVNTDEKKRAASVKDVLNAGWNIGVKPOTASDNVDVTRTDTTVEFLSADT 254
Db 236 GFQRVNSG-----AVATGTVLSGG--TQNVSSGSAISTSVYNSGVQTV-FAGATV 283
QY 255 KTTVNVESKDN---CKKTEVKIGAKTSVIKEKDKGLVTGKDKGNGSGSTDEGEGLVTA 310
Db 284 TDTTVNSGNGONISSGGIVSETTVNSGTONIYSGGSALSANIKGS-----329
QY 311 KEVIDAVNKAQWRMKTITANG-----OTQADKFETVTSNTVTFASG-----KGT 356
Db 330 ----QIVNSEGTALNTLVSDGGYQHIRNGGLASCTIVNQSGYVNISSGGVAESTIINSGG 385
QY 357 TATVSKDDQGNITVWYD--VNVGD-ALNVNQLONSQWNL-----DSKAVAGSSG--K 403
Db 386 TLRVLSGDIYARGTILNNSGRENVSNGGVSYNAMINTGNGQYIYSDGEATAAIVNTSGFOR 445
QY 404 VISGNVSPSKGMDETVNNAGN--NIEITRNKN-----IDIATSMTPQF 447
Db 446 INSGGTAPVQNSVVVTVRTVSSAAKPPDAEVYSGGQTVYLRGWIWYSNFLTAVWSMPTGT 505
QY 448 SS---VSLGAGADAPTLSDVDGDLN-----VGSKKDNKPKVRIITNVAPGV 488
Db 506 ASGANVNLGRLNFAAGNVGVTILNQEGRYQYVSGATATSTVGNNEGVEYV---LSGGI 561
QY 489 KEGDVTNVAOLKGVAQNLNRRIDNVGNAR-----GIAQAIATAGLVQAYLPKSKMAI 543
Db 562 TDGTVLNSGGILQAVSSG-----GKASATVINEGAQFVYDGGV---TGTNIK--606
QY 544 GGTYRGEAGYATGYSISDGGN 566
Db 607 NGGTIRVDSGASALNIALSSGGN 629

RESULT 5
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051; P76140; P77168;

01-OCT-1993 (Rel. 27, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR BL510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97251357; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.,
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.,
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -!- SIMILARITY: TO E. COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
CC
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CC
CC EMBL: AE000248; AAC74583.1; -;
CC EMBL: D90793; BAA15190.1; ALT_INIT.
CC EMBL: D90794; BAA15197.1; ALT_INIT.
CC EMBL: X73295; CAA51730.1; ALT_FRAME.
CC FIR: S34315; S34315.
CC EcoGene: EG11780; ydek.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 6.6%; Score 199; DB 1; Length 1325;
Best Local Similarity 21.0%; Pred. No. 0.011;
Matches 158; Conservative 91; Mismatches 244; Indels 260; Gaps 34;
QY 1 MNEILRIINWNSALNANVWVSELTR-----NHTKRASATVKTA--VLATLLFATVOAS 50
DB 1 MNRIYRIWNCITLOVFOACSELTRRACKTSTVNLKRSGLTTRFSLTLGLVLLALSASAS 60
QY 51 ANNEEDED-----LYLDPVLR-----TVAVLIIVNSDKETG 81
DB 61 GASLEVDNDQITNIDTDVAYDAYLVGWYTCVNLNLAGGNASLTITTSVIGANEDSEGT 120
QY 82 GEKEKVEENSWMAYFNEKGVLTAREITLKAGDN---LKIQKQNTNFTYSLKKDLDTLS 138
DB 121 VN-----VLGCTWRLY-----DSGNNARPLNVGQSGTG-TLNKIQ----- 154
QY 139 VCTEKLSFSANGKNVITSDTKGLNFAKTAGTNGDTTVHLNGIGSTLTDTLLNTGA--- 195
DB 155 -----KGVDGGYLRGSGTGVG-----TVNVEGSDSVLTITELFEIGSYGT 196
QY 196 -TTNVTNDNVTDDEKRAASVKDVLNAGWNIKGVPCTTASDNVDVFTVDTVEFLSADT 254
DB 197 GSNLIT-----DKGYVTSSIVAIL-----GYQAGSNGQ----- 224
QY 255 KTTTVNVES-----KDNKKTEYKIGAK-TSVIKERDKGLVTGCKGKENGSSSTDEG--- 304
DB 225 ---VVVEKGEWLKKNNDSSIEFQIGNQCTGEATIREGLVTAENTIIIGNATGICTLN 280
QY 305 -----EGLVTAKE-----VIDAVNKAGWRMK 325
DB 281 VQDQSVITVRLRYNGYFGNGTVNISNGLNNKKEYSLVGVQDGSNGVNVNVDKGHWNFL 340
QY 326 TTTTANGOTGOADKFETV-TSGTNVTFASGKG-----TTATVSKDDOGNTTVMYDVNVGD 378
DB 341 -----GTGAFRIYICDAGDELNVSSSEKGVDSGLIITACMKETGNTIVKDKNSVIT 394
QY 379 ALNVN-----QLONGWNLDKSAVAGSSGKVISGNVSPSKGKMD-----TVNI 422
DB 395 NLGTNLGYDGHGEMNISOGLVNVSGSSSLGYGETGVGNVSIITGGMWKKNVYTTIGV 454
QY 423 NAGNNITETNGK-----NIDATSMTPQFSVSLGACADAPTLSVDGDALNVGSKDKNP 478
DB 455 AGVGNLNSIDGGRFVSQNTITFLGDKASGIGTLNL---MDA-TSFDFTVGVNVG----NFG 506
QY 479 VRITNVAPGVK-----EGDVTNVAQLKGAQNLNNRNDNV-DGNARAGIAQA----- 524
DB 507 SGIVNVSNGATLNTSGYGFIGNASGKGIYINISTDSLWNKTSSTNAQLQVGLGTGEL 566
QY 525 -IATAGLVQA-----YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWI 568
DB 567 NITGGIVKARDTQIALNDKSKGDRVVDGQNSLLETENMVVGTSG--TGTTLTNNGTLN 624
QY 569 IKG-----TASGN---SRHFGASASVGY 589
DB 625 VEGGEVLYVFEPVAVGTGLNTGAAHGAADADAGE 657
RESULT 6
OMPB_RICRI STANDARD; PRT; 1654 AA.
ID OMPB_RICRI AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scd5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=783;

Best Local Similarity 21.5%; Pred. No. 0.033;

Matches 157; Conservative 83; Mismatches 266; Indels 223; Gaps 31;

```
QY 24 RNHTKRASTVTKAVLATLLFATVQASANNNEOEEDLYLDPVLRVAVLVNSDK----- 79
Db 396 REOLOQAGSTVAASGAKLI-----STQEDVKLGANVSADRAVSUKAARDVHLA 445
QY 80 GTGEKEKVEE-----NSDWAYFNEKGVLTAREITLTKAGDNLKIKQNG 122
Db 446 GLVEKDKSSERGQYRNHTSSLRGTGRWSNDESELSKASELSRSEGLTLKAGRVNSTQAG 505
QY 123 TNYTSLKDLTDLTSVGTSEKLS-----FSANGKNVNTSDTKGLNFAKET 168
Db 506 VHAQRDLTTIDADNQIGVGQKTANAKAVRDKTSMGIGGGDNKN--SNRREISHASEL 563
QY 169 AGTNGDTVTHLNG-IGSTLTDTL--NTGATTNVTNDVTDDEKKRAASVKVDLNA--- 221
Db 564 --TSGG-TLRLNGQQGVITGSKARQKQGEVATHGGLRID--NALSTVVDKIDATGT 618
QY 222 GWNKIGVKPCTASDNVDVRYTDTVEFLSADTKTTTNNVESKD-NGKKT-----EVKIGA 276
Db 619 AFNI-----TSSHKADNSYQSSTASELSKSDTNLTLSHKDADVIGSQVASSGELSVE 672
QY 277 KTSVKEKDKGLVTKDKKENGSGSTDEGELVT-----AKEVIDAVNKAGWRM-----K 325
Db 673 KTGNIINVK-----AAEROQNIDEQKTALTVPNGYAKEAGDKQYRAGLRIETHRDSEK 723
QY 326 TT-----TANGOTGOADKPFETVTSQTNVTFASGKGTTA----- 358
Db 724 TTRTENSASSLGGSVKLKAEKDVTSFGSKLVADKGDASVSGNKKVFLAADDKTSNTEQ 783
QY 359 -----TVSKDDQGNITVMYDYNVGDALN 381
Db 784 TKIGGGFYVTGGIDKLGSGVEAGYENKTKQAQSSKAITSGSDVKGNLT-----INARDKLT 839
QY 382 VNQLONGHNLDSKAVAGSGKVISGNVSPSKMDETVNNAGNNIETRNKNIDDIAT 441
Db 840 QCGAQSIVSGGAYGQENAAAGVDHLLAAADTASTTTTKTDVGVI-----GANVDYSA 888
QY 442 SMTPOQSSVSLGA-----CADAPTLVSDGDLNVSCK--DNKPVRTNVPAC 487
Db 889 VTRPVRVAVGKAAKLDATGVINDIGIGAPNVGLDIGAOGGSEKSSSSQAVVSSVQAG 948
QY 488 V-----KEGDV---TNVAQLKGVAQNLN-----NRIDNVGNARAGIAQAATAG 529
Db 949 SIDINAKGEVROGQTOYQASKG-AVLTADSHRSEAAANRQDEQSRDTR-----GSAG 1000
QY 530 LVQAYLPGKSMMAIG-----GGYRGEGAYGYSSTSDGGNW-----IKGTASGN 576
Db 1001 -VRVYTTGSDLTVDKAGGEGGTQRSSASQAVTGSIDAANGINNVNKKDAIYQGTALNG 1059
QY 577 SRGHEGASA 585
Db 1060 GRGKTAVNA 1068
```

RESULT 8
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT: 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=R;

```
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RT repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -!- PTM: GLYCOSYLATED (PROBABLE).  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC  
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CC  
CC EMBL; M31227; AAA26380.1; -  
DR PIR; A41477; A41477.  
DR InterPro; IPR003858; rOmpA_rOmpB.  
DR Pfam; PF02708; rOmpA_rOmpB; 1.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 212 286 A (TYPE I).  
FT REPEAT 287 358 B (TYPE II).  
FT REPEAT 359 430 C (TYPE II).  
FT REPEAT 431 505 D (TYPE I).  
FT REPEAT 506 577 E (TYPE II).  
FT REPEAT 578 652 F (TYPE I).  
FT REPEAT 653 724 G (TYPE II).  
FT REPEAT 725 799 H (TYPE I).  
FT REPEAT 800 874 I (TYPE I).  
FT REPEAT 875 949 J (TYPE II).  
FT REPEAT 950 1021 K (TYPE II).  
FT REPEAT 1022 1093 L (TYPE II).  
FT REPEAT 1094 1165 M (TYPE II).  
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).  
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;
```

Query Match 6.4%; Score 191; DB 1; Length 2249;

Best Local Similarity 24.4%; Pred. No. 0.051;

Matches 142; Conservative 56; Mismatches 212; Indels 172; Gaps 30;

```
QY 98 NEKGVLTAREITLTKAGDNLKIKONGTNTFTYSLKK-----DLTDLTSVGTSEKLSFSAN-----G 150
Db 766 NANAVLTGAIDNTTGDNVGV-----LNLNGLSQQVTGDTGNTNSLAT--ISVGAGTATLG 819
QY 151 NKNVITSDTKGLNFAKETAGTN-----GDT--TVHLNGIGSTLTDLLNT- 193
Db 820 GAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNGVNLNGLSQQVTGDTGNTN 879
QY 194 -----GATTNVTNDVTDDEKKRAASVKDVLNAGNWKVKPOTTTASDNV 238
Db 880 SLATISVGAGTATLGGAVIKATTTKLTN-----AASVLTLTNANAVLTGAIDNTTGDNV 934
QY 239 DFVRTYDVTVEFLSADTKTTTNNVESKDNKKTEVKIAGKTSVKEKDKGLVTGKDKGENG 298
Db 935 GVNLNGLSQQVTGDTGNT-----NSLAT--ISVGAGTATL----- 968
QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQOAKDFETVTSQTNVTFASGKGTTA 358
Db 969 -----GGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANGI-VTFGTNSTVTG 1020
QY 359 TVSKDDQGNITVMYDYNVGDALNVQLONGHNLDSKAVAGSGKVISGNVSPSKMD 418
Db 1021 NV-----GNTNALATVNVGAGL--LQVQGVVVKANTINLTNDNASAVTFTNPVVVTGAIDN 1073
QY 419 TVNINAG-----NNIEITRNGKNIDIATSWTPOFSSVSLGADAPTLSVDGDAL--NVG 471
```

Db 1074 TGNANNGIVTFTGNTVGNVGN-----TNALATVNVGAG-----LLQVQGVVVKANTI 1122
Qy 472 SKDN-KPVRTNVPAGVKEGVDVTVNAQLKGAQNLRNDRVGNARA-----GIAQIA 526
Db 1123 NLTDNASAVFTN-PVVVTGAIDNTG-----NANNGIVTFTGNTVTVGDIQNTNALA 1173
Qy 527 T-----AGL-VQAYLPKGSMA-----IGGGTYRGEAGYAIY-----SSIS 562
Db 1174 TVNVGAGITLOA---GGSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYFKGAIA 1224
Qy 563 DGGNWIK-----GTASGNSRGRH-----FGASASVG 588
Db 1225 NGNNAILNVNTKLLTASHLTICTVAEINAGNGLFTIDASVG 1266

RESULT 9

BIGA_SALTY STANDARD; PRT; 1953 AA.
ID BIGA_SALTY STANDARD; PRT; 1953 AA.
AC P25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein biga precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium r18 homolog.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A.
RP RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Willson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RN [3]
RN SEQUENCE OF 1-765 FROM N.A.
RP RC STRAIN=LT2;
RX MEDLINE=911100301; PubMed=1987123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
requirement for a cloned *cyg* plasmid to overcome limiting shiroheme
cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC -----

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CC -----

DR EMBL; AF133696; AAD39458.1; -
DR EMBL; AE008859; AAL22340.1; -
DR EMBL; M64506; AAA27042.1; ALT_FRAME.
DR EMBL; M64506; AAA27043.1; ALT_FRAME.
DR PIR; C39200; C39200.
DR PIR; D39200; D39200.

DR StyGene; SG10437; bigA.
KW Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 1953
FT
FT PUTATIVE SURFACE-EXPOSED VIRULENCE
FT PROTEIN BIGA.
FT 15 X 11 AA TANDEM REPEATS.
FT 1 (INCOMPLETE).
FT 2 (INCOMPLETE).
FT 3 (INCOMPLETE).
FT 4.
FT 5.
FT 6.
FT 7.
FT 8.
FT 9.
FT 10.
FT 11.
FT 12.
FT 13.
FT 14.
FT 15 (INCOMPLETE).
FT D -> DRGDDVTPDD (IN REF. 1).
FT A -> R (IN REF. 3).
FT CONFLICT 514 514
FT CONFLICT 1698 1698
FT CONFLICT 1795 1798
FT CONFLICT 1836 1837
FT CONFLICT SA -> T (IN REF. 1).
SQ SEQUENCE 1953 AA; 200150 MW; 611B3FIC954D91AE CRC64;

Query Match 6.3%; Score 189.5; DB 1; Length 1953;
Best Local Similarity 23.1%; Pred. No. 0.051;
Matches 126; Conservative 64; Mismatches 194; Indels 161; Gaps 29;

Qy 113 GDNLKIKONGNFYSLAKDLTSLVCTEKLSPFANGKNVNTSDTKGLNFAKETAGTN 172
Db 447 GDNATIKRNTGTS-----DISGAGSTGT-----VIDGNNAKRVND----- 480
Qy 173 GDTTVHLNGIGSTLT-DTLL-NTGATT-----NVTNDNVTDDEKKRAASVKDVLN 220
Db 481 GDMITDGGTGGHITGNDVVDNAGSTTVSGADATALIEGDNAL-----VIN 528
Qy 221 AG-WNIKGVKFTTASNDVFRVTVDFEELSAADTKTTNNVESKDKKKTEVKIGAKTS 279
Db 529 EGNQITSGGAVGTRIDGD-----DAHTTNTGDIADVAGAGAAVII----- 568
Qy 280 VIKEDKGLVTGKOKGNGSSSTDEGEGLVT--AKEVI--DAVNKAGWRMKTTTTANGQTQ 335
Db 569 -----NGDNGSLTQAGDLLVTDGAMGIIITYGTGNEA-----KNTGNATVRD 609
Qy 336 ADKFETVTSGTNVTF-----ASGKGTATVSKDDQGNITVYDVNVGDALNVNOLONS 388
Db 610 ADSVGFVVGAKNTPKKGGIDVSLNGTGLVSG-DGMSQVTLGDGINV---VSVQDSEGV 665
Qy 389 GWNLDKAVAGSSGKV-TSGNVSPS-----KGKMDETVNIAGNIEITRNGK-NI 437
Db 666 FSSATGVSVDGSDNAVDITGNVNIADYQDDLAAGAPLPTGVVYVGGNGTNTLNGALNI 725
Qy 438 ---DIATSWTQFSSVSLGAGADAPTLSDGDLANVSGKDNKPVRTITNAPGVKGDVT 494
Db 736 DNDLSATGGQYLDVVGSLVSGDDNDNDVEIDG-GINITISED--PLDGTG-----ADIT 775
Qy 495 NYAQLKGAQVNLNRRNDVNDGNARAG-----TAQAIATATAGLV-----QAYLP----- 536
Db 776 GISVSGNSTVTLNGH-STIDTNTVVGHHVLRVNVNGGSLILGDDSVVDVNVYIPTGY 834
Qy 537 ---GKSMMAIGGTYRGEAG-----YAI-----GYSSISDGGNWLKGTASNSRGHFGA 583
Db 835 TYNALLMADGEGTSTENKGDITSHGVYSVIRADNGSEVNSGDIILVIATSSNSSEDRAAI 894
Qy 584 SASVG 588
Db 895 TRASG 899


```

RN  [2]
RP  SEQUENCE OF 1-30 FROM N.A.
RC  STRAIN-DL42 / SEROTYPE B;
RX  MEDLINE=95270579; PubMed=7751272;
RA  Cope L.D., Yoge R., Mueller-Eberhard U., Hansen E.J.;
RT  "A gene cluster involved in the utilization of both free heme and
RL  heme:hemoexin by Haemophilus influenzae type b.";
RJ  J. Bacteriol. 177:2644-2653(1995).
CC  -!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  use by non-profit institutions as long as its content is in no way
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U08348; AAA74138.1; -.
KW  Transport; Signal; Repeat.
FT  SIGNAL 1 21
FT  CHAIN 22 928
FT  DOMAIN 101 679
FT  REPEAT 101 106
FT  REPEAT 205 210
FT  REPEAT 279 284
FT  REPEAT 410 415
FT  REPEAT 635 640
FT  REPEAT 674 679
FT  DOMAIN 149 172
FT  REPEAT 149 154
FT  REPEAT 155 160
FT  REPEAT 161 166
FT  REPEAT 167 172
FT  REPEAT 172 172
SQ  SEQUENCE 928 AA; 101228 MW; 67D45466A4B92390 CRC64;

Query Match
Best Local Similarity 6.1%; Score 183.5; DB 1; Length 928;
Matches 127; Conservative 92; Mismatches 253; Indels 145; Gaps 22;

QY 35 KPAVLATLLFATVQASANNEQEDLYDPVLTAVLVNSD-----KEGT----- 81
DB 3 KLVNLSLIILTCGAAVASTPDFQHHKTVFGTVTIEKTTADKWTIKGSDKAQIDWKS 62
QY 82 ---GEKEKV--EENDWAVYFNEKGVLTAREITLAKGNLKI---KQNTNFTYSLKDL 133
DB 63 FDIGQKVEYKFEQNEHAYVNRVIGGNASQIQKLTANGKYLNPNGVITTOGAENIV 122
QY 134 TDLTSVGTGTEKLSFANGKVNITSDTKGLNFAKETAGTNGDTTVH---LNGIGSTLTD- 188
DB 123 AGLLATTKDLERISNSYQTRRTKDRQVLKGLVLDKGVVKEGGVINEGNITAQDF 182
QY 189 TLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIGKVKPGTTASDNVDFVRYDTVE 248
DB 183 VVLGVDEVINKGNIV---EKNSTINGKYLSSGYNFTFLPDSGIS----- 226
QY 249 FLASADTKTTVNVESKDGKTKTEVIGAK-----TSVIKEDKGLVTG 291
DB 227 -VALEDNTVQGVTKVKEGSKAGEITSLAKGRKQALDSLVMNNGVLEATKVSNKNGKVLS 285
QY 292 KDKGE-NGSSTDEGRLVTAKEVIDAVNKAQWRMKTITANGOTGOADKFEVTSNTVTF 350
DB 286 ADNVELNENSKIGE-IVTFGADVTSNKLKDNITKTSKGVTSFKINFTGKSVNING 344
QY 351 ASGKGTATVSKDDQGNITVMYDVNVGALNVNQL---QNSGNWLDKAVAGSSGKVISG 407
DB 345 NFGREDSTTHYKDEKFKLNTENVDPDENIRIADIENTGTGTG---TCTSSFIQTG 401
QY 408 NVS----PSKGKMD---ETVNI-----NAG-----NNIEITRNK----- 435
DB 402 ALSSLLANNGKVLNKNVNSGRIHDSFRGSDSLKLTNKGHIDINNADTHSKGRLLF 461
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QY 436 -----NIDIATSMTPQFSSVSLGAGADAPTILSDVDALN-----VGSKKDKPKPVRI 483
DB 462 ITSQNEEDFKSNITITDSKINLNGCAGMLGRSVDEKDYDNRWOKTEGSRKKFDVKMSN 521
QY 484 VAPGVKEGVDVTVNAOLKQVAQNLRNIDNV---DGNARAGIAQATATAGLVQAYLPKSM 540
DB 522 VE-----FNQDDVILAGGFEKVNLDKIVAT-----GQTN 551
QY 541 MAIGGTVRGEAGYAIG 557
DB 552 FYIDGVSNRGRKRYEG 568

RESULT 13
Y741.CHLMU
ID Y741.CHLMU STANDARD; PRT: 1007 AA.
AC Q9PJUT6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Hypothetical protein TC0741 precursor.
GN TC0741.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoFn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoFn and Chlamydia
RL Nucleic Acids Res. 28:1397-1406(2000).
CC -!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE002342; AAF39550.1; -.
KW Hypothetical protein; Signal; Complete proteome.
FT SIGNAL 1 51
FT CHAIN 52 1007
FT SEQUENCE 1007 AA; 104006 MW; 84280C0871B1518 CRC64;

Query Match
Best Local Similarity 6.1%; Score 183; DB 1; Length 1007;
Matches 156; Conservative 85; Mismatches 238; Indels 248; Gaps 38;

QY 31 SATVKTAVLATLLFATVQASANNEQEDLYDPVLTAVLVNSD----- 77
DB 227 SPTDKSLLAFL--SNPNTKAKMLHSGHLVFTIDTRSSFFVPNGNWQVCSMKVQNGK 284
QY 78 -KEGTGEKEKVEE-----NSDWAVYFNEKGVLTAREITLAKGNL----- 116
DB 285 TKEDGLKD-LEDCAKCFCTGYNKFSDDWG---NRVDPVLSKAGIESGGLPSSVIINN 340
QY 117 -----KIKONGTNTFTSL--KKDLTDLTSV--GTEKLSFSAKNKNV----ITS 157
DB 341 KPFTCVAYGPNPKENGPNYTPSAMRRGRHVDGFKIFDGT-----APFNKNMGSSPT 394
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical outer membrane protein ypja.
GN YJUA OR B2647
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205937;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Shimamoto H.,
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features";
RL DNA Res. 4:91-113(1997).
CC -!- SUBCELLULAR LOCATION: Outer membrane (Potential).
CC -!- SIMILARITY: STRONG, TO BORDETTELLA PERTACTIN.
CC
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CC
CC EMBL; U36840; AAA79815.1; ALT_SEQ.
DR EMBL; AE000350; AAC75695.1; -
DR EMBL; D90889; BAAL6514.1; ALT_INIT.
DR EMBL; D90890; BAAL6518.1; ALT_INIT.
DR EcoGene; EG13213; YPJ.A.
KW Hypothetical protein; Outer membrane; Complete proteome.
SQ SEQUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;

Query Match 6.0%; Score 180.5; DB 1; Length 1569;
Best Local Similarity 19.7%; Pred. No. 0.11;
Matches 117; Conservative 102; Mismatches 277; Indels 97; Gaps 22;

QY 25 NHTKRASATVKTAVLATLL-----FATVQASANNEEEDLYLDPVLRVAVLVNS 76
DB 322 NYQHDGALKTKNTGTVSGTNSGAFSIHNVADVLLNLEGGHLD-----INA 371

QY 77 DKEGTGEKEVPENSDWAVYFNEKGVLTAREITLTKAGDNKLIKQNGTNTFTSLKKDLTDL 136
DB 372 --YGSANKTIIDKGTMSVLTNAKADAT----RIDGGVMDVAGNATN-----TI 415

QY 137 TSVGTKEKLSFSANGNKVNTSDTKGLNFAKETAGTNGDTTVHLNG-----IGST 185
DB 416 INGGTQNNINNYGIATGNTINSCTONIK-----SGKADTTIISGSRQVWEKDGTAIGN 470

QY 186 LT--DTLLNTGATTVNDVNDYDDEKKRAASVKDVLNAGWNKIG---VKPGTTASDNVD 239
DB 471 ISAGGSLIVYTGGAHGVN-----OETGSALVANT-GAGTDIEGYNKLHSFTITGGEAN 523

QY 240 FVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDKLVTKDKGENGS 299

Db 524 YVVENTGE-LTWAKTSAKNT-TIDTGGKLVQKEAKTDSRLNNGGVLEVQDGGGAH 581
QY 300 STDEGEGLV-----TAKEVIDAVNKAG--WRMKTITANGOTGOADKFEETVTSCTNV--TFA 351
DB 582 VEQQSGGALIASTTSGTLIEGTNSYGDAPYIRNSEAKNVVLENAGSLTVVTVGSRAVDTTI 641
QY 352 SGKGTATATVSKD-----DOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIS 406
DB 642 NANGKMDVYKDVGVTLNSAGTQTIYASATSDKANIKGKQTVYGLATEANIESGQIYD 701
QY 407 GNVSPSKGKMDETVINAGNNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLVSDGD 466
DB 702 GGST-----EKTHINGGTQ-TVQNYGRAIN--TDIVSGLQIQIMANGTAEGSIINGGSG 751
QY 467 ALNVGSKKDKPKVRITNVAPVKEGDVTNVQALKGVAQNLRNDRIDNVDCNARAGIAQA 526
DB 752 VYNEGGLAENSVLNDGGTLDVREKGSATGIQOSSOGALVATTRATRVGTGRADGVAFSIE 811
QY 527 TAGLVQAVLPGRKSMMAIGGTYRGEAGYAIQYSSISDGGNWI--KGTASGNS 577
DB 812 QGA-----ANNILLANGVLTVESDTSDDKTQVNMGGREIVKTKATATGTT 857

Search completed: July 3, 2002, 08:30:09
Job time: 1180 sec

GenCore version 4.5
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OM protein - protein search, using sw model
Run on: July 3, 2002, 08:28:43 ; Search time 168.02 Seconds
(without alignments)
608.499 Million cell updates/sec

Title: US-09-771-382-5
Perfect score: 2999
Sequence: 1 MNEILRIIWSALNAWVVS.....TASGNSRGHGASVGYQW 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_l9:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2999	100.0	591	2	Q93QY3	Q93qy3 neisseria m
2	2984	99.5	591	16	Q9JRI8	Q9jri8 neisseria m
3	2980	99.4	591	2	Q9JPS7	Q9jps7 neisseria m
4	2952.5	98.4	592	2	Q9AQF0	Q9aqf0 neisseria m
5	2866.5	95.6	590	2	Q9JPS3	Q9jps3 neisseria m
6	2752.5	91.8	600	2	Q9JPS6	Q9jps6 neisseria m
7	2739.5	91.3	594	2	Q93QY4	Q93qy4 neisseria m
8	2732.5	91.1	594	2	Q9JPS2	Q9jps2 neisseria m
9	2728.5	91.0	594	2	Q9JPI3	Q9jpi3 neisseria m
10	2721.5	90.7	594	2	Q9JPH7	Q9jph7 neisseria m
11	2719.5	90.7	598	2	Q9JPR9	Q9jpr9 neisseria m
12	2706.5	90.2	598	2	Q9JPT0	Q9jpt0 neisseria m
13	2706.5	90.2	598	2	Q9JPS0	Q9jps0 neisseria m
14	2705.5	90.2	598	2	Q93QY5	Q93qy5 neisseria m
15	2676	89.2	599	2	Q9JPR8	Q9jpr8 neisseria m
16	2597.5	86.6	592	2	Q9JPS9	Q9jps9 neisseria m

17	2596	86.6	599	2	Q9JPS8	Q9jps8 neisseria m
18	2555.5	85.2	598	2	Q9JPR7	Q9jpr7 neisseria m
19	2554.5	85.2	592	2	Q93QY2	Q93qy2 neisseria m
20	2523	84.1	595	2	Q9JPH0	Q9jph0 neisseria m
21	2519.5	84.0	600	2	Q9JPS5	Q9jps5 neisseria m
22	2481	82.7	589	2	Q9JPI0	Q9jpi0 neisseria m
23	2467	82.3	589	2	Q93QY1	Q93qy1 neisseria m
24	2449.5	81.7	526	2	Q9JPS4	Q9jps4 neisseria m
25	2447.5	81.6	530	2	Q9JPS1	Q9jps1 neisseria m
26	2445.5	81.5	592	16	Q9JQW4	Q9jqw4 neisseria m
27	1243	41.4	2353	2	P71401	P71401 haemophilus
28	1054.5	35.2	1098	2	Q48152	Q48152 haemophilus
29	437.5	14.6	1299	16	Q9F3X6	Q9f3x6 pasteurella
30	393	13.1	2059	16	Q9PD50	Q9pd50 xylella fas
31	375	12.5	1107	2	Q9F2D8	Q9f2d8 salmonella
32	372.5	12.4	1190	16	Q9PC04	Q9pc04 xylella fas
33	368.5	12.3	2712	16	Q9F3X5	Q9f3x5 pasteurella
34	252.5	8.4	1291	16	Q92KQ7	Q92kq7 rhizobium m
35	243	8.1	1953	16	Q98HJ2	Q98hj2 rhizobium l
36	239.5	8.0	1004	16	Q9PD63	Q9pd63 xylella fas
37	233.5	7.8	2276	2	Q93TY6	Q93ty6 staphylococ
38	231.5	7.7	3930	16	Q98E20	Q98e20 rhizobium l
39	231	7.7	1265	2	Q9FDA0	Q9fda0 xanthomonas
40	230.5	7.7	1536	2	Q48031	Q48031 haemophilus
41	230	7.7	1557	2	Q9RNI2	Q9rni2 haemophilus
42	228.5	7.6	1039	2	Q9L6T7	Q9l6t7 escherichia
43	226.5	7.6	1040	2	Q9AL50	Q9al50 shigella fl
44	222	7.4	1477	2	Q48028	Q48028 haemophilus
45	219.5	7.3	1039	2	Q9L6T8	Q9l6t8 escherichia

ALIGNMENTS

RESULT 1

Q93QY3 PRELIMINARY; PRT; 591 AA.
ID Q93QY3
AC Q93QY3;
DC 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
membrane protein of Neisseria meningitidis.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157606; AAK68867.1;
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 100.0%; Score 2999; DB 2; Length 591;
Best Local Similarity 100.0%; Pred. No. 6.8e-119;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNEILRIIWSALNAWVVS	ELTRNHTKRASATVKAVLATLLFATVQASANNEQEE	EDL	60
Db	1	MNEILRIIWSALNAWVVS	ELTRNHTKRASATVKAVLATLLFATVQASANNEQEE	EDL	60
QY	61	YLDPLVLTAVLIVNS	DKEGTGEKVEKVEKVEKVEKVEKVEKVEKVEKVEK	VEK	120
Db	61	YLDPLVLTAVLIVNS	DKEGTGEKVEKVEKVEKVEKVEKVEKVEKVEKVEK	VEK	120
QY	121	NGTNFTYSLKDLT	TSVGTGKLSFANGKNVNTSDTKGLNFAKETAGT	NTVHLN	180
Db	121	NGTNFTYSLKDLT	TSVGTGKLSFANGKNVNTSDTKGLNFAKETAGT	NTVHLN	180


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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; --
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match          99.4%; Score 2980; DB 2; Length 591;
Best Local Similarity 99.3%; Pred. No. 4.3e-118;
Matches 587; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL 60
DB 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL 60
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
DB 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 121 NGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 NGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVDF 240
DB 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVDF 240
QY 241 VRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 300
DB 241 VRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 300
QY 301 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTATV 360
DB 301 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTATV 360
QY 361 SKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDIV 420
DB 361 SKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDIV 420
QY 421 NINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 480
DB 421 NINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 480
QY 481 ITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKSM 540
DB 481 ITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKSM 540
QY 541 MAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591
DB 541 MAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591

RESULT 4
Q9AQF0
ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; --
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match          99.4%; Score 2980; DB 2; Length 591;
Best Local Similarity 99.3%; Pred. No. 4.3e-118;
Matches 587; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL 60
DB 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEQEEDL 60
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
DB 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
QY 121 NGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 NGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
QY 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVDF 240
DB 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVDF 240
QY 241 VRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 300
DB 241 VRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 300
QY 301 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTATV 360
DB 301 TDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTATV 360
QY 361 SKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDIV 420
DB 361 SKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDIV 420
QY 421 NINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 480
DB 421 NINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 480
QY 481 ITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKSM 540
DB 481 ITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKSM 540
QY 541 MAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591
DB 541 MAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591

RESULT 5
Q9JPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; --
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match          98.4%; Score 2952.5; DB 2; Length 592;
Best Local Similarity 98.5%; Pred. No. 6.1e-117;
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEE-QEED 59
DB 1 MNEILRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEE-QEED 59
QY 60 LYDLPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119
DB 60 LYDLPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119
QY 120 QNGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 179
DB 120 QNGTNTFTYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHL 179
QY 180 NGIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVD 239
DB 180 NGIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTASDNVD 239
QY 240 FVRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 299
DB 240 FVRTYDVFELSDATKTTTNNVESKDKNGKTEVKIGAKTSVKEKDKGLVTGDKDGENGS 299
QY 300 STDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTAT 359
DB 300 STDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGQADKFETVTSNTVTFASGKGTAT 359
QY 360 VSKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDET 419
DB 360 VSKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNNVSPSKGKMDET 419
QY 420 VNINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 479
DB 420 VNINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 479
QY 480 RITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKS 539
DB 480 RITNVPVKEGDTVNTVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVAQLPGKS 539
QY 540 MMAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591
DB 540 MMAIGGTYRGEAGYAIYSSISDGGNWIKGTASNSRGRHFGCASASVGYQW 591

RESULT 590
Q9JPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; --
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;
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RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42520.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 95.68; Score 2866.5; DB 2; Length 590;
Best Local Similarity 96.59; Pred. No. 2.5e-113;
Matches 571; Conservative 5; Mismatches 13; Indels 3; Gaps 2;

Qy 1 MNEILRIIWSALNAAVWVSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEDL 60
Db 1 MNKIYRIIWSALNAAVWVSELTRNHTKRASATVKTAVLATLLFATVOASATDEED- 59
Qy 61 YLDPVLRVAVLIIVNSDKGEGEKEVEENSQWAVYFNEKGVLTAREITLKAGNLKIQ 120
Db 60 -LDPVQRTVAVLIIVNSDKGEGEKEVEENSQWAVYFNEKGVLTAGTITLKAGNLKIQ 118
Qy 121 NGTFTYSLKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTHVLN 180
Db 119 NGTFTYSLKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAGTNGDTHVLN 178
Qy 181 GIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVKPGTTASDNVDF 240
Db 179 GIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVKPGTTASDNVDF 238
Qy 241 VRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSS 300
Db 239 VRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSS 298
Qy 301 TDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFETVTSCTNVTFASGKGTATV 360
Db 299 TDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFETVTSCTNVTFASGKGTATV 358
Qy 361 SKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDET 420
Db 359 SKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDET 418
Qy 421 NINAGNTEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDGD-ALNVGSKDNKP 479
Db 419 NINAGNTEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDGDALNVGSKDNKP 478
Qy 480 RITNVAPCKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQYLPK 539
Db 479 RITNVAPCKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQYLPK 538
Qy 540 MMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591
Db 539 MMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 590

RESULT 6
Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RN SEQUENCE FROM N.A.
RP STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.8%; Score 2752.5; DB 2; Length 600;
Best Local Similarity 91.3%; Pred. No. 1.6e-108;
Matches 549; Conservative 16; Mismatches 25; Indels 11; Gaps 3;

Qy 1 MNEILRIIWSALNAAVWVSELTRNHTKRASATVKTAVLATLLFATVOASANN---EEQ 56
Db 1 MNKIYRIIWSALNAAVWVSELTRNHTKRASATVKTAVLATLLFATVOASADNVQASDN 60
Qy 57 EEDLYLDPVLRVAVLIIVNSDKGEGEKEVEENSQWAVYFNEKGVLTAREITLKAGNL 116
Db 61 EEEYELPVVTPAPVLSFYSDAEDTGEKE-VTENTNGIYFDKNGVIKAGTITLKAGNL 119
Qy 117 KIKO-----NGTFTYSLKDLTDLTSVGTKEKLSFANGKNVITSDTKGLNFAKETAG 170
Db 120 KIKQNTDENTNASSFTYSLKELTDLTSVGTKEKLSFGANGKNVITSDTKGLNFAKETAG 179
Qy 171 TNGDTTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVK 230
Db 180 TNGDTTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVK 239
Qy 231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 290
Db 240 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 299
Qy 291 GKDKGENSSVDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFETVTSCTNVTF 350
Db 300 GKDKGENSSVDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFETVTSCTNVTF 359
Qy 351 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNV 410
Db 360 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNV 419
Qy 411 PSKGMDETVMINAGNTEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDGDALNV 470
Db 420 PSKGMDETVMINAGNTEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDGDALNV 479
Qy 471 GSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGL 530
Db 480 GSKDANKPVRTITNVAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGL 539
Qy 531 VQAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 590
Db 540 VQAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 599
Qy 591 W 591
Db 600 W 600

RESULT 7
Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NHHA OUTER MEMBRANE PROTEIN.
 GN NHHA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=EG327;
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 membrane protein of Neisseria meningitidis."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF157605; AAK68866.1; -.
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 91.3%; Score 2739.5; DB 2; Length 594;
 Best Local Similarity 91.8%; Pred. No. 5.5e-108;
 Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNEILRIWNSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEDL 60
 DB 1 MNKIYRIWNSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASTTD---DDDL 57
 QY 61 YLDPVLTAVLVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIQ 120
 DB 58 YLEPVQRTAVLVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIQ 116
 QY 121 -----NGTFTVSLKDLTDLTSVGTPEKLSFSAANGKVNITSDTKGLNFAKETAGTNGD 174
 DB 117 NTNENTNASSFTVSLKDLTDLTSVGTPEKLSFSAANGKVNITSDTKGLNFAKETAGTNGD 176
 QY 175 TTVHLNGIGSTLTDLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 234
 DB 177 TTVHLNGIGSTLTDLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236
 QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDK 294
 DB 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDK 296
 QY 295 GENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTQADKFEVTSCTNVTFSAGK 354
 DB 297 GENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTQADKFEVTSCTNVTFSAGK 356
 QY 355 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
 DB 357 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
 QY 415 KMDETVINAGNIEITRNKNIDIAFMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
 DB 417 KMDETVINAGNIEITRNKNIDIAFMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 476
 QY 474 KDNKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQA 533
 DB 477 DANKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQA 536
 QY 534 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 591
 DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 594

RESULT 8
 Q9JPS2 PRELIMINARY; PRT; 594 AA.
 ID Q9JPS2
 AC Q9JPS2
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE OUTER MEMBRANE PROTEIN GNA992.
 GN GNA992.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EG31;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Broecker M., Hurdit E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 Meningococcus by Whole-Genome Sequencing."
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226379; AAF42528.1; -.
 SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 91.1%; Score 2732.5; DB 2; Length 594;
 Best Local Similarity 91.6%; Pred. No. 1.1e-107;
 Matches 548; Conservative 14; Mismatches 25; Indels 11; Gaps 4;

QY 1 MNEILRIWNSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEDL 60
 DB 1 MNKIYRIWNSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASTTD---DDDL 57
 QY 61 YLDPVLTAVLVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIQ 120
 DB 58 YLEPVQRTAVLVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIQ 116
 QY 121 -----NGTFTVSLKDLTDLTSVGTPEKLSFSAANGKVNITSDTKGLNFAKETAGTNGD 174
 DB 117 NTNENTNASSFTVSLKDLTDLTSVGTPEKLSFSAANGKVNITSDTKGLNFAKETAGTNGD 176
 QY 175 TTVHLNGIGSTLTDLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 234
 DB 177 TTVHLNGIGSTLTDLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236
 QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDK 294
 DB 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGDK 296
 QY 295 GENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTQADKFEVTSCTNVTFSAGK 354
 DB 297 GENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTQADKFEVTSCTNVTFSAGK 356
 QY 355 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
 DB 357 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
 QY 415 KMDETVINAGNIEITRNKNIDIAFMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 473
 DB 417 KMDETVINAGNIEITRNKNIDIAFMTQFSSVSLGAGADAPTLSDVGD-ALNVGSK 476
 QY 474 KDNKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQA 533
 DB 477 DANKPVRTITNAPGVKEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQAIAATAGLVQA 536
 QY 534 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 591
 DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 594

RESULT 9
 Q9JPI3 PRELIMINARY; PRT; 594 AA.
 ID Q9JPI3
 AC Q9JPI3
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE OUTER MEMBRANE PROTEIN GNA992.
 GN GNA992.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
DR EMBL; AF226376; AAF42525.1; -;
DR EMBL; AF226369; AAF42518.1; -;
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B6 CRC64;

Query Match 91.0%; Score 2728.5; DB 2; Length 594;
Best Local Similarity 91.5%; Pred. No. 1.6e-107;
Matches 547; Conservative 14; Mismatches 26; Indels 11; Gaps 4;
Qy 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOASANNEQEEDL 60
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOASTD---DDL 57
Qy 61 YLDPVLRVAVLIVNSDKGEGTEKESVSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 YLEPQRTAVPLSFHDSGEGTEKE-VTEDSNMGVYFDKGVLTAGTITLKAGDNLKIQ 116
Qy 121 -----NCTNFTYSLKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNGD 174
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 NTDENTNASSFTYSLKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
Qy 175 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASKVDVLNAGWNKGVKPGTTA 234
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASKVDVLNAGWNKGVKPGTTA 236
Qy 235 SDNVDFVRYDTVPELSADTKTTTVNVEKONGKTEVKGAKTSVKEKDGKLVTKGDK 294
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 SDNVDFVRYDTVPELSADTKTTTVNVEKONGKTEVKGAKTSVKEKDGKLVTKGDK 296
Qy 295 GENGSTDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFEVTSGTNVTFSAGK 354
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 GENGSTDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFEVTSGTNVTFSAGK 356
Qy 355 GTTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
Qy 415 KMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 KMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSK 476
Qy 474 KDNKPVRTITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNRAGIAQAATAGLVQA 533
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 DANKPVRITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNRAGIAQAATAGLVQA 536
Qy 534 YLPGRSMAIGGTYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYQW 591
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 537 YLPGRSMAIGGTYRGEAGYAGYSSISDGNWIKGTASGNSRGHFGASASVGYQW 594

RESULT 10
Q9JPH7 PRELIMINARY; PRT; 594 AA.
AC Q9JPH7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198, AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
DR EMBL; AF226369; AAF42518.1; -;
DR EMBL; AF226358; AAF42507.1; -;
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 90.7%; Score 2721.5; DB 2; Length 594;
Best Local Similarity 91.6%; Pred. No. 3.1e-107;
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

Qy 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOASANNEQEEDL 60
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : |||
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOANATD---DDL 57
Qy 61 YLDPVLRVAVLIVNSDKGEGTEKESVSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 YLEPQRTAVPLSFHDSGEGTEKESVSDWAVYFNEKGVLTAREITLKAGDNLKIQ 116
Qy 121 -----NCTNFTYSLKDLTDLTSVTEKLSFANGKNVITSDTKGLNFAKETAGTNGD 174
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 NTDENTNASSFTYSLKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
Qy 175 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASKVDVLNAGWNKGVKPGTTA 234
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASKVDVLNAGWNKGVKPGTTA 236
Qy 235 SDNVDFVRYDTVPELSADTKTTTVNVEKONGKTEVKGAKTSVKEKDGKLVTKGDK 294
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 SDNVDFVRYDTVPELSADTKTTTVNVEKONGKTEVKGAKTSVKEKDGKLVTKGDK 296
Qy 295 GENGSTDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFEVTSGTNVTFSAGK 354
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 GENGSTDEGGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFEVTSGTNVTFSAGK 356
Qy 355 GTTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
Qy 415 KMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDG-ALNVGSK 473
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 KMDETVINAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSK 476
Qy 474 KDNKPVRTITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNRAGIAQAATAGLVQA 533
||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 DANKPVRITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNRAGIAQAATAGLVQA 536

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QY 534 YLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGYQW 591
|||||
Db 537 YLPKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGYQW 594
|||||

RESULT 11
QJUPR9
ID QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-WAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 90.7%; Score 2719.5; DB 2; Length 598;
Best Local Similarity 91.0%; Pred. No. 3.8e-107;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNEILRIIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQASANNEDEEDL 60
|||
Db 1 MNKRIIWIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATD ---DDDL 57
|||
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||
Db 58 YLEPQRTAVVLSFRSDKEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIQ 116
|||
QY 121 -----NCTNTYSLKDLTDLTSVGTSEKLSFANGKVNITSDTKGLNFAKETAG 170
|||
Db 117 NTNENTNENTNDSSFTYSLKDLTDLTSVETSEKLSFGANGKVNITSDTKGLNFAKETAG 176
|||
QY 171 TNGDPTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKKRAASVKDVLNAGNKGKVP 230
|||
Db 177 TNGDPTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKKRAASVKDVLNAGNKGKVP 236
|||
QY 231 GTTASDNVDFVRYTDFEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 290
|||
Db 237 GTTASDNVDFVRYTDFEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 296
|||
QY 291 GKDKGENSSDDEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFTVTSNTVTF 350
|||
Db 297 GKDKGENSSDDEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFTVTSNTVTF 356
|||
QY 351 ASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGWNLDKAVAGSSKVISGNYS 410
|||
Db 357 ASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGWNLDKAVAGSSKVISGNYS 416
|||
QY 411 PSKGMDETIVNAGNIIETIRNGKNIDATSWTPQFSSVSLGAGADPTLSVDGD-ALN 469
|||
Db 417 PSKGMDETIVNAGNIIETIRNGKNIDATSWTPQFSSVSLGAGADPTLSVDDEGALN 476
|||
QY 470 VGSKDNKPKVRIITNVPAGVKEGDTVNAQLKGVAQNLNRRIDNVGNAAGIAATAG 529
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Db 477 VGSKDNKPKVRIITNVPAGVKEGDTVNAQLKGVAQNLNRRIDNVGNAAGIAATAG 536
QY 530 LVQAVLPKGSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 589
|||||
Db 537 LVQAVLPKGSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 596
|||||
QY 590 QW 591
|||
Db 597 QW 598
|||

RESULT 12
QJUPTO
ID QJUPTO PRELIMINARY; PRT; 598 AA.
AC QJUPTO;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-WAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 90.2%; Score 2706.5; DB 2; Length 598;
Best Local Similarity 90.4%; Pred. No. 1.3e-106;
Matches 544; Conservative 14; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNEILRIIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQASANNEDEEDL 60
|||
Db 1 MNKRIIWIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATD ---DDDL 57
|||
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||
Db 58 YLEPQRTAVVLSFRSDKEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIQ 116
|||
QY 121 -----NCTNTYSLKDLTDLTSVGTSEKLSFANGKVNITSDTKGLNFAKETAG 170
|||
Db 117 NTNENTNENTNDSSFTYSLKDLTDLTSVETSEKLSFGANGKVNITSDTKGLNFAKETAG 176
|||
QY 171 TNGDPTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKKRAASVKDVLNAGNKGKVP 230
|||
Db 177 TNGDPTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKKRAASVKDVLNAGNKGKVP 236
|||
QY 231 GTTASDNVDFVRYTDFEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 290
|||
Db 237 GTTASDNVDFVRYTDFEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 296
|||
QY 291 GKDKGENSSDDEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFTVTSNTVTF 350
|||
Db 297 GKDKGENSSDDEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFTVTSNTVTF 356
|||
QY 351 ASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGWNLDKAVAGSSKVISGNYS 410
|||
Db 357 ASGKGTATVSKDDQGNITVMYDVNVGDALNVQLNSGWNLDKAVAGSSKVISGNYS 416
|||
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QY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLV 290
|||||
Db 237 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLV 296
|||||
QY 291 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEVTVTSGTNVTF 350
|||||
Db 297 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEVTVTSGTKVTF 356
|||||
QY 351 ASGKGTATVSKDDOGNTVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 410
|||||
Db 357 ASGKGTATVSKDDOGNTVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 416
|||||
QY 411 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN 469
|||||
Db 417 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 476
|||||
QY 470 VGSKDKNKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNIDVNDGNARAGIAQAIAATAG 529
|||||
Db 477 VGSKDKNKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNIDVNDGNARAGIAQAIAATAG 536
|||||
QY 530 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFGASASVGY 589
|||||
Db 537 LQAVYLPKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFGTSASVGY 596
|||||
QY 590 QW 591
||
Db 597 QW 598

RESULT 15
QJPR8
ID QJPR8 PRELIMINARY; PRT; 599 AA.
AC QJPR8
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 15, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -;
DR EMBL: AF157608; AAK68869.1; -;
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;
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Query Match 89.2%; Score 2676; DB 2; Length 599;
Best Local Similarity 89.0%; Pred. No. 2.6e-105;
Matches 536; Conservative 18; Mismatches 34; Indels 14; Gaps 4;
QY 1 MNEILRIIWNLSALNAAVAVSELNRHTRKASATVKTAVLATLLFATVQANATDEDEEE 60
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Db 1 MNKIYRIIWNLSALNAAVAVSELNRHTRKASATVKTAVLATLLFATVQANATDEDEEE- 59
|||||
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEKVEKNSDVAWYFNEKGVLTAREITLKAGDNLIKIKO 120
|||||
Db 60 -LEPVVRSALVIOFMIDKEGGENEST-CNIGWSIYDNNHTLHGATVTLKAGDNLIKIKO 117
|||||
QY 121 -----NGTNFTYSLKDLTDLTSVTEKLSFANGKNVNTSDTKGLNFAKETAG 170
|||||
Db 118 NTNKNWNTNDSPTYSLLKDLTDLTSVETEKLSFANGKNVNTSDTKGLNFAKETAG 177
|||||
QY 171 TNGDVTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNNIKGVKP 230
|||||
Db 178 TNGDVTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGNNIKGVKP 237
|||||
QY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLV 290
|||||
Db 238 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDGKLV 297
|||||
QY 291 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEVTVTSGTNVTF 350
|||||
Db 298 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEVTVTSGTNVTF 357
|||||
QY 351 ASGKGTATVSKDDOGNTVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 410
|||||
Db 358 ASGKGTATVSKDDOGNTVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 417
|||||
QY 411 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDG-DALN 469
|||||
Db 418 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 477
|||||
QY 470 VGSKDKNKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNIDVNDGNARAGIAQAIAATAG 529
|||||
Db 478 VGSKDKNKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNIDVNDGNARAGIAQAIAATAG 537
|||||
QY 530 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFGASASVGY 589
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Db 538 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFGASASVGY 597
|||||
QY 590 QW 591
||
Db 598 QW 599
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Search completed: July 3, 2002, 08:28:45
Job time: 1166 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:07 ; Search time 168.6 Seconds
(without alignments)
389.351 Million cell updates/sec

Title: US-09-771-382-5

Perfect score: 2999
Sequence: 1 MNEILRIIMNSALNAMYVS.....TASGNSRGHCASASVGYQW 591

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	100.0	591	20	AAV23741
2	2999	100.0	591	22	AAU06175
3	2984	99.5	591	20	AAV22702
4	2984	99.5	591	20	AAV23746
5	2984	99.5	591	22	AAU06171
6	2958	98.6	591	21	AAV57045
7	2952.5	98.4	592	20	AAV23737
8	2739.5	91.3	594	21	AAV23740
9	2739.5	91.3	594	21	AAV57044
10	2739.5	91.3	594	22	AAU06174
11	2721.5	90.7	594	20	AAV23739

12	2721.5	90.7	594	22	AAU06179	N. meningitidis BZ
13	2706.5	90.2	598	20	AAV23742	A surface protein
14	2706.5	90.2	598	22	AAU06177	N. meningitidis H1
15	2705.5	90.2	598	20	AAV23738	A surface protein
16	2705.5	90.2	598	22	AAU06178	N. meningitidis BZ
17	2676	89.2	599	20	AAV23743	A surface protein
18	2676	89.2	599	22	AAU06176	N. meningitidis H3
19	2554.5	85.2	592	20	AAV23744	A surface protein
20	2554.5	85.2	592	22	AAU06172	N. meningitidis H4
21	2538.5	84.6	512	22	AAU06182	N. meningitidis PM
22	2467	82.3	589	20	AAV23745	A surface protein
23	2467	82.3	589	22	AAU06173	N. meningitidis P2
24	2447.5	81.6	502	22	AAU06186	N. meningitidis PM
25	2445.5	81.5	592	22	AAU06180	N. meningitidis Z2
26	2416.5	80.6	592	20	AAV27203	Amino acid sequenc
27	2395	79.9	513	22	AAU06183	N. meningitidis H4
28	2230.5	74.4	604	22	AAU06181	N. meningitidis su
29	2096	69.9	433	22	AAU06185	N. meningitidis PM
30	1949	65.0	407	22	AAU06184	N. meningitidis PM
31	1245	41.5	2411	21	AAV23860	Haemophilus influe
32	1243	41.4	2353	17	AAV23856	Haemophilus influe
33	1221	40.7	245	20	AAV27201	Amino acid sequenc
34	1064.5	35.5	1094	21	AAV23858	Haemophilus influe
35	1054.5	35.2	1098	17	AAV23859	Haemophilus influe
36	985	32.8	679	21	AAV23855	Haemophilus influe
37	985	32.8	679	21	AAV23855	Haemophilus influe
38	749.5	25.0	1004	21	AAV23857	Haemophilus influe
39	738.5	24.6	1002	21	AAV23854	Haemophilus influe
40	694.5	23.2	1104	21	AAV23856	Haemophilus influe
41	694.5	23.2	1104	21	AAV23859	Haemophilus influe
42	600	20.0	116	21	AAV37832	Neisseria conserv
43	390.5	13.0	1778	22	AAV2677	Escherichia coli P
44	388	12.9	2314	22	AAV69136	M. catarrhalis tes
45	381.5	12.7	2053	22	AAV69135	M. catarrhalis str

ALIGNMENTS

```
RESULT 1
AAV23741
AAV23741 standard; protein; 591 AA.
XX
AC AAV23741:
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998: 98WO-AU01031.
XX
PR 12-DEC-1997: 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX (UYOU) UNIT QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX WPI, 1999-418754/35.
XX N-PSDB: AAV85793.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
```



```
QY 1 MNEILRIINWSALNMAWVVSSELTNRHTRASATVKTAVLATLTFATVQASANNEOEEDL 60
DB 1 meilriinsalnawvvseltlrhtrkrsatvtktavlatlllfatvgasanneegee1 60
QY 61 YLDPVLRTVAVLIVNSDKREGTEKEKEVEENSDMAVVFENEKGYLTAREITLKAGDNLIKIKO 120
DB 61 yldpvlrtvavllivnsdkegtegekeveensdwayvfnekyvltarelitlkagdnlikixy 120
QY 121 NCTNPFYSLKKDLDTSVGTGTEKLSFANGKNVNTSDPKGLNFAKETAGTNDPTVHLN 180
DB 121 nctnfyyslkkdldtstvgteklsfsangknvnitsdtkglnfaketagtndptvhl 180
QY 181 GIGSTLFDLTLNGATTNTNDVDEKERRAASVADVNAGNINIKGVPPTTASDNVDF 240
DB 181 gigestldtldlntgattntndvdekkrraasvkdvnagwnikgvppttasdnvdf 240
QY 241 VRTYDVEFLSADTKTTTVNVESKDKNGKTEVYKIGAKTSVIREKDKLVTGDKGENSS 300
DB 241 vrtydveflsadtktttvneskdngkktevki gaktsvirekdglvtgdkgenss 300
QY 301 TDEGEGLYTAKKEYIDAVNKAQNRKMTTANQOTGQADKEFTVSGTNVTFASGKTGTATV 360
DB 301 tdegelytakyeyidavnkagmrkmttanqotgqadkefvtsgtnvtfasgkgtatv 360
QY 361 SKDDGNTITVMYDVNVDALNNQLONSGMNLSKAVAGSSGKVIISGNVSPSKGMDFTV 420
DB 361 skddgntitvm ydvnvdalnnqlo nsgmnl skavagssgkviisgnvpsk gmdftv 420
QY 421 NINAGNNIEITRGNKIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKNKPVR 480
DB 421 ninagnnieitrngknidatstmpqfssvslgagadaptlisvdgalnvgs kdknpvr 480
QY 481 ITNVAPGVKEGQVTVNAQIKGYAQNINNRIDVNDGNAKRGIAQAIATAGLVQAYLPGKSM 540
DB 481 itnvapgvkegqvtvnaqikgyaqninnridvndgnaragiagailvqaylpgksm 540
QY 541 MAIGGTYRGEAGYALGYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 591
DB 541 maiggtyrgeagyalgyssisdgmwlikgtasgnsrghfgasasvgyqw 591

RESULT 3
ID AAY27202 standard; Protein: 591 AA.
XX
AC AAY27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX
OS Neisseria meningitidis.
XX
PN WO9936544-A2.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-1B00103.
XX
PR 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
XX (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizsa M, Rappuoli R, Scarlato V;
XX
DR WPI; 1999-444400/37.
XX
DR N-PSDB; AAX99124.
XX
```

```
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AAY27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA:

Query Match 99.5%; Score 2984; DB 20; Length 591;
Best Local Similarity 99.5%; Pred. No. 4.5e-168;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIINWSALNMAWVVSSELTNRHTRASATVKTAVLATLTFATVQASANNEOEEDL 60
DB 1 mneilriinsalnawvvseltlrhtrkrsatvtktavlatlllfatvgasanneegee1 60
QY 61 YLDPVLRTVAVLIVNSDKREGTEKEKEVEENSDMAVVFENEKGYLTAREITLKAGDNLIKIKO 120
DB 61 yldpvlrtvavllivnsdkegtegekeveensdwayvfnekyvltarelitlkagdnlikixy 120
QY 121 NCTNPFYSLKKDLDTSVGTGTEKLSFANGKNVNTSDPKGLNFAKETAGTNDPTVHLN 180
DB 121 nctnfyyslkkdldtstvgteklsfsangknvnitsdtkglnfaketagtndptvhl 180
QY 181 GIGSTLFDLTLNGATTNTNDVDEKERRAASVADVNAGNINIKGVPPTTASDNVDF 240
DB 181 gigestldtldlntgattntndvdekkrraasvkdvnagwnikgvppttasdnvdf 240
QY 241 VRTYDVEFLSADTKTTTVNVESKDKNGKTEVYKIGAKTSVIREKDKLVTGDKGENSS 300
DB 241 vrtydveflsadtktttvneskdngkktevki gaktsvirekdglvtgdkgenss 300
QY 301 TDEGEGLYTAKKEYIDAVNKAQNRKMTTANQOTGQADKEFTVSGTNVTFASGKTGTATV 360
DB 301 tdegelytakyeyidavnkagmrkmttanqotgqadkefvtsgtnvtfasgkgtatv 360
QY 361 SKDDGNTITVMYDVNVDALNNQLONSGMNLSKAVAGSSGKVIISGNVSPSKGMDFTV 420
DB 361 skddgntitvm ydvnvdalnnqlo nsgmnl skavagssgkviisgnvpsk gmdftv 420
QY 421 NINAGNNIEITRGNKIDATSMTPQFSSVSLGAGADAPTLISVDGALNVGSKDKNKPVR 480
DB 421 ninagnnieitrngknidatstmpqfssvslgagadaptlisvdgalnvgs kdknpvr 480
QY 481 ITNVAPGVKEGQVTVNAQIKGYAQNINNRIDVNDGNAKRGIAQAIATAGLVQAYLPGKSM 540
DB 481 itnvapgvkegqvtvnaqikgyaqninnridvndgnaragiagailvqaylpgksm 540
QY 541 MAIGGTYRGEAGYALGYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 591
DB 541 maiggtyrgeagyalgyssisdgmwlikgtasgnsrghfgasasvgyqw 591

RESULT 4
ID AAY23746 standard; Protein: 591 AA.
XX
AC AAY23746;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
DR Surface protein; surface glycoprotein; infection; vaccine;
XX
```

KW immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 PN W09931132-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-AU01031.
 XX
 PR 12-DEC-1997; 97GB-0026398.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 XX (UYOU) UNIV QUEENSLAND.
 XX
 PI Jennings MP, Moxon ER, Peak IRA;
 XX
 DR WPI: 1999-418754/35.
 DR N-PSDB: AAX85798.
 XX
 PT Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1; Page 127-128; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 SQ Sequence 591 AA;

Query Match 99.5%; Score 2984; DB 20; Length 591;
 Best Local Similarity 99.5%; Pred. No. 4.5e-168;
 Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNANWVSELTNRHTRKASATVTAVALTLLEFATVOASANNEQEDDL 60
 DB 1 mkkiyriiwnsalnawvseltrnhtrkasatvtavlatillfatvqasannegeedl 60
 QY 61 YIDPLRLVAVLIIVNSDEKGEKKEVEENSDMAYFNEKGVLTARETTIKAGDLKIKQ 120
 DB 61 yldpqrivaavliivnsdegekegekevendswavyfnekgyltareltikagdnkikq 120
 QY 121 NGNTFYSLKDLDTLTSVGETKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTVHLN 180
 DB 121 ngntfyslkkdltdltsvgteklsfsangknvntstdtkglnfaketaagtngdttvhl 180
 QY 181 GIGSLTDTLTNTGATVNTNDNTDDEKRRASVKDVLNAGMNIRKGVKPGTASDNVDF 240
 DB 181 gisgsltdtllntgactvntndndvdekkraasvkdvlmagmnirkgykpgtasadndf 240
 QY 241 VRTYPTVFELSDTTRTVNVNVEKNGKTEYKIGAKTSYIKERKGLVGTGDKENGSS 300
 DB 241 vrtlyptvfelsdtktltnvveskngktekigaktsvlikekgklytgdkengss 300
 QY 301 TDEGGLVTAKFVIDAVNKAQRMAKTTTANGOTGOADFEETVTSCTNVTFAAGKGTATV 360
 DB 301 tdegglvtakevidavnkagwrmktcttanqgtgqadkfetvstnvtfaagkgtatv 360
 QY 361 SKDDGNTTVMYDVNVGDALNVNQLNSGWNLSKAVAGSSGKVSIGNVSPSKGMDETV 420
 DB 361 skddgnttvmvdyvngdalanvnglqnsqwnlskavagssgkvsignvspskgmdetv 420
 QY 421 NINAGNNFEITRNGKNIDIAITMTPOFSSVSIGAGADAPLTSLVDGDALNVGSKKNKPPR 480
 DB 421 ninaagnfeitrngknidiatmtppfssvsigagadapltslvdgdalnvsgkknkppr 480

QY 481 ITTNAPGVKEGDVNTVNAQLKVAQNLNNRIDNVGNARAGIAQATATAGLVQAYLPCKSM 540
 DB 481 itnvapgvkegdvntvnaqlkvaqnlmnridnvdgnaaragiagataglvqaylpcksm 540
 QY 541 MAIGGTYRGAGYATIGYSSISDGNMIIKGTASGNSGHRGASASVYQW 591
 DB 541 maiggtyrgaayaigysisdgnwlikglaasgrhigasasvyqyw 591

RESULT 5
 AAU06171
 ID AAU06171 standard; Protein; 591 AA.
 XX
 AC AAU06171;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
 XX
 KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
 XX
 OS Neisseria meningitidis strain PMC21.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..51
 FT /label= Signal_peptide
 FT 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT 51..108
 FT /label= V1
 FT /note= "Variable region 1"
 FT 52..591
 FT /label= Mature_Nhha
 FT /note= "Predicted mature protein, specifically
 claimed in claim 12."
 FT 109..120
 FT /label= C2
 FT /note= "Conserved region 2"
 FT 121..124
 FT /label= V2
 FT /note= "Variable region 2"
 FT 125..188
 FT /label= C3
 FT /note= "Conserved region 3"
 FT 189..210
 FT /label= V3
 FT /note= "Variable region 3"
 FT 211..229
 FT /label= C4
 FT /note= "Conserved region 4"
 FT 230..236
 FT /label= V4
 FT /note= "Variable region 4"
 FT 237..591
 FT /label= C5
 FT /note= "Conserved region 5"

W0200155182-A1.
 PD 02-AUG-2001.
 XX
 PD 25-JAN-2001; 2001WO-AU00069.
 XX
 PR 25-JAN-2000; 2000US-0177917.
 XX
 PA (UYOU) UNIV QUEENSLAND.
 XX
 PI Peak IRA, Jennings MP;
 XX
 DR WPI: 2001-488774/53.
 DR N-PSDB: AAS09161.

XX New Nhma surface antigen polypeptides and polynucleotides from
 PT *Neisseria meningitidis*, useful in producing vaccines for treating or
 PT preventing broad spectrum of *Neisseria meningitidis*.
 XX
 XX
 PS Claim 9: Fig 1: 91pp: English.

CC The present invention relates to the isolation of novel *Neisseria*
 CC *meningitidis* mutant polypeptides of the surface antigen Nhma
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
 CC characterized by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of *N. meningitidis*, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of *N. meningitidis* strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhma
 CC from *N. meningitidis* strain PMC21 is 1 of 10 Nhma polypeptide sequences
 CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in
 CC the present invention.
 XX
 XX Sequence 591 AA:

Query Match 99.5%; Score 2984; DB 22: Length 591;
 Best Local Similarity 99.5%; Pred. No. 4, 5e-168;
 Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEIIRIINNSALNMAVVSSELRNHTKRSATVKTAVLATLLEFATVQASANNEOEEDL 60
 DB 1 mmkylrllnsalnawvvseltlrhltkrasatvktavlatllefavqsannegeedl 60
 QY 61 YLDPVLRVAVLIVNSDEKGEKEKEVEENSDMAVVFENEKGVLTAREITLKAGDNLKIKQ 120
 DB 61 yldpvrvaavlivnsdekgekekeveensdawayfnekgyvltareitlckagdnlikq 120
 QY 121 NGTNFTYSKAKDLDLTSTGTEKLSFANGKNVNTSDPKGLNFAKETAGTNGDTVHLN 180
 DB 121 ngtnftyslkakldltstgteklsfsangknvntsdtkglnfaketagtngdtvhl 180
 QY 181 GIGSTLTDLTLMWATNTVNTDDEKRRASVQDVNAGNIRKGVPGTASDNVDF 240
 DB 181 gigtstltdltmlwattntvntddekrrasvqdvnnagnikgvpgtassdnvdf 240
 QY 241 VRTYDVEFLSADTKTTTVNVEKDKGKTEVKGAKTSVIREKDGKLVYTGDKGENSS 300
 DB 241 vrtydveflsadtktttvneskdngkktvkgaktsvirekdglvtygdkgenss 300
 QY 301 TPEGELVYAKREVDAVKNKAGRMKTTTANGOTGADKEFTYSGTNTVPASGKTITATV 360
 DB 301 tpegelvyakevldavknkagrmktttlangotgadkeftysgtntvpasgkttatv 360
 QY 361 SKDDGNTIVMYDVNYGDALNNOLONGMNLDSKAVASSGCVISGNTSPSKGKMDERV 420
 DB 361 skddgntivmydvnygdalnnolongsnmnlkskavassgcvisgntspskgkmderv 420
 QY 421 NINAGNIEITRNKNIDIASMTPOFSSVSISAGADAPTLVSDGALNVGSKKDKR 480
 DB 421 ninagnieitrnknidiasmtpfssvsisagadaptlvsdgalnvsgkdkdkr 480
 QY 481 IINVAPGVESGVTNVAOLKGYAQNINNRIDVNDGNARAGIAQATITAGLVQATLFGKSM 540
 DB 481 iinvapgvsgvtvnvaolkgyaqninnrldvndgnaragiatitaglvqatlfpgksm 540
 QY 541 MAIGGTYGEGAGYAIGSYISDGNMIIKGTASGNSRHFSGASASVQW 591
 DB 541 maiggttygeagyaigsysisdgnmiikgtasgnsrhfgasasvqgw 591

RESULT 6
 AA57045
 ID AA57045 standard: Protein: 591 AA.

XX
 AC AA57045;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE BAS029 amino acid sequence from *N. meningitidis* strain H44/76.
 XX
 KW BAS029; *Neisseria meningitidis*; surface fibrin protein; HSF; diagnosis;
 KW infection; treatment; prevent; antibacterial drug.
 XX
 XX *Neisseria meningitidis*.

Key Location/Qualifiers
 FT Misc-difference 90
 FT /note= "Encoded by AAT"
 FT Misc-difference 92
 FT /note= "Encoded by GAT"
 FT Misc-difference 98
 FT /note= "Encoded by AAC"
 FT Misc-difference 108
 FT /note= "Encoded by AATC"
 FT Misc-difference 123
 FT /note= "Encoded by ACA"
 FT Misc-difference 269
 FT /note= "Encoded by AAA"
 FT Misc-difference 389
 FT /note= "Encoded by CGT"

PN W0958683-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-EP03255.
 XX
 PR 13-MAY-1998; 98GB-0010276.
 XX

PA (SMK) SMTTKLINE BECHAM BIOLOGICALS.

PI Ruelle J;

DR WPI: 2000-053103/04.
 DR N-PSDB: AA239865.

PT New polypeptide from *neisseria meningitidis* useful for diagnosis,
 PT treatment or prevention of bacterial infections in mammal

PS Claim 4: Fig 2: 74pp: English.

CC This is the *Neisseria meningitidis* BAS029 amino acid sequence from
 CC serogroup B strain H44/76. The BAS029 protein is homologous to the
 CC Haemophilus influenzae surface fibrin (HSF) protein. The invention
 CC relates to BAS029 polynucleotide sequences (AA239864-239865) and
 CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.
 CC BAS029 polypeptides are useful in a method of diagnosing a *Neisseria*
 CC *meningitidis* infection in a mammal. Compositions containing BAS029
 CC polynucleotides and polypeptides are useful for generating an immune
 CC response in an animal. A therapeutic composition comprising an antibody
 CC directed against BAS029 is useful in treating humans with *Neisseria*
 CC *meningitidis* disease. The polynucleotide is useful in the diagnosis of
 CC the stage of infection, type of infection, susceptibility to an
 CC infection which results from increased or decreased expression of the
 CC polynucleotide, and for therapeutic or prophylactic purposes,
 CC particularly genetic immunisation. Antibodies against BAS029
 CC polynucleotides and polypeptides are also useful for treating infections
 CC particularly bacterial infections. The protein is useful in the
 CC screening and development of antibacterial drugs. Fused recombinant
 CC protein is useful for the stimulation of the immune system of an organism
 CC receiving the protein.
 XX
 XX Sequence 591 AA:

Query Match 98.6%; Score 2958; DB 21: Length 591;

DE A surface protein of Neisseria meningitidis.
 XX Surface protein: surface glycoprotein; infection; vaccine;
 KW immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 PN W09931132-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-AU01031.
 XX
 PR 12-DEC-1997; 97GB-0026398.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 PA (OYUO) UNITV QUEENSLAND.
 XX
 PI Jennings MP, Moxon ER, Peak IRA;
 XX
 DR WPI: 1999-418754/35.
 DR N-PSDB: AAX85792.
 XX
 PT Neisseria meningitidis surface proteins useful for treating N.
 PT meningitidis infections
 XX
 PS Claim 1; Page 100-101; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 CC
 SO Sequence 594 AA:

Query Match 91.3%; Score 2739.5; DB 20; Length 594;
 Best Local Similarity 91.8%; Pred. No. 1.2e-153;
 Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNEILRIIWNGLNMAVYVSELTNRNTRKASATVATLTLFATVQASANNEOEEDL 60
 DB 1 mkkiyrlwnsalnawavseltrnhckrasatavataiacllfaavgastld--dddl 57
 QY 61 YLDPVLRVAVLVNSDKRGTEKEKEVENSDMAVYENFKGVTAREILKAGDNLKIKO 120
 DB 58 ylepqvtaavsvftrsdkegke- vtedsmgyvfdkkytltagtlckagdnlkikq 116
 QY 121 -----NGTNFTYSLKKDLTDLTSVTEKLSFANGNKVNITSDFGLNFAKETAGTNGD 174
 DB 117 ntneutnasstfyslkldtldtsvgtelksfsansknitsdctqlnfakktactnd 176
 QY 175 TVVHLNGICSTLTDLTLNLTGATNTVNDVTDDEKKRAASVQDVNLAGNNIKGVPGTTA 234
 DB 177 tcvhngjstldtldlmgatlnvndvtddekkraasvqdvlnagynikgvkpgtta 236
 QY 235 SUNVDPVRVRYDVEFLSATRTTTTVNVEKDKGKTEVIGAKTSYIKRKDKGLVNGXK 294
 DB 237 shnvdyrvrydveflsatrttttvnveskdkngkrevlignaktsyikdkglvngkxk 296
 QY 295 GENGSTDEGEGLVTAKEYIDA VNKAGMRKTTTANGQTQADKFEFTVTSGTWTFASGK 354
 DB 297 gendstckgeglvtakeyidavnkagvrmktttangqgqadkfctvscgnvltasgk 356
 QY 355 GTTATVSKDDQGNITVYVNVGDALNVNQLONGSNLDSKAVAGSSGKAVISGNVSPSKG 414
 DB 357 gttatvskddqgnitvymvngvdalnvnqlqsgvsnldskavagssgkavvisgnvpskxg 416

QY 415 KMEFVNINAGNNIEITRNGKNIDIA TSMTPQFSSVSLGADAPLTVSDG-ALNWGSK 473
 DB 417 kmefvniagnnielttrngknidiatmtbpqfssvsjagadaprlsvddegalnvgsk 476
 QY 474 KDNKPVRTTNVAPGKVEGDTVNYAOLKGYAQNINRDNVDGNARAGIAOATATAGLVQA 533
 DB 477 dknkpvrttnvapgkvegdtnvayolkgyaqninrhdvndgnaragialagatlvga 536
 QY 534 YLPGRSMMAIGCGTYRGEAGYATGSSISDGGWIIKGTASGRGHPGASASVGYOW 591
 DB 537 ylpgrsmma1gg9cyrgeagyalgysisdggwllkgtasgrghfgasasvgyow 594

RESULT 9
 AAY57044
 ID AAY57044 standard; Protein; 594 AA.
 XX
 AC AAY57044;
 XX
 DT 21-FEB-2000 (first entry)
 XX
 DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
 XX
 KW BASB029; Neisseria meningitidis; surface fibrin protein; HSF; diagnosis;
 KW infection; treatment; prevent; antibacterial drug.
 XX
 OS Neisseria meningitidis.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 104
 FT "/note="Encoded by AATC"
 XX
 PN W09958683-A2.
 XX
 PD 18-NOV-1999.
 XX
 PF 07-MAY-1999; 99WO-EP03255.
 XX
 PR 13-MAY-1998; 98GB-0010276.
 XX
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 XX
 DR Ruelle J;
 DR WPI: 2000-053103/04.
 DR N-PSDB: AAZ39864.
 XX
 PT New polypeptide from neisseria meningitidis useful for diagnosis,
 PT treatment or prevention of bacterial infections in mammal
 PS Claim 4; Fig 2; 74pp; English.
 XX

This is the Neisseria meningitidis BASB029 amino acid sequence from serogroup B strain ATCC13090. The BASB029 protein is homologous to the Haemophilus influenzae surface fibrin (HSF) protein. The invention relates to BASB029 polynucleotide sequences (AAZ39864-239865) and polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a Neisseria meningitidis infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with Neisseria meningitidis disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.


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FT      /note= "Conserved region 2"
FT      117..126
FT      /label= V2
FT      /note= "Variable region 2"
FT      127..190
FT      /label= C3
FT      /note= "Conserved region 3"
FT      191..212
FT      /label= V3
FT      /note= "Variable region 3"
FT      213..231
FT      /label= C4
FT      /note= "Conserved region 4"
FT      232..238
FT      /label= V4
FT      /note= "Variable region 4"
FT      239..594
FT      /label= C5
FT      /note= "Conserved region 5"
FT      WO20015182-A1.
XX      PN
XX      PD
XX      02-AUG-2001.
XX      PF
XX      25-JAN-2001; 2001WO-AU00069.
XX      PR
XX      25-JAN-2000; 2000US-0177917.
XX      PA
XX      (UYOU ) UNIV QUEENSLAND.
XX      PI
XX      Peak IRA, Jennings MP;
XX      DR
XX      WPI: 2001-488774/53.
XX      DR
XX      N-PSDB: AAS09169.
XX      PT
XX      New Nhma surface antigen polypeptides and polynucleotides from
XX      PT
XX      Neisseria meningitidis, useful in producing vaccines for treating or
XX      PT
XX      preventing broad spectrum of Neisseria meningitidis .
XX      PS
XX      Claim 9; Fig 1; 91pp; English.
XX      CC
XX      The present invention relates to the isolation of novel Neisseria
XX      CC
XX      meningitidis mutant polypeptides of the surface antigen Nhma
XX      CC
XX      (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX      CC
XX      characterised by deletions of non-conserved amino acids, particularly
XX      CC
XX      the deletion of variable regions. The deletion mutants are useful in
XX      CC
XX      diagnostics, therapeutic and prophylactic vaccines against a broader
XX      CC
XX      spectrum of N. meningitidis, and in designing and/or screening of
XX      CC
XX      medicaments. The mutant proteins when used as a vaccine can effectively
XX      CC
XX      immunise against a broader spectrum of N. meningitidis strains than
XX      CC
XX      would be expected from a corresponding wild-type surface antigen.
XX      CC
XX      The present sequence representing the wild type surface antigen Nhma
XX      CC
XX      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX      CC
XX      the present invention.
XX      CC
XX      Sequence      594 AA:
SQ

```

```

Query Match      90.7%: Score 2721.5; DB 22; Length 594;
Best Local Similarity 91.6%: Pred. No. 1.3e-152;
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

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QY      1 MNEILRIITWNSALNAAWVVSFLTRNHRKRASATKATLALTLATVQASANNEQEDL 60
DB      1 muklyriiwsalnawvvseltrnhkrasatvatavatlalatyqanad--dddl 57
QY      61 YLDVLTVAALYINSDKEGKEKVEENDMAVYENKGVLTARETTLKAGDNLKIKO 120
DB      58 yldvltvavllsfrsdeggekegedt-snwavyfiekrvllkagatllkagdnllkikg 116
QY      121 -----NCTNFYSLKRDLDLTJSGTEKLSFSANGKNVNTSDPTKGLNFAKETAGTNGD 174
DB      121 -----NCTNFYSLKRDLDLTJSGTEKLSFSANGKNVNTSDPTKGLNFAKETAGTNGD 174

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DB      117 ntuenndsflysllkklldltsvetekisfgangnkvnltsldtqlnfeketagtngd 176
QY      175 TTVHLNGIGSTFTDPLNTGATNTVNDNTVDDEKRRASVYKDVNLNGMNIKGVKPGTTA 234
DB      177 pcvhnglgsclldtllntgatctvndnvtddckkraasvkvdylnagwnlkgykpgtta 236
QY      235 SDNVDVARTYDVEFLSADTKTTTVNESKDNKGRKTEVKIGAKTSVIKEDGKLVGTGDK 294
DB      237 sdndvfrtyltvflsadtktltvneskdngrkktvksvllkekqkvlvtgkqk 296
QY      295 GENSSSTDEGGLYTAKEVIDAVNKKACRMKMTTANOTGTGADKFEVYTSSTNTTFPSGK 354
DB      297 dengsstdegeglvtakevidavnkagwrmktltanqtgqadkfetvstqnlvtfsqk 356
QY      355 GTTATVSKDDGNTTVMVDVWGDALNNVNOJNSGMNIDSKAVVSSGKTVSGNVSPSKG 414
DB      357 gttatvskddgntltvkvdydvovgdalnvnqngsqwnlidsavagssgkvtsngvpskg 416
QY      415 KMDETVINAGNNIEITRNGKNIDIAATSMRPFSSVSLGACADAPPLSYDGD-ALNMGSK 473
DB      417 kmdetvlnagnnleltrngknidiatstmapfssvslgagadapllsvddegalnvgsk 476
QY      474 KDNKPVRTTNVAPGVKESDVTNVAQLKGVQNLNKRIDNVGNKARAGIAAIAATAGLVQA 533
DB      477 dlnkpvrltnvapgvksgdvtnvaqlkgyvaqnlmnrldnvgnaraglaaglaiaaglvqa 536
QY      534 YLPGKSMVAIGGTYRGAGYAIGYSSISDGGNMITGTASGRGHGASAVGYOW 591
DB      537 ylpgksmmaigdytgrgeaygaigysisdggnmlkgytasgrghgasaavgyow 594

RESULT 13
AAV23742
ID      AAV23742 standard; Protein: 598 AA.
XX      AC
XX      AAV23742:
XX      DT
XX      08-SEP-1999 (first entry)
XX      DE
XX      A surface protein of Neisseria meningitidis.
XX      KW
XX      Surface protein; surface glycoprotein; infection; vaccine;
XX      KW
XX      Immunoreactive peptide.
XX      OS
XX      Neisseria meningitidis.
XX      PN
XX      W09931132-A1.
XX      PD
XX      24-JUN-1999.
XX      PF
XX      14-DEC-1998; 98WO-AU01031.
XX      PR
XX      12-DEC-1997; 97GB-0026398.
XX      PA
XX      (ISIS-) ISIS INNOVATION LTD.
XX      PA
XX      (UYOU ) UNIV QUEENSLAND.
XX      PI
XX      Jennings MP, Moxon ER, Peak IRA;
XX      DR
XX      WPI: 1999-418754/35.
XX      DR
XX      N-PSDB: AAX85794.
XX      PT
XX      Neisseria meningitidis surface proteins useful for treating N.
XX      PT
XX      meningitidis infections
XX      PS
XX      Claim 1; Page 108-110; 132pp; English.
XX      CC
XX      The present sequence represents a surface protein of Neisseria
XX      CC
XX      meningitidis which is approximately 62 kDa. The N. meningitidis
XX      CC
XX      surface glycoproteins, nucleic acids, the primers and optionally
XX      CC
XX      a thermostable polymerase, or antibodies are useful in a kit for
XX      CC
XX      the detection or diagnosis of N. meningitidis infection in humans.
XX      CC
XX      The N. meningitidis surface glycoproteins can also be used to

```

CC prevent or treat *N. meningitidis* infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.

XX Sequence 598 AA:

Query Match 90.2%; Score 2706.5; DB 20; Length 598;
 Best Local Similarity 90.5%; Pred. No. 1e-151;
 Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

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QY 1 MNEILRIINNSALINAWVVSELTRNHTKRASATVKATVATLTLFATVQASANNEQEDL 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 mkiylriwmsalawvsvseltrnhtkrasatvatlatllfatvganad---dddl 57

QY 61 YLDPLVARTAVILVNSDKGTGEGKEVEENSDMAVVFNEGCVLTAEETIKAGDNLIKQ 120
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 58 ylepvgrtavlvsfrsdekgteqged-snavyidekrvllkagallkagdnlikq 116

QY 121 -----NGTNYSLKKDLTDLTSVGTETKLSFSAANGKNVINSDFKGLNFAKETAG 170
  |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 ntntentntndsfyslkkdltdltsveteklsifgankvnltsdtkglnfaketag 176

QY 171 TNGDTRVHLNGIGSTLTDPLTNGATTNVTNDVTDDEKKRAASVYKDVLAGNNIKGVK 230
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 177 tngdtrvhlnglsgstltdclntgatntvndvndvtddekkraasvkvdlvlnagvnlkgvkr 236

QY 231 GTTASNDVFRITVYVERLSADTKTTTVNVEKDKNGKTEVIGAKTSYIKRDKGLVT 290
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 237 gttasndvfritydvefrlsadtkltlvvesekdngkktvkvigaktvikekdqklyv 296

QY 291 GKDKGENSGSTDEGLVTAKEVIDAVNKGAMKTTTANNGOTGADKPEVTNSGTNVVF 350
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 297 gkdkengsgstdegevlvakevidavnkagvrmkcltanngtqgadtclvtsqtklyv 356

QY 351 ASGKGTATVSKDDQCNITVMYDVNVDALINVLQNSGNLDSKAVAGSSGKVISGNVS 410
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 357 asgngtatsvskddqgnltvkvdyvngdalinvglnsgnldskavagssgkvisgnvs 416

QY 411 PSKGKDETVNINAGNNIETTRNGKNIDTASMTPOFSSVSLGADAPTLVSVDG-ALN 469
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 417 pskgkndetvnlagnnielttrngknidatmtcpqfssvslgagadaptlvsddegah 476

QY 470 VGSKKNKRPVTRTNVAPGVKEGDVTNVAQLKGAQNLNRRIDVDNARRAGIAQATATAG 529
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Db 477 vgskdnkprvtrtnvapgvegdvtvnaqlkgyaqlnrridvdnarraglaqatag 536

QY 530 LVQAVLPGRSKMAIGGTYRGEAGYAIIGYSISIDCGNMIIKGTASGNSRCHFGASASGV 589
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Db 537 lagaylpgrskmmaiggtyrgeagaylgysslsidcgnmwikgtasgnsrghfgasasgv 596

QY 590 QW 591
  ||:
Db 597 qw 598

```

RESULT 14

ID AAU06177 standard; Protein; 598 AA.

AC AAU06177;

DT 24-OCT-2001 (first entry)

DE *N. meningitidis* H15 surface antigen Nhma polypeptide sequence.

KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.

OS *Neisseria meningitidis* strain H15.

XX Key Location/Qualifiers

FT Region 1..50 /label= C1

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FT FT /note= "Conserved region 1"
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  FT /label= V1
  FT /note= "Variable region 1"
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  FT /label= C2
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  FT /label= V2
  FT /note= "Variable region 2"
  FT Region 131..194
  FT /label= C3
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  FT /label= V3
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  FT /label= C4
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  FT Region 236..242
  FT /label= V4
  FT /note= "Variable region 4"
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  FT /label= C5
  FT /note= "Conserved region 5"

PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PD 25-JAN-2001; 2001MO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
PI WPI; 2001-488774/53.
XX
DR N-PSDB; AAS059167.
XX
PT New Nhma surface antigen polypeptides and polynucleotides from
  PT Neisseria meningitidis, useful in producing vaccines for treating or
  PT preventing broad spectrum of Neisseria meningitidis -
  PS Claim 9; Fig 1; 91pp; English.
XX
XX
XX The present invention relates to the isolation of novel Neisseria
  CC meningitidis mutant polypeptides of the surface antigen Nhma
  CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
  CC characterised by deletions of non-conserved amino acids, particularly
  CC the deletion of variable regions. The deletion mutants are useful in
  CC diagnostics, therapeutic and prophylactic vaccines against a broader
  CC spectrum of N. meningitidis, and in designing and/or screening of
  CC medicaments. The mutant proteins when used as a vaccine can effectively
  CC immunise against a broader spectrum of N. meningitidis strains than
  CC would be expected from a corresponding wild-type surface antigen.
  CC The present sequence representing the wild type surface antigen Nhma
  CC from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences
  CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
  CC the present invention.
XX
XX Sequence 598 AA:
SQ

```

Query Match 90.2%; Score 2706.5; DB 22; Length 598;

Best Local Similarity 90.5%; Pred. No. 1e-151;
 Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

```

QY 1 MNEILRIINNSALINAWVVSELTRNHTKRASATVKATVATLTLFATVQASANNEQEDL 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 mkiylriwmsalawvsvseltrnhtkrasatvatlatllfatvganad---dddl 57

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OY 61 YLDPVLRVAVLIIVNSDEKTEGKEKEVENSMDWAYFNEKGVLFAREITLAKGDNLIKIQ 120
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Db 58 ylepyrtravlsfrsfdckgeygeked -snwayfidekrvlykagaltlkagdnllklyk 116
OY 121 -----NCTNFTYSLKKDLTDLTIVSGTEKLSFSANGKNVITSTQKLNPKETAG 170
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 117 ntneuntenntdsfitylkkdltdltsveleklsfganghkvntsdtkglnfaketaag 176
OY 171 TNGDPTVHLNGISLTPTLTINTGATVNTNDNVTDDEKKRAASAKVDLNGMNIKGYKP 230
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 177 tngdptvhlngisltlcltllntgaltvntdnvdekkraasakvdlngmnikgykp 236
OY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKGKRTTEYKIGAKTSVIREKDKGLVT 290
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 237 gttasdnvdfvrydtveflsadtktttvnveskngkrtteykgaktsvirekdkglvt 296
OY 291 GKDKGENSSSTDEGGLVTAKEVIDAVNKAQRMTTANQOTGQADFEVYTSCTNVT 350
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 297 gkdkgenssstdegeglvtakevidavnkagwrmttanqotgqadkfeytsqtkvlf 356
OY 351 ASGKGTATVSKDDOGNTTVMVDVNGDALNVNOLONGSMNIDSKAVAGSSGKVTSGNVS 410
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 357 asnggtatvskddognltvkvdydvngdahnvnglqnsqwnldskavagssgkvlsqnv 416
OY 411 PSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSPVGD-ALN 469
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 417 pskgmdetvlnagnnieitrngknidiatstmpofssvslgagadaptlsvddegaln 476
OY 470 VGSKKDNKPVRTITNAPGVKESDVTNVAOLKGVAONLNRRIDNVGNARAGIAOLAATAG 529
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 477 vgskdanpvriltvnagpvksgdvtnvaqlkyvaqnlmrridnvgnaraglaqalaatag 536
OY 530 LVOAVLPKSMMAIGGGRYRGAGYAIGYSSISDGNMNIKGTAGSNGRGHGASASGY 589
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 537 laqaylpkssmmaiggyrgygeagyaigysslstgmnwlykgtasngsrghfgasasvgy 596
OY 590 QW 591
   ||
Db 597 qw 598

RESULT 15
AA23738
ID AAY23738 standard; Protein: 598 AA.
XX
AC AAY23738;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
   immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN MO9931132-A1.
PD 24-JUN-1999.
PE 14-DEC-1998; 98WO-A001031.
PR 12-DEC-1997; 97GB-0026398.
PA (ISIS-) ISIS INNOVATION LTD.
   (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI: 1999-418754/35.
XX
DR N-PSDB; AAX85790.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
```

```
PT meningitidis infections
XX
PS Claim 1, Page 91-93; 132pp: English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 90.2%; Score 2705.5; DB 20; Length 598;
Best Local Similarity 90.4%; Pred. No. 1.2e-151;
Matches 544; Conservative 14; Mismatches 29; Indels 15; Gaps 4;

OY 1 MNEILRIIWSALNMYVSELRHTKRASATVKTAVLATLTPATVOASNNNEQEDL 60
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 1 mkslriiwsalna myvselrhtkrasatvktavlatltpatvoasnnneqedl 57

OY 61 YLDPVLRVAVLIIVNSDEKTEGKEKEVENSMDWAYFNEKGVLFAREITLAKGDNLIKIQ 120
   |||||  |||  |||||  |||  |||||  |||  |||||  |||  |||||  |||
Db 58 ylepyrtravlsfrsfdckgeygeked -snwayfidekrvlykagaltlkagdnllklyk 116
OY 121 -----NCTNFTYSLKKDLTDLTIVSGTEKLSFSANGKNVITSTQKLNPKETAG 170
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Search completed: July 3, 2002, 08:09:09
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:17 ; Search time 64.11 Seconds

(without alignments)
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Title: US-09-771-382-5

Sequence: 1 MNEILRIINMSALNAMYVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents.AA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2999	100.0	591	US-09-377-155-11	Sequence 11, Appl
2	2999	100.0	591	US-09-669-974-11	Sequence 11, Appl
3	2984	99.5	591	US-09-377-155-21	Sequence 21, Appl
4	2984	99.5	591	US-09-669-974-21	Sequence 21, Appl
5	2952.5	98.4	592	US-09-377-155-2	Sequence 2, Appl
6	2952.5	98.4	592	US-09-669-974-2	Sequence 2, Appl
7	2739.5	91.3	594	US-09-377-155-9	Sequence 9, Appl
8	2739.5	91.3	594	US-09-669-974-9	Sequence 9, Appl
9	2721.5	90.7	594	US-09-377-155-7	Sequence 7, Appl
10	2721.5	90.7	594	US-09-669-974-7	Sequence 7, Appl
11	2706.5	90.2	598	US-09-377-155-13	Sequence 13, Appl
12	2706.5	90.2	598	US-09-669-974-13	Sequence 13, Appl
13	2705.5	90.2	598	US-09-377-155-5	Sequence 5, Appl
14	2705.5	90.2	598	US-09-669-974-5	Sequence 5, Appl
15	2676	89.2	599	US-09-377-155-15	Sequence 15, Appl
16	2676	89.2	599	US-09-669-974-15	Sequence 15, Appl
17	2554.5	85.2	592	US-09-377-155-17	Sequence 17, Appl
18	2554.5	85.2	592	US-09-669-974-17	Sequence 17, Appl
19	2467	82.3	589	US-09-377-155-19	Sequence 19, Appl
20	2467	82.3	589	US-09-669-974-19	Sequence 19, Appl
21	1245	41.5	2411	US-09-268-347-36	Sequence 36, Appl
22	1243	41.4	2353	US-09-377-155-33	Sequence 33, Appl
23	1243	41.4	2353	US-08-913-942-4	Sequence 4, Appl
24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
25	1242	41.4	2354	US-09-268-347-30	Sequence 30, Appl
26	1180.5	39.4	607	US-08-409-995-6	Sequence 6, Appl
27	1180.5	39.4	607	US-08-685-467-6	Sequence 6, Appl

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32	1054.5	35.2	1098	US-08-409-995-2	Sequence 2, Appl
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35	1054.5	35.2	1098	US-08-913-942-32	Sequence 32, Appl
36	1054.5	35.2	1098	US-09-669-974-32	Sequence 32, Appl
37	1054.5	35.2	1098	US-09-268-347-44	Sequence 44, Appl
38	1036.5	34.6	658	US-08-409-995-5	Sequence 5, Appl
39	1036.5	34.6	658	US-08-685-467-5	Sequence 5, Appl
40	1036.5	34.6	658	US-08-913-942-5	Sequence 5, Appl
41	985	32.8	679	US-09-268-347-26	Sequence 26, Appl
42	985	32.8	679	US-09-268-347-30	Sequence 30, Appl
43	749.5	25.0	1004	US-09-268-347-30	Sequence 30, Appl
44	738.5	24.6	1002	US-09-268-347-24	Sequence 24, Appl
45	694.5	23.2	1104	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1	US-09-377-155-11
Sequence 11	Application US/09377155
Patent No. 6197312	
GENERAL INFORMATION:	
APPLICANT: PEAK, Ian Richard Anselm	
APPLICANT: JENNINGS, Michael Paul	
APPLICANT: MOXON, E. Richard	
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN	
FILE REFERENCE: 065064/0128	
CURRENT APPLICATION NUMBER: US/09/377,155	
CURRENT FILING DATE: 1999-08-19	
PRIOR APPLICATION NUMBER: PCT/AU98/01031	
PRIOR FILING DATE: 1998-12-14	
PRIOR APPLICATION NUMBER: GB 9726398.2	
PRIOR FILING DATE: 1997-12-12	
NUMBER OF SEQ ID NOS: 33	
SOFTWARE: Patentin Ver. 2.0	
SEQ ID NO 11	
LENGTH: 591	
TYPE: PRT	
ORGANISM: Neisseria meningitidis	
US-09-377-155-11	
Query Match	100.0%; Score 2999; DB 4; Length 591;
Best Local Similarity	100.0%; Pred. No. 4.8e-224;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
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RESULT 2

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US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11
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Query Match 100.0%; Score 2999; DB 4; Length 591;

Best Local Similarity 100.0%; Pred. No. 4.8e-224;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3

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; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
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Query Match 99.5%; Score 2984; DB 4; Length 591;

Best Local Similarity 99.5%; Pred. No. 6.9e-223;

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US-09-669-974-21
: Sequence 21, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669, 974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 21
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-21
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Query Match 99.5%; Score 2984; DB 4; Length 591;
Best Local Similarity 99.5%; Pred. No. 6.9e-223;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Db 61 YLDPVLRVAVAVLIYNSDEKGEKGEKVEENSDMAVYFNEKGYLTAARETLAKAGDLKIK 120
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Db 121 NCTNFTYSLKRLDLISVGTSEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTTVALN 180
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: Sequence 2, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-2
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Query Match 98.4%; Score 2952.5; DB 4; Length 592;
Best Local Similarity 98.5%; Pred. No. 1.9e-220;
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

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QY 60 YLDPVLRVAVAVLIYNSDEKGEKGEKVEENSDMAVYFNEKGYLTAARETLAKAGDLKIK 119
Db 61 YLDPVLRVAVAVLIYNSDEKGEKGEKVEENSDMAVYFNEKGYLTAARETLAKAGDLKIK 120
QY 120 NCTNFTYSLKRLDLISVGTSEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTTVALN 179
Db 121 NCTNFTYSLKRLDLISVGTSEKLSFSANGKVNITSDTKGLNFAKETAGTNGDTTVALN 180
QY 180 NGIGSTLTDLTLTGATNTNDNVTDDEKKRAASVYKDVNAGMNIKGYKPGTTASDNVDF 239
Db 181 NGIGSTLTDLTLTGATNTNDNVTDDEKKRAASVYKDVNAGMNIKGYKPGTTASDNVDF 240
QY 240 VRTYDVEFLSADTKTTTVNVNVEKDKGKTEYKIGAKTSVIEKDGKLVTKDKGENSS 299
Db 241 VRTYDVEFLSADTKTTTVNVNVEKDKGKTEYKIGAKTSVIEKDGKLVTKDKGENSS 300
QY 300 TDEGEGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKEFEYVTSNTVTFASGKTATATV 359
Db 301 TDEGEGLVTAKEVIDAVNKAAGRMKTTTANGOTGADKEFEYVTSNTVTFASGKTATATV 360
QY 360 VSKDDGNTITVMVDVNVGDLNVNOLNSGMNLDKRAVASSCKVTSIGNVSPSKGMDETV 419
Db 361 VSKDDGNTITVMVDVNVGDLNVNOLNSGMNLDKRAVASSCKVTSIGNVSPSKGMDETV 420
QY 420 VINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 479
Db 420 VINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 479
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Db 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPV 480
QY 480 RITNVAPEGKGDVYTNVAQLKGVAONLNRRIDNDVGNARAGIAAIAIATAGLVQAYLPCKS 539
Db 481 RITNVAPEGKGDVYTNVAQLKGVAONLNRRIDNDVGNARAGIAAIAIATAGLVQAYLPCKS 540
QY 540 MMAIGGTYRGEAGYALGYSISIDGWNIIKGTASGNSRGHFGASASVGYOM 591
Db 541 MMAIGGTYRGEAGYALGYSISIDGWNIIKGTASGNSRGHFGASASVGYOM 592

RESULT 6
US-09-669-974-2
Sequence 2, Application US/09669974
Patent No. 633173
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/669,974
CURRENT FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 592
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 98.4%; Score 2952.5; DB 4; Length 592;
Best Local Similarity 98.4%; Pred. No. 1.9e-220;
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;
QY 1 MNELIRITMNSALNAAWVVSSELTNRHTRKASATYKATVATLTLFATYQASANNEDQED 59
Db 1 MNKIVRIIMNSALNAAWVVSSELTNRHTRKASATYKATVATLTLFATYQASANNEDPRKD 60
QY 60 LYLDPLVLTAVLVNSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 119
Db 61 LYLDPLVLTAVLVNSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 120
QY 120 QNGNFTYSLKDLTDLTSVTEKLSFSGANGKNVITSDTGLNFAKTAGNGDTVHL 179
Db 121 QNGNFTYSLKDLTDLTSVTEKLSFSGANGKNVITSDTGLNFAKTAGNGDTVHL 180
QY 180 NGISSTLTDLLNTGATTVNDVYTDDEKRRASVSKDVLNAGWNIKVKKGTASDNDV 239
Db 181 NGISSTLTDLLNTGATTVNDVYTDDEKRRASVSKDVLNAGWNIKVKKGTASDNDV 240
QY 240 FVRTYDYVEFLSADTKTTTVNESKNGKTEVKIGAKTSVYKEKDKLVYKDKGENGS 299
Db 241 FVRTYDYVEFLSADTKTTTVNESKNGKTEVKIGAKTSVYKEKDKLVYKDKGENGS 300
QY 300 STDGEGLVYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEVYVSGTVTFASGKGTAT 359
Db 301 STDGEGLVYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEVYVSGTVTFASGKGTAT 360
QY 360 VSKDQGNITVYVNVGDALNVNOLONGWNLDSKAAVAGSSGKVISGNVSPSKKMDT 419
Db 361 VSKDQGNITVYVNVGDALNVNOLONGWNLDSKAAVAGSSGKVISGNVSPSKKMDT 420
QY 420 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPV 479

Db 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPV 480
QY 480 RITNVAPEGKGDVYTNVAQLKGVAONLNRRIDNDVGNARAGIAAIAIATAGLVQAYLPCKS 539
Db 481 RITNVAPEGKGDVYTNVAQLKGVAONLNRRIDNDVGNARAGIAAIAIATAGLVQAYLPCKS 540
QY 540 MMAIGGTYRGEAGYALGYSISIDGWNIIKGTASGNSRGHFGASASVGYOM 591
Db 541 MMAIGGTYRGEAGYALGYSISIDGWNIIKGTASGNSRGHFGASASVGYOM 592

RESULT 7
US-09-377-155-9
Sequence 9, Application US/09377155
Patent No. 6197312
GENERAL INFORMATION:
APPLICANT: PEAK, Ian Richard Anselm
APPLICANT: JENNINGS, Michael Paul
APPLICANT: MOXON, E. Richard
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
FILE REFERENCE: 065064/0128
CURRENT APPLICATION NUMBER: US/09/377,155
CURRENT FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: PCT/AU98/01031
PRIOR FILING DATE: 1998-12-14
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 594
TYPE: PRT
ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 91.3%; Score 2739.5; DB 4; Length 594;
Best Local Similarity 91.8%; Pred. No. 5.7e-204;
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;
QY 1 MNELIRITMNSALNAAWVVSSELTNRHTRKASATYKATVATLTLFATYQASANNEDQED 60
Db 1 MNKIVRIIMNSALNAAWVVSSELTNRHTRKASATYKATVATLTLFATYQASANNEDPRKD 57
QY 61 LYLDPLVLTAVLVNSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 120
Db 58 YLEPVQRTAVLVNSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 116
QY 121 -----NGNFTYSLKDLTDLTSVTEKLSFSGANGKNVITSDTGLNFAKTAGNGD 174
Db 117 NTNEVTNASSFTYSLKDLTDLTSVTEKLSFSGANGKNVITSDTGLNFAKTAGNGD 176
QY 175 TTVHLNGISSTLTDLLNTGATTVNDVYTDDEKRRASVSKDVLNAGWNIKVKKGTASDNDV 234
Db 177 TTVHLNGISSTLTDLLNTGATTVNDVYTDDEKRRASVSKDVLNAGWNIKVKKGTASDNDV 236
QY 235 SDNVDFVRYTVEFLSADTKTTTVNESKNGKTEVKIGAKTSVYKEKDKLVYKDKGENGS 294
Db 237 SDNVDFVRYTVEFLSADTKTTTVNESKNGKTEVKIGAKTSVYKEKDKLVYKDKGENGS 296
QY 295 GENGSTDEGEGLVYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEVYVSGTVTFASGK 354
Db 297 GENGSTDEGEGLVYTAKEVIDAVNKAQRMKTTTANGOTGQADKFEVYVSGTVTFASGK 356
QY 355 GTTATVSKDQGNITVYVNVGDALNVNOLONGWNLDSKAAVAGSSGKVISGNVSPSKKMDT 414
Db 357 GTTATVSKDQGNITVYVNVGDALNVNOLONGWNLDSKAAVAGSSGKVISGNVSPSKKMDT 416
QY 415 KMDFTVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPV 473
Db 417 KMDFTVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGDLNVGSKKDNKPV 476
QY 474 KDNRPVRLITNVAPEGKGDVYTNVAQLKGVAONLNRRIDNDVGNARAGIAAIAIATAGLVQ 533

|||||
Db 477 DANKPVRITNVA PGVEGDVTNVAOLKGVAQNLMNNHIDVDGNARAGIAQAIALATAGLVQA 536
QY 534 YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGASGNSRHFASASVGYOW 591
|||||
Db 537 YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGASGNSRHFASASVGYOW 594

RESULT 8

US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 91.3%; Score 2739.5; DB 4; Length 594;
Best Local Similarity 91.8%; Pred. No. 5.7e-204;
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNELIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLLEFATVOASANNEDEEDL 60
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :||
Db 1 MNKIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLLEFATVOASTD--DDDL 57
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 YLDPVLRVAVLI VNSDKRGEKEKEVEENSDMAVYFENKGYLTAREITLKAGDNLKIQ 120
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 YLEPQRTAVLVSPRSDEKTEGEKE-VIEDSNMGVYFEDKGVLTAGTITLKAGDNLKIQ 116
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 -----NGTNPYSLKKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGD 174
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 NTNEMTNMSSFTYSLKKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGD 176
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 TTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKRRASVVDVLAAGNINIGVKPGTTA 234
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 TTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKRRASVVDVLAAGNINIGVKPGTTA 236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVATGAKTSYIKKDKGLVYGKDK 294
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVATGAKTSYIKKDKGLVYGKDK 296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 354
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 356
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 GTTATVSKDQGNITVMYVNGDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSGK 414
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 GTTATVSKDQGNITVMYVNGDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSGK 416
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 KMDFTVINAGNNIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 473
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 KMDFTVINAGNNIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 476
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 KMKPVRITNVA PGVEGDVTNVAOLKGVAQNLMNNHIDVDGNARAGIAQAIALATAGLVQA 533
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 477 DANKPVRITNVA PGVEGDVTNVAOLKGVAQNLMNNHIDVDGNARAGIAQAIALATAGLVQA 536
QY 534 YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGASGNSRHFASASVGYOW 591
|||||
Db 537 YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGASGNSRHFASASVGYOW 594

RESULT 9

US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 90.7%; Score 2721.5; DB 4; Length 594;
Best Local Similarity 91.6%; Pred. No. 1.4e-202;
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

QY 1 MNELIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLLEFATVOASANNEDEEDL 60
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : :||
Db 1 MNKIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLLEFATVOANATD--DDDL 57
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 YLDPVLRVAVLI VNSDKRGEKEKEVEENSDMAVYFENKGYLTAREITLKAGDNLKIQ 120
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 58 YLEPQRTAVLVSPRSDEKTEGEKE-SMNAVYFEDKRVLKAGATITLKAGDNLKIQ 116
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 -----NGTNPYSLKKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGD 174
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 NTNEMTNMSSFTYSLKKDLTDLTSVTEKLSFSAANGKNVITSDTKGLNFAKETAGTNGD 176
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 175 TTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKRRASVVDVLAAGNINIGVKPGTTA 234
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 TTVHLNGIGSTLTDPLNTGATTNTNDVTDDEKRRASVVDVLAAGNINIGVKPGTTA 236
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVATGAKTSYIKKDKGLVYGKDK 294
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVATGAKTSYIKKDKGLVYGKDK 296
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 295 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 354
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 356
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 355 GTTATVSKDQGNITVMYVNGDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSGK 414
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 GTTATVSKDQGNITVMYVNGDALNVNQLONGSNLDSKAVAGSSGKVIISGNVSPSGK 416
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 415 KMDFTVINAGNNIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 473
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 KMDFTVINAGNNIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 476
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 474 KMKPVRITNVA PGVEGDVTNVAOLKGVAQNLMNNHIDVDGNARAGIAQAIALATAGLVQA 533
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 477 DTKKPVRTNVA PGVEGDVTNVAOLKGVAQNLMNNHIDVDGNARAGIAQAIALATAGLVQA 536
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 534 YLPKGSMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGASGNSRHFASASVGYOW 591

Db 537 YLPKSMMAIGGDTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 10

US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 90.7%; Score 2721.5; DB 4; Length 594;

Best Local Similarity 91.6%; Pred. No. 1.4e-202;
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

QY 1 MNEIIRIIMNSALAAWVVSSELTNRNHRKASATYKATVATLFLFATYQASANNEOEEDL 60
DB 1 MNKIRIIMNSALAAWVVSSELTNRNHRKASATYKATVATLFLFATYQANATD---DDDL 57
QY 61 YLDPVLTAAVLIVNSDEKGEKEKEEENSMAVYFNEKGVLTAREITLAKGNLKI 120
DB 58 YLEPVQRTAAVLSRSPDEKGEKEGED-SNMAVYFDEKGVLTAREITLAKGNLKI 116
QY 121 -----NGNFTYSLKDLDTLSVTEKLSFSGANGKVNITSDTKGLNFAKETAGTNGD 174
DB 117 NTNENTNDSSFTYSLKDLDTLSVTEKLSFSGANGKVNITSDTKGLNFAKETAGTNGD 176
QY 175 TTVHLNGIGSTLDTLTNTGATTVTNDNTDDEKRRASVYKDVLANGMNIIKGYK 234
DB 177 PTVHLNGIGSTLDTLTNTGATTVTNDNTDDEKRRASVYKDVLANGMNIIKGYK 236
QY 235 SDNDVFRYDTVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVIREKDGKLVY 294
DB 237 SDNDVFRYDTVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVIREKDGKLVY 296
QY 295 GENGSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGQTQADKFEVYTGSTNTV 354
DB 297 DENSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGQTQADKFEVYTGSTNTV 356
QY 355 GTTATVSKDDGNTITVYDVNVDGALNVNOLONGSGWNLDSKAAGSSGKVI 414
DB 357 GTTATVSKDDGNTITVYDVNVDGALNVNOLONGSGWNLDSKAAGSSGKVI 416
QY 415 KMDTVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDD-ALN 473
DB 417 KMDTVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDD-ALN 476
QY 474 KDNFVITNVAAPGVKEDVYVNAOLKGVANLNRRIDNVGNARAGIAQAIAATAG 533
DB 477 DTNKPVITNVAAPGVKEDVYVNAOLKGVANLNRRIDNVGNARAGIAQAIAATAG 536
QY 534 YLPKSMMAIGGDTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 591

Db 537 YLPKSMMAIGGDTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 594

RESULT 11

US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 90.2%; Score 2706.5; DB 4; Length 598;

Best Local Similarity 90.5%; Pred. No. 2.1e-201;
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNEIIRIIMNSALAAWVVSSELTNRNHRKASATYKATVATLFLFATYQASANNEOEEDL 60
DB 1 MNKIRIIMNSALAAWVVSSELTNRNHRKASATYKATVATLFLFATYQANATD---DDDL 57
QY 61 YLDPVLTAAVLIVNSDEKGEKEKEEENSMAVYFNEKGVLTAREITLAKGNLKI 120
DB 58 YLEPVQRTAAVLSRSPDEKGEKEGED-SNMAVYFDEKGVLTAREITLAKGNLKI 116
QY 121 -----NGNFTYSLKDLDTLSVTEKLSFSGANGKVNITSDTKGLNFAKETAG 170
DB 117 NTNENTNDSSFTYSLKDLDTLSVTEKLSFSGANGKVNITSDTKGLNFAKETAG 176
QY 171 TNGDTVHLNGIGSTLDTLTNTGATTVTNDNTDDEKRRASVYKDVLANGMNIIKGYK 230
DB 177 TNGDTVHLNGIGSTLDTLTNTGATTVTNDNTDDEKRRASVYKDVLANGMNIIKGYK 236
QY 231 GTTASDNDVFRYDTVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVIREKDGKLVY 290
DB 237 GTTASDNDVFRYDTVEFLSADTKTTTVNVEKNGKTEVKIGAKTSVIREKDGKLVY 296
QY 291 GKDGENGSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGQTQADKFEVYTGSTNTV 350
DB 297 GKDGENGSSSTDEGEGLYTAKEVIDAVNKAAGRMKTTTANGQTQADKFEVYTGSTNTV 356
QY 351 ASGKGTATVSKDDGNTITVYDVNVDGALNVNOLONGSGWNLDSKAAGSSGKVI 410
DB 357 ASGKGTATVSKDDGNTITVYDVNVDGALNVNOLONGSGWNLDSKAAGSSGKVI 416
QY 411 PSKGMDETVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDD-ALN 469
DB 417 PSKGMDETVNINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDD-ALN 476
QY 470 VGSKDKNKPVITNVAAPGVKEDVYVNAOLKGVANLNRRIDNVGNARAGIAQAIAATAG 529
DB 477 VGSKDKNKPVITNVAAPGVKEDVYVNAOLKGVANLNRRIDNVGNARAGIAQAIAATAG 536
QY 530 LVOAYLPGKSMMAIGGDTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 589
DB 537 LAQAYLPGKSMMAIGGDTYRGEGAGYAIGYSSISDGNMIIKGTASGNSRGHFGASASVGYOW 596
QY 590 QW 591

[illegible]

RESULT 14
US-09-669-974-5

```

1  Sequence 5, Application US/09669974
2  Patent No. 6333173
3  GENERAL INFORMATION:
4  APPLICANT: PEAK, Ian Richard Anselm
5  APPLICANT: JENNINGS, Michael Paul
6  APPLICANT: MOXON, E. Richard
7  TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
8  FILE REFERENCE: 065064/0128
9  CURRENT APPLICATION NUMBER: US/09/669,974
10 CURRENT FILING DATE: 2000-09-26
11 PRIOR APPLICATION NUMBER: US 09/377,155
12 PRIOR FILING DATE: 1998-08-19
13 PRIOR APPLICATION NUMBER: PCT/AU98/01031
14 PRIOR FILING DATE: 1998-12-14
15 PRIOR APPLICATION NUMBER: GB 9726398.2
16 PRIOR FILING DATE: 1997-12-12
17 NUMBER OF SEQ ID NOS: 33
18 SOFTWARE: Patentln Ver. 2.0
19 SEQ ID NO 5
20 LENGTH: 598
21 TYPE: PRT
22 ORGANISM: Neisseria meningitidis
23 US-09-669-974-5

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Query Match:	90.28:	Score 2705.5:	DB: 4	Length 598;
Best Local Similarity:	90.48:	Pred. No. 2.5e-201;		
Matches 544;	Conservative 14;	Mismatches 29;	Indels 15;	Gaps 4;

[illegible]

DB	477	VGSKAMPVRITVNAPEVKEGDDTVNAQOLKGVNQNNRNRIDNVQNAARAGIAQAIATAG	536
QY	530	LVOAATLPKSMMAIGGGTYREGAGYATIGYSTISDGGNMHTIKGTASGNSRQHPGASASVGY	589
DB	537	LAQATLPKSMMAIGGGTYREGAGYATIGYSTISDGTGMNVIKGTASGNSRQHPGASASVGY	596
QY	590	QM 591	
DB	597	QM 598	

RESULT 15
HS-09-377-155-15

1. Sequence 15, Application US/093771155
 2. Patent No. 6197312
 3. GENERAL INFORMATION:
 4. APPLICANT: PEAK, Ian Richard Anselm
 5. APPLICANT: JENNINGS, Michael Paul
 6. APPLICANT: MOXON, E. Richard
 7. TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
 8. FILE REFERENCE: 065064/0128
 9. CURRENT APPLICATION NUMBER: US/09/377,155
 10. CURRENT FILING DATE: 1999-08-19
 11. PRIOR APPLICATION NUMBER: PCT/AU98/01031
 12. PRIOR FILING DATE: 1998-12-14
 13. PRIOR APPLICATION NUMBER: GB 9726398.2
 14. PRIOR FILING DATE: 1997-12-12
 15. NUMBER OF SEQ ID NOS: 33
 16. SOFTWARE: PatentIn Ver. 2.0
 17. SEQ ID NO 15
 18. LENGTH: 599
 19. TYPE: PRT
 20. ORGANISM: Neisseria meningitidis
 21. US-09-377-155-15

Query Match	89.2%	Score 2676	DB 4	Length 599
Best Local Similarity	89.0%	Pred No. 4.8e-199		
Matches 356; Conservative	18;	Mismatches 34;	Indels 14;	Gaps 4

Oy	1	MNEIIRITIMNSALNAAWVVSLELTENHNRKRASATYKTVLTLLEFATQOASANNDEGEDD	60
Oy	1	MNEIIRITIMNSALNAAWVVSLELTENHNRKRASATYKTVLTLLEFATQOASANNDEGEDD	60
Dd	1	MNKITRIITIMNSALNAAWVVSLELTENHNRKRASATYKTVLTLLEFATQOAAATDEDEEE	59
Oy	61	YLDPLVLTVAVLIVNSDEKGTGEKEKVEENSQWAVFNEKGVLTAREITLKADNLKIKO	120
Dd	60	-LEPVRSALVLOCMIDKEKGENGENEST-GNTGMSIYYDNNHTLHGAIVTLKADNLKIKO	117
Oy	121	-----NGTNEPTYSLKDKLIDLTVSGEKESIFSGANKNVITSDTGLMPAKETAG	170
Dd	118	NTNKNNTENNTWDSSTFTYSLKDLIDLTVSETEKLSFEGANKNVITSDTGLMPAKETAG	177
Oy	171	TNGDPTVHLNGISGTLTDFTLTLNTGATTNVTNDNVTDDEKKRAASVKNVLAAGNNIKGVP	230
Dd	178	TNGDPTVHLNGISGTLTDFTLTLNTGATTNVTNDNTDDKKRAASVKNVLAAGNNIKGVP	237
Oy	231	GTTASDNDVFRATDPTVEELSAOKRTTTVVNESKDNCKRTVEKIGATSVYKEDGLVTF	290
Dd	238	GTTASDNDVFRATDPTVEELSAOKRTTTVVNESKDNCKRTVEKIGATSVYKEDGLVTF	297
Oy	291	GKDKGENSSSTDEGEGVLTAKVEYIDAANKAGWRRKTTTJANGQGTQADKFEVTVSGTWTF	350
Dd	298	GKDKGENSSSTDEGEGVLTAKVEYIDAANKAGWRRKTTTJANGQGTQADKFEVTVSGTWTF	357
Oy	351	ASGKGTATVSKDDOQGNITVTVYDVNNGDALNVNQLONSQNNLDSKANVAGSSGVIISGNVS	410
Dd	358	ASGKGTATVSKDDOQGNITVTVYDVNNGDALNVNQLONSQNNLDSKAAGSSGVIISGNVS	417
Oy	411	PSKGMDETVIMNAGNNIEIRNRKNIDIAITSMTPQFSSVSLAGADAPLTVSDG-DALN	469
Dd	418	PSKGMDETVIMNAGNNIEIRNRKNIDIAITSMTPQFSSVSLAGADAPLTVSDVDGALN	477
Oy	470	VGSKDKNKPVRITVAPGVKEGDVTNAOLKGYAQNLRNIBNDVNGNARAGIAQAIATAG	529

Db	478	VGSKDANKPVRTNVPVKEGDPVTNVAQLKGVAQNLNRRIDNDVGNARAGIAQAIAATAG	537
QY	530	LVQAYLPGKSMMAIGGCTYRGEGAYTAIGYSSISDGGNMIKGTASGNSRGRHFGASASVGY	589
Db	538	LVQAYLPGKSMMAIGGCTYRGEGAYTAIGYSSISDGGNMIKGTASGNSRGRHFGASASVGY	597
QY	590	QW 591	
Db	598	QW 599	

Search completed: July 3, 2002, 08:10:19
Job time: 531 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:09 ; Search time 168.6 Seconds
(without alignments)
394.622 Million cell updates/sec

Title: US-09-771-382-6
Perfect score: 3060
Sequence: 1 MNKIYRIWNSALNAWAVS.....TASGSRGHFGASAVGVQW 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3060	100.0	599	20 AAY23743	A surface protein
2	3060	100.0	599	22 AAU06176	N. meningitidis H3
3	2824.5	92.3	598	20 AAY23742	A surface protein
4	2824.5	92.3	598	22 AAU06177	N. meningitidis H1
5	2821.5	92.2	598	20 AAY23738	A surface protein
6	2821.5	92.2	598	22 AAU06178	N. meningitidis B2
7	2802.5	91.6	594	20 AAY23739	A surface protein
8	2802.5	91.6	594	22 AAU06179	N. meningitidis B2
9	2762.5	90.3	594	20 AAY23740	A surface protein
10	2762.5	90.3	594	21 AAY57044	BAS029 amino acid
11	2762.5	90.3	594	22 AAU06174	N. meningitidis EG

12	2699.5	88.2	592	20 AAY23744	A surface protein
13	2699.5	88.2	592	21 AAU06172	N. meningitidis H4
14	2696	88.1	591	21 AAY57045	BAS029 amino acid
15	2694	88.0	589	20 AAY23745	A surface protein
16	2694	88.0	589	22 AAU06173	N. meningitidis P2
17	2685	87.7	591	20 AAY27202	Amino acid sequenc
18	2685	87.7	591	22 AAY23746	A surface protein
19	2685	87.7	591	22 AAU06171	N. meningitidis PM
20	2676	87.5	591	20 AAY23741	A surface protein
21	2676	87.5	591	22 AAU06175	N. meningitidis EG
22	2663.5	87.0	592	20 AAY23737	A surface protein
23	2587.5	84.6	592	22 AAU06180	N. meningitidis Z2
24	2551.5	83.4	592	20 AAY27203	Amino acid sequenc
25	2472	80.8	513	22 AAU06183	N. meningitidis H4
26	2453.5	80.2	512	22 AAU06182	N. meningitidis PM
27	2371.5	77.5	502	22 AAU06186	N. meningitidis PM
28	2231.5	72.9	604	22 AAU06181	N. meningitidis su
29	2032	66.4	433	22 AAU06185	N. meningitidis PM
30	1886	61.6	407	22 AAU06184	N. meningitidis PM
31	1271	41.5	2353	17 AAR99393	Haemophilus adhesi
32	1246	40.7	2411	21 AAB23860	Haemophilus influe
33	1070.5	35.0	1098	17 AAR99392	Haemophilus influe
34	1053.5	34.4	1094	21 AAB23858	Haemophilus influe
35	1008	32.9	679	17 AAR99394	Haemophilus adhesi
36	1008	32.9	679	21 AAB23855	Haemophilus influe
37	970.5	31.7	245	20 AAY27201	Amino acid sequenc
38	758.5	24.8	1004	21 AAB23857	Haemophilus influe
39	743.5	24.3	1002	21 AAB23854	Haemophilus influe
40	701.5	22.9	1104	21 AAB23856	Haemophilus influe
41	701.5	22.9	1104	21 AAB23859	Haemophilus influe
42	600	19.6	116	21 AAB37832	Neisserial conserv
43	401.5	13.1	2123	22 AAE00701	Moraxella catarrha
44	398.5	13.0	1992	17 AAW04505	Moraxella 200 kDa
45	398.5	13.0	1992	22 AAB69133	M. catarrhalis str

ALIGNMENTS

RESULT 1
AA23743
ID AAY23743 standard; Protein; 599 AA.
XX
AC AAY23743;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW Immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-AL.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAY85795.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX

```

PS Claim 1; Page 114-115; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 599 AA;

Query Match 100.0%; Score 3060; DB 20; Length 599;
Best Local Similarity 100.0%; Pred. No. 7.9e-171;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVCAANATDEDEEL 60
Db 1 mnkiyriiwsalnawavseltrnhtkrasatvktavlatllfatvqanatedeheel 60

Qy 61 EPVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120
Db 61 epvrsalvlqfmidkegngengestgnigwsiyydnhntlhgatvtlkagdnllkikqntn 120

Qy 121 KNTNENTNDSSTYSLLKDLTDLASVTEKLSFGANGKXVNTSDTKCLNFAKETAGTNG 180
Db 121 kntnentndsstysllkdltdlasvteklsgfngangkvnitstktclnfaaketagtn 180

Qy 181 DTTVHLNGIGSTLDTLNTGATNTVNDNTDDKKRAASVKDVLNAGWNKIGVKPGTT 240
Db 181 dttvhlngigstltdlntgattntvndntddkkraasvkdvlngagwnikgvpqgtt 240

Qy 241 ASDNVDFVHTYDVEFLSADTKTNTVNVESKDNGKRTVEKTKTAKTSVIKEKDGKLVTKG 300
Db 241 asdnvdfvhtydvelfsadtknttnvneskdngkrtevkigaktsvikekdglvtgk 300

Qy 301 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFEVTSCTNVTFASG 360
Db 301 kgengstdegeglvtakevldavnkagwrmtttangotqadkfetvtsctnvtfasg 360

Qy 361 KGTATVSKDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 420
Db 361 kgtatvskdqqnitvkydynvgdalnvnlqnsqwnldskavagsgkvisgnvpsk 420

Qy 421 GKMDETVNIAGNIEITRNKNIIDIAFSWTPQFSSVSLGAGADAPTLSDYDKGALNVGS 480
Db 421 gkmdetvniagnieitrngkniidiatsmtppfssvslgagadaptilsvdkgalnvgs 480

Qy 481 KDANKPVRITNAPVQKGEVDVTVNAOLKGAQNLNRRIDNVDGNARAGIAAIATAGLVQ 540
Db 481 kdanpvrtnvapvqkgevdvtnvaqlkgvaqnlrridnvdgnaragiaaiaataglvq 540

Qy 541 AYLPGKSMMAIGGTYRGEAGYAIYCSISDGGNWIKGTASGNSRHFASASVGYQW 599
Db 541 aylpgksmmaiggtyrgeagyaigyssisdggnwikgtasgnsrghfgasasvgyqw 599

RESULT 2
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX
AC AAU06176;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H38 surface antigen Nhba polypeptide sequence.
XX
KW Surface antigen Nhba; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H38.

```

```

XX FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..105
FT /label= V1
FT /note= "Variable region 1"
FT Region 106..117
FT /label= C2
FT /note= "Conserved region 2"
FT Region 118..131
FT /label= V2
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FT Region 132..195
FT /label= C3
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FT /label= C4
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FT Region 237..243
FT /label= V4
FT /note= "Variable region 4"
FT Region 244..599
FT /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09166.
XX
PT New Nhba surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhba
CC (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhba
CC from N. meningitidis strain H38 is 1 of 10 Nhba polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 599 AA;

Query Match 100.0%; Score 3060; DB 22; Length 599;
Best Local Similarity 100.0%; Pred. No. 7.9e-171;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
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Db 1 mnkiyriiwnlsalnawavseltrnhtkrasatvktavlatllfatvqanatede 60
QY 61 EPVRSALVQPMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGDNLKIKQNTN 120
Db 61 epvrsalvqpmidkegngengestgnigwsiyddhntlhgatvtlkagdnlikqntn 120
QY 121 KTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
Db 121 ktnentndssfyslkkdltdltsveteklsfgangknvntsdtkglnfaketagtn 180
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKIKGVPKGT 240
Db 181 dttvhlngigstltdllntgattnvtndvddkkraasvkdvlnagwnikgvkpgtt 240
QY 241 ASDNVDFVHTYDVEFLSADTKTTTNNVESKONGKRTVEKIGAKTSVIEKDGKLVTKG 300
Db 241 asdnvdfvhtydtveflsadtktttvnveskdngkrtvekigaktsviekdgklvtkg 300
QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKT TTTANGOTGOADKFTETVTSGTNVTFASG 360
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QY 361 KGTATVSKDDQGNITVKYDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 361 kgtatvskddqgnitvkydnnvgdlnvnlqnsqwnldskavagssgkvisgnvspk 420
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Db 421 gkmdetvnnagnnieitrngknidatmtptqfssvslgagadaptlsvddkgalnvg 480
QY 481 KDANKPVRITNVAPVKGEGDVTVNAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540
Db 481 kdankpvrntnvapvkegdvtnvaqlkgvaqlnrridnvdgnaraglaaiaataglvq 540
QY 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFASASVGYQW 599
Db 541 aylpgksmmaigggtyrgeagyaigyssisdggnwlikgtasgnsrghfgasasvgyqw 599
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RESULT 3

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AA06177
ID AA06177 standard; Protein; 598 AA.
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AC AA06177;
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DT 08-SEP-1999 (first entry)
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XX A surface protein of Neisseria meningitidis.
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DE Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
```

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XX Neisseria meningitidis.
```

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OS WO9931132-A1.
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XX 24-JUN-1999.
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PF 14-DEC-1998; 98WO-AU01031.
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PR 12-DEC-1997; 97GB-0026398.
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XX (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
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PI Jennings MP, Moxon ER, Peak IRA;
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XX WPI; 1999-418754/35.
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DR N-PSDB; AAX85794.
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XX Neisseria meningitidis surface proteins useful for treating N.
```

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PT meningitidis infections
```

```
PS Claim 1; Page 108-110; 132pp; English.
```

```
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
```

```
XX Sequence 598 AA;
```

```
Query Match 92.3%; Score 2824.5; DB 20; Length 598;
Best Local Similarity 92.7%; Pred. No. 4.4e-157;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;
```

```
QY 1 MNKIYRIIWNLSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
```

```
Db 1 mnkiyriiwnlsalnawavseltrnhtkrasatvktavlatllfatvqanated-d 59
```

```
QY 61 EPVRSALVQPMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGDNLKIKQNTN 120
```

```
Db 60 epvrtavlsfrsdegtgektedsnwavyfdekrvfkagailkagdnlikqntn 119
```

```
QY 121 KTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
```

```
Db 120 entnentndssfyslkkdltdltsveteklsfgangknvntsdtkglnfaketagtn 179
```

```
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKIKGVPKGT 240
```

```
Db 180 dptvhlngigstltdllntgattnvtndvddkkraasvkdvlnagwnikgvkpgtt 239
```

```
QY 241 ASDNVDFVHTYDVEFLSADTKTTTNNVESKONGKRTVEKIGAKTSVIEKDGKLVTKG 300
```

```
Db 240 asdnvdfvhtydtveflsadtktttvnveskdngkrtvekigaktsviekdgklvtkg 299
```

```
QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKT TTTANGOTGOADKFTETVTSGTNVTFASG 360
```

```
Db 300 kgensstdegeglvtakevidavnkgwrmttttangotgoadkftetvtsgtntvtfasg 359
```

```
QY 361 KGTATVSKDDQGNITVKYDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
```

```
Db 360 ngttatvskddqgnitvkydnnvgdlnvnlqnsqwnldskavagssgkvisgnvspk 419
```

```
QY 421 GKMDETVNNAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS 480
```

```
Db 420 gkmdetvnnagnnieitrngknidatmtptqfssvslgagadaptlsvddkgalnvg 479
```

```
QY 481 KDANKPVRITNVAPVKGEGDVTVNAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540
```

```
Db 480 kdankpvrntnvapvkegdvtnvaqlkgvaqlnrridnvdgnaraglaaiaataglaq 539
```

```
QY 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFASASVGYQW 599
```

```
Db 540 aylpgksmmaigggtyrgeagyaigyssisdggnwlikgtasgnsrghfgasasvgyqw 598
```

RESULT 4

```
AAU06177
ID AAU06177 standard; Protein; 598 AA.
```

```
XX AAU06177;
```

```
XX 24-OCT-2001 (first entry)
```

```
XX N. meningitidis H15 surface antigen Noha polypeptide sequence.
```

```
XX Surface antigen Noha; meningococcal disease; meningitis vaccine.
```

```

XX OS Neisseria meningitidis strain H15.
XX FH Key Location/Qualifiers
XX FT Region 1..50
XX FT /label= C1
XX FT /note= "Conserved region 1"
XX FT Region 51..104
XX FT /label= V1
XX FT /note= "Variable region 1"
XX FT Region 105..116
XX FT /label= C2
XX FT /note= "Conserved region 2"
XX FT Region 117..130
XX FT /label= V2
XX FT /note= "Variable region 2"
XX FT Region 131..194
XX FT /label= C3
XX FT /note= "Conserved region 3"
XX FT Region 195..216
XX FT /label= V3
XX FT /note= "Variable region 3"
XX FT Region 217..235
XX FT /label= C4
XX FT /note= "Conserved region 4"
XX FT Region 236..242
XX FT /label= V4
XX FT /note= "Variable region 4"
XX FT Region 243..598
XX FT /label= C5
XX FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09167.
XX
XX New Nhma surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis .
XX
XX Claim 9; Fig 1; 9lpp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhma
XX (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhma
XX from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 598 AA;

Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;
Qy 1 MNKIVRIIWNNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEBEL 60
Db 1 mmklyriiwnsalnawvsvseltrnhtkrasatvatavlatllfatvqanad-dddlyl 59
Qy 61 EPVVRSAVLQFMIDKEGNGENESTGNIGWISYDNNHNTLHGATVTLKAGDNKLTKQNTN 120
Db 60 epvqrtavvlfsrdskegkegednswavfdekrvilkagaitlkagdnklkqntn 119
Qy 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG 180
Db 120 entnentndssftyslkkdldtsveteklsfgangnkvnitstdtkglnfaketagtn 179
Qy 181 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDKRAASVKDVLNAGWNIKGVKPGTT 240
Db 180 dptvhlngigstltdltllntgattntvndvtddekkraasvkdvlhagwnikgvkpgtt 239
Qy 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTKIGAKTSVTKEDGKLVTGKG 300
Db 240 asdnvdfvrtvdtveflsadtktttvnveskdngkktvkgaktsvikekdglvtgkg 299
Qy 301 KGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQADKFEFTVTSCTNVTTFASG 360
Db 300 kdengsstdegeglvtakevidavnkagwrmtttangotgadkfeftvtsctnvttfasg 359
Qy 361 KGTATVSKDDQGNITVKYDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVSPSK 420
Db 360 ngttatvskddqgnitvkdydvngdalnvnqlngsgwnldskavagssgkvisgnvpsk 419
Qy 421 GKMDETVNIAGNNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 420 gkmdetvniagnnieitrngknidiatsmtppqfssvslgagadaptlsvddegalnvg 479
Qy 481 KDANKPVRITNWAPGVKEGDTNVAQLKGVAQNLRNIDVNGHARAGIAIAIATAGLVQ 540
Db 480 kdanpvrnitnwapgvkegdtnvaqlkgvaqnlrnrnidvngnaragiaiaiataglaq 539
Qy 541 AYLPGKSMMAITGGTYRGEAGYAIGYSSISDGNWIKGTASGNSRHFASASVGYQW 599
Db 540 aylpgksmmaiggytyrgeagyaigyssisdgtnwnwilkgtasgnsrghfgasasvgyqw 598

RESULT 5
AAV23738
ID AAV23738 standard; Protein; 598 AA.
XX
AC AAV23738;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAX85790.

```

Query Match 92.3%; Score 2824.5; DB 22; Length 598;
 Best Local Similarity 92.7%; Pred. No. 4.4e-157;

```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX Claim 1; Page 91-93; 132pp; English.
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX Sequence 598 AA;
SQ
Query Match 92.2%; Score 2821.5; DB 20; Length 598;
Best Local Similarity 92.7%; Pred. No. 6.5e-157;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 1 MKKIIRIINWSALNAWVSELTNRHTKRASATVTAVALTLFATVQANATDEDEEEL 60
Db 1 mkkisriiwnsalnawvsvseltrnhtkrasatvatavlatllfatvqanatl-dddl 59
QY 61 EPVRSALVLPQWIDKGENECSTIGWSIYYDHNHNTLHGATVTLKAGDNLIKQNTN 120
Db 60 epvqrtavvlvirsdkgegtgekedtwnwvfydekrvfkagaitcagdnlikqncn 119
QY 121 KNTNENTNDSSEFYSLLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
Db 120 entnentndssftyslkkdlttsveteklsfgangkvnitsdtkglinfaketagtn 179
QY 181 DRTVHLNGIGSLTDLTLNLTGATFNTVNDVDDKKRAASVKDVLNAGWNKKGKPGTT 240
Db 180 dptvhlngigsltdtlntgattntvndvdddkkraasvkdvltnagwnkkgvkpgtt 239
QY 241 ASDNVDFVHTYDVFELSADTFTTVNVESKDKGRTEVKIGAKTSVKEKDKGLVTGK 300
Db 240 asdnvdfvrydtvelfsadtkttvtnveskdkgrtkrtvkgaktsvikekgklvtgk 299
QY 301 KGENSSSTDEGELVTAKEVIDAVNKAQWRMKTTFANGQTQADKPETVTSCTNVTFAAG 360
Db 300 kgensstdegeglvtakevidavnkagwrmtkttfangtqgqadkfetvtsctkvtfaag 359
QY 361 KGTATVSKDDGNTVTKYDVNVGDALNVNQIQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 360 ngttatvskddgnttkydydvngdnlvnqilqnswnldskavagssgkvisgnvpsk 419
QY 421 GKMDETVNTNAGNNIEITRNGKNIDTATSWTPQFSSVSLGAGADAPTLSDVDKGLNVGS 480
Db 420 gkmdetvntnagnnleitrngknidatstmpqfssvslgagadaptlsvddgelnvgs 479
QY 481 KDANKPVRTITNVPAGKEGDVNTVAQLKGAQNLNRRIDVNGNARAGIAQAIAATAGLVQ 540
Db 480 kdankpvrtnvpagkegdvntvnaqlkgvaqnlrridvngnarnaragiataglaq 539
QY 541 AYLPGKSMMAIGGTVRGAGYAIGYSSISDGNWIIKTAGSNGRHFASASVGYQW 599
Db 540 aylpgksmmaiggtvrygeaygaigyssisdtnwnviktagasngsrghfgtasvgyqw 598
RESULT 6
AAU06178
ID AAU06178 standard; Protein; 598 AA.
XX AC AAU06178;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis Bz10 surface antigen Nhha polypeptide sequence.
```

```
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain BZ10.
OS
XX
FH Key Location/Qualifiers
Region 1..50 /label= C1
Region 51..104 /note= "Conserved region 1"
Region 105..116 /label= V1
Region 117..130 /note= "Variable region 1"
Region 131..194 /label= C2
Region 195..216 /note= "Conserved region 2"
Region 217..235 /label= V2
Region 236..242 /note= "Variable region 2"
Region 243..598 /label= C3
Region 243..598 /note= "Conserved region 3"
Region 243..598 /label= V3
Region 243..598 /note= "Variable region 3"
Region 243..598 /label= C4
Region 243..598 /note= "Conserved region 4"
Region 243..598 /label= V4
Region 243..598 /note= "Variable region 4"
Region 243..598 /label= C5
Region 243..598 /note= "Conserved region 5"
WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
PR 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09168.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain BZ10 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
SQ Sequence 598 AA;
```

Query Match 92.2%; Score 2821.5; DB 22; Length 598;
Best Local Similarity 92.7%; Pred. No. 6.5e-157;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSALNAWAVASELTHNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mnkisirliwsalnawvvseltrnhtrkrasatvatavlatllfatvqanad-dddlyl 59

QY 61 EPVVRSAVLQFMIDKREGNGENESTGNIGWSIYYDNIHTLHGATVTLKAGDNLIKIKONTN 120
DB 60 epvqrtavvlfsrdskegtednsnwavfyfdekrvfkagaitlkagdnlikikontn 119

QY 121 KNTNENTNDSFTYSLKKDLTDLTSVTEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
DB 120 entnentndsfstyslkkdltsveteklsfgangknvniitstdtkglnfaketagtn 179

QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 240
DB 180 dptvhlngigstltdtllntgattnvndvddkkraasvkdvlalnagwnikvkgpgtt 239

QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
DB 240 asdnvdfvhtydtveflsadtktttvnveskdngkrtvekgikagtsvikekgklvtgk 299

QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTFASS 360
DB 300 kgensstdegeglvtakevidavnkgawrmktttangtqgqadkfetvtsgtkvtfass 359

QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 420
DB 360 ngttatvskddqgnitvkydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpsk 419

QY 421 GKMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
DB 420 gkmdetvinagnieitrngknidiatstmpqfssvslgagadaptlsvddkalgavgs 479

QY 481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGNARAGIAQAATAGLVQ 540
DB 480 kdanpvrntnvapgvkegdvtnvaqlkgvaqnlnnridnvgnaragiagaataglaq 539

QY 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYQW 599
DB 540 aylpgkmmaiggytyrgeagyaigyssisdggnwiiikgtasgnsrghfgasasvgyqw 598

RESULT 7
AAU06179
ID AAY23739 standard; Protein; 594 AA.
XX
AC AAY23739;
XX
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX

DR WPI; 1999-418754/35.
DR N-PSDB; AAX85791.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections
XX
PS Claim 1; Page 95-97; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;

Query Match 91.6%; Score 2802.5; DB 20; Length 594;
Best Local Similarity 92.5%; Pred. No. 8.3e-156;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

QY 1 MNKIYRIIWSALNAWAVASELTHNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mnkisirliwsalnawvvseltrnhtrkrasatvatavlatllfatvqanad-dddlyl 59

QY 61 EPVVRSAVLQFMIDKREGNGENESTGNIGWSIYYDNIHTLHGATVTLKAGDNLIKIKONTN 120
DB 60 epvqrtavvlfsrdskegtednsnwavfyfdekrvfkagaitlkagdnlikikontn 116

QY 121 KNTNENTNDSFTYSLKKDLTDLTSVTEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
DB 117 -ntnentndsfstyslkkdltsveteklsfgangknvniitstdtkglnfaketagtn 175

QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 240
DB 176 dptvhlngigstltdtllntgattnvndvddkkraasvkdvlalnagwnikvkgpgtt 235

QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
DB 236 asdnvdfvhtydtveflsadtktttvnveskdngkrtvekgikagtsvikekgklvtgk 295

QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTFASS 360
DB 296 kgensstdegeglvtakevidavnkgawrmktttangtqgqadkfetvtsgtntvtfass 355

QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSK 420
DB 356 kgtatvskddqgnitvkydvnvgdalnvnlqnsqwnldskavagssgkvisgnvpsk 415

QY 421 GKMDETVINAGNIEITRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
DB 416 gkmdetvinagnieitrngknidiatstmpqfssvslgagadaptlsvddkalgavgs 475

QY 481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVGNARAGIAQAATAGLVQ 540
DB 476 kdnkpvrntnvapgvkegdvtnvaqlkgvaqnlnnridnvgnaragiagaataglaq 535

QY 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYQW 599
DB 536 aylpgkmmaiggytyrgeagyaigyssisdggnwiiikgtasgnsrghfgasasvgyqw 594

RESULT 8
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX
AC AAU06179;
XX
DT 24-OCT-2001 (first entry)

XX N. meningitidis Bz198 surface antigen Nhha polypeptide sequence.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain Bz198.
OS
XX Key Location/Qualifiers
FH 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..126
FT /label= V2
FT /note= "Variable region 2"
FT 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT 191..212
FT /label= V3
FT /note= "Variable region 3"
FT 213..231
FT /label= C4
FT /note= "Conserved region 4"
FT 232..238
FT /label= V4
FT /note= "Variable region 4"
FT 239..594
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
PN
XX 02-AUG-2001.
PD
XX 25-JAN-2001; 2001WO-AU00069.
PF
XX 25-JAN-2000; 2000US-0177917.
PR
XX (UYQU) UNIV QUEENSLAND.
PA
XX Peak IRA, Jennings MP;
PI
XX WPI; 2001-488774/53.
DR N-PSDB; AAS09169.
DR
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis .
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC immunisants. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain Bz198 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX Sequence 594 AA;
SQ

Query Match 91.6%; Score 2802.5; DB 22; Length 594;
Best Local Similarity 92.5%; Pred. No. 8.3e-156;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIIWNNSALNAWVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDEDEEEL 60
DB 1 mkiyriiwnsalnawvvseilrnhtrkrasatavlatlilfatvqanad-dddlyl 59
QY 61 EPVRSALVQLQFMIDKEGNESTONIGWSIYYDNHNLHGATVTLKAGDNLIKIKONTN 120
DB 60 epvrtavvlslfrskdtegektednsawyfdkrlkagaitlkagdnlikikg--- 116
QY 121 KNTNENTNDSSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
DB 117 -ntnentndssftyslkkdltdltsveteklsfgangknvntsdckglnfaketagtng 175
QY 181 DTTVHLNGIGSTLTDTLNTGATTNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTT 240
DB 176 dptvhlingigstltdtlntgattntvndvddkkraasvkdvlmagwnlkgvkpgtt 235
QY 241 ASDNVDVHTYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKDKGLVTGKG 300
DB 236 asdnvdfvrtvdtveflsadtktttvnveskdngkktvkgaktsviekdkglvtgkg 295
QY 301 KGENSSDDEGLVTAKVIDAVNKAGWRMKTTTTANGOTGOADKPTETVTSCTNVTFASG 360
DB 296 kdengssdtegeglvtakevidavnkagwrmttttangotgqadkftetvtsctnvtfasg 355
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNLDSKAVAGSGKVIISGNVSPSK 420
DB 356 kgtatvskddqgnitvkydvnvvgdalnvnqlnsgnldskavagsgkviisgnvpsk 415
QY 421 GKMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTSLVDDKGLNVGS 480
DB 416 gkmdetvniagnnieitrngknidiatsmapqfssvslgagadaptslvddkglnvgs 475
QY 481 KDANKPVRITNVAPGVKEGDTVNAOLKGAONLNRIIDNVGNARAGTAQATATAGLVQ 540
DB 476 kdnkpvritnvapgvkegdtvnvaolkgaonlnriidnvgnaraglaqataglvq 535
QY 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWTIKGTASGNSRGHFGASVGYQW 599
DB 536 aylpgksmmaiggyrgeagyaigyssisdggnwiikgtasgnsrghfgaasvgyqw 594
RESULT 9
AAY23740
ID AAY23740 standard; Protein; 594 AA.
XX
AC AAY23740;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX

```
PI Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85792.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 100-101; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 594 AA;
SQ
Query Match 90.3%; Score 2762.5; DB 20; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.8e-153;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;
Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTVATLTLFATVQANATDEDEEL 60
Db 1 mnklyriiwsalnawavseltrnhktrasatvatatliffatvqastdd-dddlyl 59
Qy 61 EPVVRSAVLQFMIDKEGNGENESTGNIGWYIYDNNHTLHGATVTLKAGDNLKIKQNTN 120
Db 60 epvqrtavvlfrsdkegtgekednsnwgvyfdkkgvltagtitikagdnllkqg--- 116
Qy 121 KNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
Db 117 -ntnentnassfyslkkdltlsvgteklfsfnsnknvntsdtkglnfakkttaetng 175
Qy 181 DTTVHLNGIGSLTDLTLTLCATNTVNTDNDVTDKRAASVKDVLNAGWNKGVKPGCTT 240
Db 176 dttvhlngigsltdltlntgatctnvdndvtddekkraasvkdvlnagwnkvgkpgtt 235
Qy 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKNDNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
Db 236 asdnvdfvtydtveflsadtktttvnveskdngkrtvekgikaktsvikekdglvtgkd 295
Qy 301 KGENGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFETVTSCTWVTASG 360
Db 296 kgensdstdkgelivtakevidavnkagwrmtttangqtgqadkfetvtsctwvtfasg 355
Qy 361 KGTATVSKDQGNITTVKYDYNVGDALNVNOLNSGWNLDKAVAGSGKVIYSGNVSPSK 420
Db 356 kgtatvskddqgnitvmydvnygdalnvnglqnsqwnldskavagsgkviysgnvpsk 415
Qy 421 GKMDETVINAGNIEITRNKNIDIAITSMTPQFSVSLGAGADAPTLSDVDKGLNNGVS 480
Db 416 gkmdetvinagnieitrnknidiatsmtpqfssvslgagadaptlsvddegalnvg 475
Qy 481 KDANKPVRIITNAPGVKEGDVTNVAQLKGVAQNLRNDRDNDVGNARAGIAQIATAGLVQ 540
Db 476 kdankpvritnapgvkegdvtnvaqlkgvaqnlrnhidnvdgnaragiaqiataglvq 535
Qy 541 AYLPGKSMMAIGGGTYRGEAGYATIGYSSISDGGNWIITKGASNGSRHFGASASVGGQW 599
Db 536 aylpgksmmaigggtyrgeagyaigysisidgggnwiitkgasngsrhfgasasvgyq 594
RESULT 10
AAY57044
ID AAY57044 standard; Protein; 594 AA.
XX
AC AAY57044;
```

```
XX 21-FEB-2000 (first entry)
DT
XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
DE
XX BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
XX Neisseria meningitidis.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 104 /note= "Encoded by AATC"
FT
XX WO9958683-A2.
XX
XX 18-NOV-1999.
PD
XX 07-MAY-1999; 99WO-EP03255.
PF
XX 13-MAY-1998; 98GB-0010276.
PR
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Ruelle J;
PI
XX
XX WPI: 2000-053103/04.
DR N-PSDB; AAZ39864.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
PT
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
XX Sequence 594 AA;
```

```
Query Match 90.3%; Score 2762.5; DB 21; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.8e-153;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;
Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTVATLTLFATVQANATDEDEEL 60
Db 1 mnklyriiwsalnawavseltrnhktrasatvatatliffatvqastdd-dddlyl 59
Qy 61 EPVVRSAVLQFMIDKEGNGENESTGNIGWYIYDNNHTLHGATVTLKAGDNLKIKQNTN 120
Db 60 epvqrtavvlfrsdkegtgekednsnwgvyfdkkgvltagtitikagdnllkqg--- 116
Qy 121 KNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
Db 117 -ntnentnassfyslkkdltlsvgteklfsfnsnknvntsdtkglnfakkttaetng 175
```



```
QY 181 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDKKRAASVKDVLNAGWNIKGKPGTT 240
DB 176 dtvhlngigstltdltllntgattntvndvtddekkraasvkdvlnagwnikgkpgtt 235
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTNNVESKDKNGRTEVKIGAKTSVIEKDKGLVTGK 300
DB 236 asdnvdfvhtydtveflsadtktttvnnveskdngkrtvkgaktsviekdkglvtgk 295
QY 301 KGENSGSTDEGEGLVTAKEVIDAVNKAAGRMTTANGQTGQADKPEETVTSCTNVTFSAG 360
DB 296 kgensgstdegglvtakevidavnkagwrmtttangtqgqadkfetvtsctnvtfsg 355
QY 361 KGTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDLSKAVAGSSGKVISGNNVSPSK 420
DB 356 kgtatvskddognitvmydvngdnlvngqlnsgwnldskavagssgkvisgnvpsk 415
QY 421 GKMDFTVNIAGNIIETRNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKGLNVS 480
DB 416 gkmdetvniagniietrngknidiatsmtpqfssvslgagadaptlsvddgklnvsg 475
QY 481 KDANKPVRTNVPAGVKEGDVTVNAQLKGAQNLANNRIDNVGNARAGIAQAIAATAGLVQ 540
DB 476 kdankpvrtnvpagvkegdvtnvaqlkgvaqnlannhldnvdgnaraglaqalataglvq 535
QY 541 AYLPKSMMAIGGTYRGAGYAIGYSSTSDGNNWIIKGTASGNSRHFSGASASVGYOW 599
DB 536 aylpksmmaiggytyrgaagyaygysissdgnwlikgtasgnsrghfsgasasvgyow 594

RESULT 11
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DT 24-OCT-2001 (first entry)
DE N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX
```

```
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
XX
DR N-PSDB; AAS09164.
XX
PT New NhhA surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen NhhA
CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen NhhA
CC from N. meningitidis strain EG327 is 1 of 10 NhhA polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
SQ Sequence 594 AA;
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```
Query Match 90.3%; Score 2762.5; DB 22; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.8e-153;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MNKIYRIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mkiyriwnsalnawvavseltrnhtkrasatvatvlatllfatvqasttd-dddlyl 59
QY 61 EPVRSALVLPQFMIDKEGENESTGNIGWSIYYDNNHTLHGATVTLKAGDNLKIKONTN 120
DB 60 epvrtavvlsfrskdgtgektevdsnwgvyfdkkgvltagtitlkagdnlikkq--- 116
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
DB 117 -ntnentnassftyslkkdltltsvgtklsfsaansknvntsdtkgnfakktetng 175
QY 181 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDKKRAASVKDVLNAGWNIKGKPGTT 240
DB 176 dtvhlngigstltdltllntgattntvndvtddekkraasvkdvlnagwnikgkpgtt 235
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTNNVESKDKNGRTEVKIGAKTSVIEKDKGLVTGK 300
DB 236 asdnvdfvhtydtveflsadtktttvnnveskdngkrtvkgaktsviekdkglvtgk 295
QY 301 KGENSGSTDEGEGLVTAKEVIDAVNKAAGRMTTANGQTGQADKPEETVTSCTNVTFSAG 360
DB 296 kgensgstdegglvtakevidavnkagwrmtttangtqgqadkfetvtsctnvtfsg 355
QY 361 KGTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDLSKAVAGSSGKVISGNNVSPSK 420
DB 356 kgtatvskddognitvmydvngdnlvngqlnsgwnldskavagssgkvisgnvpsk 415
QY 421 GKMDFTVNIAGNIIETRNKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKGLNVS 480
DB 416 gkmdetvniagniietrngknidiatsmtpqfssvslgagadaptlsvddgklnvsg 475
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Db 416 gkndetvnnagnnieitrrngknidiatsmtpqfssvslgagadapltlsvddgalnvgs 475
QY 481 KDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQ 540
Db 476 kdankpvrirtnvapgvkegdvtnvaqlkgvaqnlhnhidnvdnragiaaiaataglvq 535
QY 541 AYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 599
Db 536 aylpksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 12
AAY23744
ID AAY23744 standard; Protein; 592 AA.
XX
AC AAY23744;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UTQU ) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI: 1999-418754/35.
DR N-PSDB; AAX85796.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 118-120; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;

Query Match 88.2%; Score 2699.5; DB 20; Length 592;
Best Local Similarity 91.2%; Pred. No. 8.5e-150;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY 1 MNKLYRIIWNALNANWAVAVSELFRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 mnklyriiwnalnawavavseltrnhkrasatvktavlatllfratvqanatedeeseel 60
QY 61 EPVVRSAVLVQFMIDKEGNGENESTGNIGWSIYYDNIHLHG-ATVTLKAGDNLKIKQNT 119
Db 61 esvqrs-vvgsiqasmeqvelet---islsmtdnskefdvpyivtlkagdnlkikq-- 114
QY 120 NKNTNENTNDSSFTYSLKKDLTLTSTVETEKLSFGANGKNVNITSDPKGLNFAKETAGTN 179
```

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Db 115 --ntnentnassfyslkkdltglinveteklsifgankkvnllsdcckglnfaketagtn 172
QY 180 GDTTVHLNGIGSLTDTLLNTGATTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGT 239
Db 173 gdtvhlngigsltdmlntgattnvtdndvtddekkraasvkdvlnagwnkgvkpgt 232
QY 240 TASDNVDVFVHTYDTEFLSADTKTTVTNNVESKDNKRTEYKIGAKTSVVIKEKDGKLVTK 299
Db 233 tasdnvdfvrtvteflsadtktttcnveskdngkktvkigaktsvikekgdklvtkg 292
QY 300 GKGENSSDTEGEGLYTAKEVIDAVNKGWRMKTITTANGOTGQADKRETTVTSGTNVTFAS 359
Db 293 gkgengsstdegeglvtakevidavnkagwrmttttangtgdqdkfetytsgtkvtfas 352
QY 360 GKGTATTATVSKDDOGNITVKYDVNVGDALNVNQLNSQWMLDSKAVAGSSGKVTSGNVSPS 419
Db 353 gngttatvskddggnitvkvdyvngdnlvngnlqnsqwnlidskavagssgkvsgnvsp 412
QY 420 KGKMDETVNNAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 479
Db 413 kgkmdetvnnagnnieitrrngknidiatsmtpqfssvslgagadapltlsvddgalnv 472
QY 480 SKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLV 539
Db 473 skdankpvrirtnvapgvkegdvtnvaqlkgvaqnlhnhidnvdnragiaaiaataglv 532
QY 540 QAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 599
Db 533 qaylpksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 592

RESULT 13
AAU06172
ID AAU06172 standard; Protein; 592 AA.
XX
AC AAU06172;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H41 surface antigen NnhA polypeptide sequence.
XX
KW Surface antigen NnhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H41.
XX
FH Key Location/Qualifiers
FT Peptide 1..51 /label= Signal_peptide
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..102 /label= V1
FT /note= "Variable region 1"
FT Protein 52..592
FT /label= Mature_NnhA
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
FT Region 103..114 /label= C2
FT /note= "Conserved region 2"
FT Region 115..124 /label= V2
FT /note= "Variable region 2"
FT Region 125..188 /label= C3
FT /note= "Conserved region 3"
FT Region 189..210 /label= V3
FT /note= "Variable region 3"
FT Region 211..229 /label= C4
FT
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FT Region /note= "Conserved region 4"
FT 230..236 /label= V4
FT /note= "Variable region 4"
FT 237..592
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UQUU) UNIV QUEENSLAND.
XX PA Peak IRA, Jennings MP;
XX PI WPI: 2001-488774/53.
XX DR N-PSDB; AAS09162.
XX
XX New Nhaa surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis
XX
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhaa
CC (AAU06182-AAU06186). The modified or mutant Nhaa polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhaa
CC from N. meningitidis strain H41 is 1 of 10 Nhaa polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 592 AA;

Query Match 88.2%; Score 2699.5; DB 22; Length 592;
Best Local Similarity 91.2%; Pred. No. 8.5e-150;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY 1 MNKIYRIIWSNALNWAWSVSELRHTRKRASATVTVTAVALTLFATVQANATDEDEEEL 60
DB 1 mnkiyriiwsnalnwaawseltrhtrkrasatvktavlatllfatvqanatedeeseel 60

QY 61 EPVRSALVLPQFMIDKEGENESGTGSIYSDGNWIIKGTASGNSRHFHGASASVGYQW 119
DB 61 esvqrs-vvgsiqasmegsvelet---slsmtndskefvdpyivvtlkgadnlkikq-- 114

QY 120 NKNTNENTNDSFTYSLKDLFDLTVSETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 179
DB 115 --ntnentnassftyllkldlglinveteklsfsgangkknvniisdtkglnfaketagn 172

QY 180 GDTTVHLNIGIGSTLTDTLTLLTGATTVNDVTDKRRKRAASVKDVLNAGWNIKGVKPGT 239
DB 173 gdttvhlngigstldmlntgattntdntdndvtddekkraasvkdvlngwnikgvkpgt 232

QY 240 TASDNVDFVHTYDVFELISADFTTNNVESKDNGKRTVEKIGAKTSVTKEDGKLVGCK 299
DB 233 tasdnvdfvrtvdytvefilsadktttnvveskdngkrtvekigaktsvikekdgkvlvgck 292

QY 300 KGKNGSSSTDEGLVTAKEVIDAYNKAGWRMKTITANGQTQADKFETVTSCTNVTFAS 359
DB 300 kgkngssstdeglvtakevidaynkagwrmtttangqtqadkfetvtsctnvtfas 352

DB 293 gkngssstdeglvtakevidavnkagwrmtttangqtqadkfetvtsctnvtfas 352
QY 360 KGKTTATVSKDDQGNITVYDVNVGDALNVNOLQNSGNLDSKAVAGSSGKVTSGNVSPS 419
DB 353 gngttatvskddqgnitvkydvngdalinvgdnlqnswnldskavagsgkvtisgnvps 412
QY 420 KGKMDETVNIAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDKALNYG 479
DB 413 kgkmdetvniagnnieitrcngknidiatmpqfssvslgagadaptsvdddegalnyg 472
QY 480 SKDANKPVRITNWAPGVREGDVTNVAQLKGVQNLNNDVNDGNARAGIAQAIATAGLV 539
DB 473 skdankpvrtnvapgvgkegvtvnaqlkgvagnlnndvngnarnaraglaiaataglv 532
QY 540 QAYLPGKSMWAIIGGTYRGEAGYATIGYSSISDGGNWIKGTASGNSRHFHGASASVGYQW 599
DB 533 qaylpgksmmaigggtyrgeagyaigysisaggnwilkgtasgnrghfgasasvgyq 592

RESULT 14

AAV57045
ID AAV57045 standard; Protein; 591 AA.

XX
AC AAV57045;

XX
DT 21-FEB-2000 (first entry)

XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

XX
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.

XX
OS Neisseria meningitidis.

XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX
PN WO9958683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI: 2000-053103/04.
XX DR N-PSDB; AAZ39865.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
XX treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.

XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention

QY 359 SGKGTATVSKDDQGNITVKYDVNVGDALNVNOLQNSGWNLDKAVAGSGKVISGNVSP 418
|| |||||
Db 349 sgngttatvskddqgnitvkydvnvgdalnvnlqnsqwnldskavagsgkvvisgnvsp 408
|| |||||
QY 419 SKGKMDETVNIAGNNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDDKCALNV 478
|| |||||
Db 409 skgkmdetvniagnnietrnngknidiatmtptqfssvslgagadaptilsvddegaln 468
|| |||||
QY 479 GSKDANKPVRITNVAPGVKEGDTNVAQLKGVNAQNLNRRIDNVNDRAGIAQAIATAGL 538
|| |||||
Db 469 gskdankpvrtnvapgvkegdvtnvaqlxgvaqnlrrldnvnngnaraglaiaiatagl 528
|| |||||
QY 539 VQAYLPCKSMAIIGGTYRGEAGYAICYSSISDGNWIIKGTASGNSRGHFGASASVGYQ 598
|| |||||
Db 529 aqaylpqksmmaiggytlygeagyaigyssisdtgnwvkgtagsgnsrghfgtsasvgyq 588
|| |||||
QY 599 W 599
|
Db 589 w 589

Search completed: July 3, 2002, 08:09:11
Job time: 497 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:19 ; Search time 64.11 Seconds
(without alignments)
228.216 Million cell updates/sec

Title: US-09-771-382-6
Perfect score: 3060
Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHGASASVGYQW 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pap: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pap: *
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pap: *
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3060	100.0	599	4	US-09-377-155-15
2	3060	100.0	599	4	US-09-669-974-15
3	2824.5	92.3	598	4	US-09-377-155-13
4	2824.5	92.3	598	4	US-09-669-974-13
5	2821.5	92.2	598	4	US-09-377-155-5
6	2821.5	92.2	598	4	US-09-669-974-5
7	2802.5	91.6	594	4	US-09-377-155-7
8	2802.5	91.6	594	4	US-09-669-974-7
9	2762.5	90.3	594	4	US-09-377-155-9
10	2762.5	90.3	594	4	US-09-669-974-9
11	2699.5	88.2	592	4	US-09-377-155-17
12	2699.5	88.2	592	4	US-09-669-974-17
13	2694	88.0	589	4	US-09-377-155-19
14	2694	88.0	589	4	US-09-669-974-19
15	2685	87.7	591	4	US-09-377-155-21
16	2685	87.7	591	4	US-09-669-974-21
17	2676	87.5	591	4	US-09-377-155-11
18	2676	87.5	591	4	US-09-669-974-11
19	2663.5	87.0	592	4	US-09-377-155-2
20	2663.5	87.0	592	4	US-09-669-974-2
21	1271	41.5	2353	4	US-09-377-155-33
22	1271	41.5	2353	4	US-08-913-942-4
23	1271	41.5	2353	4	US-09-669-974-33
24	1270	41.5	2354	4	US-09-268-347-30
25	1246	40.7	2411	4	US-09-268-347-36
26	1199.5	39.2	607	1	US-08-409-995-6
27	1199.5	39.2	607	3	US-08-685-467-6

28	1199.5	39.2	607	4	US-08-913-942-6	Sequence 6, Appli
29	1199.5	39.2	1912	1	US-08-409-995-4	Sequence 4, Appli
30	1199.5	39.2	1912	3	US-08-685-467-4	Sequence 4, Appli
31	1070.5	35.0	1098	1	US-08-409-995-2	Sequence 2, Appli
32	1070.5	35.0	1098	3	US-08-685-467-2	Sequence 2, Appli
33	1070.5	35.0	1098	4	US-09-377-155-32	Sequence 32, Appli
34	1070.5	35.0	1098	4	US-08-913-942-2	Sequence 2, Appli
35	1070.5	35.0	1098	4	US-09-669-974-32	Sequence 32, Appli
36	1070.5	35.0	1098	4	US-09-268-347-44	Sequence 44, Appli
37	1053.5	34.3	1094	4	US-09-268-347-32	Sequence 32, Appli
38	1050.5	34.3	658	1	US-08-409-995-5	Sequence 5, Appli
39	1050.5	34.3	658	3	US-08-685-467-5	Sequence 5, Appli
40	1050.5	34.3	658	4	US-08-913-942-5	Sequence 5, Appli
41	1008	32.9	679	4	US-08-913-942-15	Sequence 15, Appli
42	1008	32.9	679	4	US-09-268-347-26	Sequence 26, Appli
43	758.5	24.8	1004	4	US-09-268-347-30	Sequence 30, Appli
44	743.5	24.3	1002	4	US-09-268-347-24	Sequence 24, Appli
45	701.5	22.9	1104	4	US-09-268-347-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAR, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match	100.0%	Score 3060;	DB 4;	Length 599;
Best Local Similarity	100.0%;	Pred. No. 7.2e-233;		
Matches 599;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVKAVLATLTLFATVQANATDEDEEEL	60	
Db	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVKAVLATLTLFATVQANATDEDEEEL	60	
QY	61	EPVRSALVQFMIDKEGNESTGNIGSIYDHNHTLHGATVTLKAGDNLKIKQNTN	120	
Db	61	EPVRSALVQFMIDKEGNESTGNIGSIYDHNHTLHGATVTLKAGDNLKIKQNTN	120	
QY	121	KNTNENTNDSSTYSLSKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG	180	
Db	121	KNTNENTNDSSTYSLSKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG	180	
QY	181	DTTVHLNGTSLTDFLLNLTGATVNTNDVDDKKRAASVKDVLNAGWNIGKVPKPTT	240	
Db	181	DTTVHLNGTSLTDFLLNLTGATVNTNDVDDKKRAASVKDVLNAGWNIGKVPKPTT	240	
QY	241	ASDNVDFVHTYDFVFLSADTKTTTNNVESKNGKTEYKIGAKTSVIEKDGKLVTKG	300	
Db	241	ASDNVDFVHTYDFVFLSADTKTTTNNVESKNGKTEYKIGAKTSVIEKDGKLVTKG	300	
QY	301	KGNSSTDBEGELVTAKEVIDAVNKAGRMKTNTTANGQTQADKPEVTVTSGTNTVTFASG	360	

Db 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSGTNVTASG 360
Qy 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSGKVISGNVSPSK 420
Qy 421 GKMDETVINAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVINAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Qy 481 KDANKPVRITNAPGVKEGDTVNVQAQLKGAQNINNRIDNDVGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRITNAPGVKEGDTVNVQAQLKGAQNINNRIDNDVGNARAGIAQAATATAGLVQ 540
Qy 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASVGYQW 599
Db 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASVGYQW 599

RESULT 2

US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 633173

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 100.0%; Score 3060; DB 4; Length 599;
Best Local Similarity 100.0%; Pred. No. 7.2e-233;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Caps 0;
Qy 1 MNKIYRIIWSALNAWAVASELTRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWAVASELTRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60
Qy 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGNLKIKONTN 120
Db 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGNLKIKONTN 120
Qy 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180
Qy 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGNINIKVKPGTT 240
Db 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGNINIKVKPGTT 240
Qy 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300
Db 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300
Qy 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSGTNVTASG 360

Db 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSGTNVTASG 360
Qy 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSGKVISGNVSPSK 420
Qy 421 GKMDETVINAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVINAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Qy 481 KDANKPVRITNAPGVKEGDTVNVQAQLKGAQNINNRIDNDVGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRITNAPGVKEGDTVNVQAQLKGAQNINNRIDNDVGNARAGIAQAATATAGLVQ 540
Qy 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASVGYQW 599
Db 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASVGYQW 599

RESULT 3

US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312

; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 92.3%; Score 2824.5; DB 4; Length 598;
Best Local Similarity 92.7%; Pred. No. 2.5e-214;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MNKIYRIIWSALNAWAVASELTRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWAVASELTRNHTKRASATVKTAVLATLFLPATVOANATD-DDDLXL 59
Qy 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGNLKIKONTN 120
Db 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGNLKIKONTN 119
Qy 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 179
Qy 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGNINIKVKPGTT 240
Db 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGNINIKVKPGTT 239
Qy 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300
Db 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 299
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Db 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSGTNVTASG 359
Qy 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSGKVISGNVSPSK 420

Db 360 NCTTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419
QY 421 GKMDETVNIAGNNITRNGKNIDTATSWTQFSSVSLGACADAPTLSVDDKGLALNVGS 480
Db 420 GKMDETVNIAGNNITRNGKNIDTATSWTQFSSVSLGACADAPTLSVDDKGLALNVGS 479
QY 481 KDANKPVRTNTPAVGKGDVTVNAQLKGVQAOVLNLRIDNVGNARAGIAQAIAATAGLVQ 540
Db 480 KDANKPVRTNTPAVGKGDVTVNAQLKGVQAOVLNLRIDNVGNARAGIAQAIAATAGLVQ 539
QY 541 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNIIKGTASGNSRGHFGASASVGYQW 599
Db 540 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 4

US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match 92.3%; Score 2824.5; DB 4; Length 598;
Best Local Similarity 92.7%; Pred. No. 2.5e-214;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;
QY 1 MNKIYRIIWSALNAWVAVSELTNRHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTNRHTKRASATVKTAVLATLLFATVQANATD-DDDLVL 59
QY 61 EPVRSALVQPMIDKEGNESTGNIWSIYYDNHNTHLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVQRTAVVLSFRSDKEGTGEKEDTSNWAYVFDKRVLKAGAITLKAGDNLKIKQNTN 119
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTG 180
Db 120 ENTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTG 179
QY 181 DPTVHLNGIGSLTDLTLNLTGATTVNTDNDVDDKKRAASVKDVLNAGWNIKGVKPGT 240
Db 180 DPTVHLNGIGSLTDLTLNLTGATTVNTDNDVDDKKRAASVKDVLNAGWNIKGVKPGT 239
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKDKNGKRTKVEIKAKTSVKEKDKGLVTGK 300
Db 240 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKDKNGKRTKVEIKAKTSVKEKDKGLVTGK 299
QY 301 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 360
Db 300 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 359
QY 361 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 360 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419

Db 360 NCTTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419
QY 421 GKMDETVNIAGNNITRNGKNIDTATSWTQFSSVSLGACADAPTLSVDDKGLALNVGS 480
Db 420 GKMDETVNIAGNNITRNGKNIDTATSWTQFSSVSLGACADAPTLSVDDKGLALNVGS 479
QY 481 KDANKPVRTNTPAVGKGDVTVNAQLKGVQAOVLNLRIDNVGNARAGIAQAIAATAGLVQ 540
Db 480 KDANKPVRTNTPAVGKGDVTVNAQLKGVQAOVLNLRIDNVGNARAGIAQAIAATAGLVQ 539
QY 541 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNIIKGTASGNSRGHFGASASVGYQW 599
Db 540 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNVIKGTASGNSRGHFGASASVGYQW 598

RESULT 5

US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 92.2%; Score 2821.5; DB 4; Length 598;
Best Local Similarity 92.7%; Pred. No. 4.3e-214;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 1 MNKIYRIIWSALNAWVAVSELTNRHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTNRHTKRASATVKTAVLATLLFATVQANATD-DDDLVL 59
QY 61 EPVRSALVQPMIDKEGNESTGNIWSIYYDNHNTHLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVQRTAVVLSFRSDKEGTGEKEDTSNWAYVFDKRVLKAGAITLKAGDNLKIKQNTN 119
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTG 180
Db 120 ENTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTG 179
QY 181 DPTVHLNGIGSLTDLTLNLTGATTVNTDNDVDDKKRAASVKDVLNAGWNIKGVKPGT 240
Db 180 DPTVHLNGIGSLTDLTLNLTGATTVNTDNDVDDKKRAASVKDVLNAGWNIKGVKPGT 239
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKDKNGKRTKVEIKAKTSVKEKDKGLVTGK 300
Db 240 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKDKNGKRTKVEIKAKTSVKEKDKGLVTGK 299
QY 301 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 360
Db 300 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFSAG 359
QY 361 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 360 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419
QY 421 GKMDETVNIAGNNITRNGKNIDTATSWTQFSSVSLGACADAPTLSVDDKGLALNVGS 480

Db 420 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479
QY 481 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540
Db 480 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 539
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGTGNWVTKGTASGNSRHFSGASVGYQW 599
Db 540 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGTGNWVTKGTASGNSRHFSGASVGYQW 598

RESULT 6
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match 92.2%; Score 2821.5; DB 4; Length 598;
Best Local Similarity 92.7%; Pred. No. 4.3e-214; Indels 1; Gaps 1;
Matches 555; Conservative 13; Mismatches 30;
QY 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDDEEEL 60
Db 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATD-DDDLXL 59
QY 61 EPVRSALVLFQMDKEGNGENESTGNISYIYDNTLHGATVTLKAGDNLKIKONTN 120
Db 60 EPVQRTAVLFSRDKGEGTEGKEDSNWAVFDEKRVLKAGAITLKGADNLKIKONTN 119
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 120 ENTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
QY 181 DTTVHLNGIGSTLTDLLNTGATTVNTNDVTDKKRAASVKDVLNAGWNIKVKPGETT 240
Db 180 DPTVHLNGIGSTLTDLLNTGATTVNTNDVTDKKRAASVKDVLNAGWNIKVKPGETT 239
QY 241 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDKGLVTKGK 300
Db 240 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDKGLVTKGK 299
QY 301 KGENSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVSGTNVTFASG 360
Db 300 KGENSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVSGTNVTFASG 359
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSGKVISGNVSPSK 420
Db 360 NGTATVSKDDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSGKVISGNVSPSK 419
QY 421 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480

Db 420 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479
QY 481 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540
Db 480 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 539
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGTGNWVTKGTASGNSRHFSGASVGYQW 599
Db 540 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGTGNWVTKGTASGNSRHFSGASVGYQW 598

RESULT 7
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 91.6%; Score 2802.5; DB 4; Length 594;
Best Local Similarity 92.5%; Pred. No. 1.3e-212;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDDEEEL 60
Db 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATD-DDDLXL 59
QY 61 EPVRSALVLFQMDKEGNGENESTGNISYIYDNTLHGATVTLKAGDNLKIKONTN 120
Db 60 EPVQRTAVLFSRDKGEGTEGKEDSNWAVFDEKRVLKAGAITLKGADNLKIKO- 116
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 117 -NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
QY 181 DTTVHLNGIGSTLTDLLNTGATTVNTNDVTDKKRAASVKDVLNAGWNIKVKPGETT 240
Db 176 DPTVHLNGIGSTLTDLLNTGATTVNTNDVTDKKRAASVKDVLNAGWNIKVKPGETT 235
QY 241 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDKGLVTKGK 300
Db 236 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDKGLVTKGK 295
QY 301 KGENSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVSGTNVTFASG 360
Db 296 KGENSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVSGTNVTFASG 355
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSGKVISGNVSPSK 420
Db 356 KGTATVSKDDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSGKVISGNVSPSK 415
QY 421 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480
Db 416 GKMDETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475
QY 481 KDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540

Db 476 KDTNKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 535
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHCASASVGYOW 599
Db 536 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHCASASVGYOW 594

RESULT 8

US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 91.6%; Score 2802.5; DB 4; Length 594;
Best Local Similarity 92.5%; Pred. No. 1.3e-212;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIIWSALNNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANAT- DDDL 59
QY 61 EPVRSALVQFMIDKEGGENESTGNIWSIYDHNHTLHGATVTLKAGDNLIKIKONTN 120
Db 60 EPVQRTAVLSFRSDKEGTEGKEDTSNWAYFDEKRVLKAGAITLKAGDNLIKIKO--- 116
QY 121 KNTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 117 -NTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
QY 181 DTTVHLNGIGSTLTDTLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 240
Db 176 DPTVHLNGIGSTLTDTLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 235
QY 241 ASDNVDFVHTDYDFEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLVTKG 300
Db 236 ASDNVDFVHTDYDFEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLVTKG 295
QY 301 KGENSGSTDEGGLVTAKEVIDAVNAGWRMKTTTTANGQTGQADKEFTVSGTNVTFASG 360
Db 296 KGENSGSTDEGGLVTAKEVIDAVNAGWRMKTTTTANGQTGQADKEFTVSGTNVTFASG 355
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 420
Db 356 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 415
QY 421 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS 480
Db 416 GKMDETVNIAGNNIETRNKKNIDATSMAPQFSSVSLGAGADAPTLSVDDKGALNVGS 475
QY 481 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 540
Db 476 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 535

Db 476 KDTNKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 535
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHCASASVGYOW 599
Db 536 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHCASASVGYOW 594

RESULT 9

US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 90.3%; Score 2762.5; DB 4; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.9e-209;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;
QY 1 MNKIYRIIWSALNNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNNAWVAVSELTRNHTKRASATVKAVLATLLFATVQASTTD- DDDL 59
QY 61 EPVRSALVQFMIDKEGGENESTGNIWSIYDHNHTLHGATVTLKAGDNLIKIKONTN 120
Db 60 EPVQRTAVLSFRSDKEGTEGKEDTSNWAYFDEKRVLKAGAITLKAGDNLIKIKO--- 116
QY 121 KNTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 117 -NTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
QY 181 DTTVHLNGIGSTLTDTLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 240
Db 176 DTTVHLNGIGSTLTDTLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 235
QY 241 ASDNVDFVHTDYDFEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLVTKG 300
Db 236 ASDNVDFVHTDYDFEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLVTKGD 295
QY 301 KGENSGSTDEGGLVTAKEVIDAVNAGWRMKTTTTANGQTGQADKEFTVSGTNVTFASG 360
Db 296 KGENSGSTDEGGLVTAKEVIDAVNAGWRMKTTTTANGQTGQADKEFTVSGTNVTFASG 355
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 420
Db 356 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 415
QY 421 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS 480
Db 416 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGS 475
QY 481 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 540
Db 476 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 535
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRHFHCASASVGYOW 599

Db 536 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 594
|||||

RESULT 10
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 90.3%; Score 2762.5; DB 4; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.9e-209;
Matches 549; Conservative 32; Mismatches 32; Indels 5; Gaps 2;
Qy 1 MNKYRIIWSALNNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60
Db 1 MNKYRIIWSALNNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVOASTD-DDDLVL 59
Qy 61 EPPVRSALVLFQFMDKEGNGENESTGNIGWSIYYDNNHTLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVORTAVLFRSDKEGTGEKEVETDSNMGVYFDKGVLTAGTITLKAGDNLKIKQ--- 116
Qy 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180
Db 117 -NTNENTNASSFTYSLKKDLTDLTSVETEKLSFSANSKNVITSDTKGLNFAKTAETNG 175
Qy 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGMNIKGVKPGTT 240
Db 176 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGMNIKGVKPGTT 235
Qy 241 ASDNVDFVHTYDVEFLSADTKTTTVNVESKDKNGKRTVEVIGAKTSVIKEKDGKLVTKG 300
Db 236 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEVIGAKTSVIKEKDGKLVTKG 295
Qy 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVTSCTNVTASG 360
Db 296 KGENSSTDKEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVTSCTNVTASG 355
Qy 361 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKSKAVAGSGKVISGNVSPSK 420
Db 356 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKSKAVAGSGKVISGNVSPSK 415
Qy 421 GKMDETVNIAGNNIETIRNGKNIDTATSMPTQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 416 GKMDETVNIAGNNIETIRNGKNIDTATSMPTQFSSVSLGAGADAPTLSDVDDKALNVGS 475
Qy 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 540
Db 476 KDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLVQ 535
Qy 541 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 599
|||||

Db 536 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 594
RESULT 11
US-09-377-155-17
; Sequence 17, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-17

Query Match 88.2%; Score 2699.5; DB 4; Length 592;
Best Local Similarity 91.2%; Pred. No. 1.7e-204;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;
Qy 1 MNKYRIIWSALNNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60
Db 1 MNKYRIIWSALNNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60
Qy 61 EPPVRSALVLFQFMDKEGNGENESTGNIGWSIYYDNNHTLHG-ATVTLKAGDNLKIKQNT 119
Db 61 ESVQRS-VVGSIOASMEGSVELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 114
Qy 120 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 179
Db 115 --NTNENTNASSFTYSLKKDLTGLINVEETEKLSFGANGKNVITSDTKGLNFAKETAGTN 172
Qy 180 GDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGMNIKGVKPGT 239
Db 173 GDTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGMNIKGVKPGT 232
Qy 240 TASDNVDFVHTYDVEFLSADTKTTTVNVESKDKNGKRTVEVIGAKTSVIKEKDGKLVTKG 299
Db 233 TASDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEVIGAKTSVIKEKDGKLVTKG 292
Qy 300 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVTSCTNVTAS 359
Db 293 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVTSCTNVTAS 352
Qy 360 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKSKAVAGSGKVISGNVSPS 419
Db 353 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKSKAVAGSGKVISGNVSPS 412
Qy 420 KGKMDETVNIAGNNIETIRNGKNIDTATSMPTQFSSVSLGAGADAPTLSDVDDKALNVG 479
Db 413 KGKMDETVNIAGNNIETIRNGKNIDTATSMPTQFSSVSLGAGADAPTLSDVDDKALNVG 472
Qy 480 SKDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLV 539
Db 473 SKDANKPVRIITNAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLV 532
Qy 540 QAYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 599
Db 533 QAYLPGKSMMAIGGTYLGEAGYATGYSSISAGGNWIILKGTASGNSRHFHGASASVGYQW 592

RESULT 12

US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match 88.2%; Score 2699.5; DB 4; Length 592;
Best Local Similarity 91.2%; Pred. No. 1.7e-204;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY 1 MNKIYRIIWNLSALNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 MNKIYRIIWNLSALNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

QY 61 EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHG-ATVTLKAGDNLIKQNT 119
DB 61 ESVQRS-VVGSIOASMEGSEVELET---ISLMTNDSKEFVDPIVTVTLKAGDNLIKQ-- 114

QY 120 NKTNTNNTDSSFTYSILKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 179
DB 115 --NTNENTNASSFTYSILKKDLTGLINIVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 172

QY 180 GDTTVHLNGIGSLTDLTLNTGATTNVDNVDKRAASVKDVLNAGWNKGVKPGT 239
DB 173 GDTTVHLNGIGSLTDLTLNTGATTNVDNVDKRAASVKDVLNAGWNKGVKPGT 232

QY 240 TASDNVDVHTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDKGLVTGK 299
DB 233 TASDNVDVHTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDKGLVTGK 292

QY 300 KKGENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSCTNVTFA 359
DB 293 KKGENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSCTNVTFA 352

QY 360 KGCTTATVSKDDOGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPS 419
DB 353 GNGTATVSKDDOGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPS 412

QY 420 KGKMDETVINAGNNTIETRNKNIDDIATSMTPQFSSVSLGAGADAPTLVSDDKGLNNG 479
DB 413 KGKMDETVINAGNNTIETRNKNIDDIATSMTPQFSSVSLGAGADAPTLVSDDKGLNNG 472

QY 480 SKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNANRINDVNGNARAGIAQAIATAGLV 539
DB 473 SKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNANRINDVNGNARAGIAQAIATAGLV 532

QY 540 QAYLPKSKMMAIGGGTYLGEAGYAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 599
DB 533 QAYLPKSKMMAIGGGTYLGEAGYAIYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 13

US-09-377-155-19

; Sequence 19, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-19

Query Match 88.0%; Score 2694; DB 4; Length 589;
Best Local Similarity 89.7%; Pred. No. 4.6e-204;
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;

QY 1 MNKIYRIIWNLSALNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 MNKIYRIIWNLSALNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

QY 61 EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLIKQNTN 120
DB 61 ESVRSALVQFMIDKEGNGEIESTGDIGWSIYYDDHTLHGATVTLKAGDNLIKQ-- 117

QY 121 KNTNENTDSSFTYSILKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 180
DB 118 -----SGKDFYSLKKELDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 170

QY 181 DTVVHLNGIGSLTDLTLNTGATTNVDNVDKRAASVKDVLNAGWNKGVKPGT 240
DB 171 DTVVHLNGIGSLTDLTLNTGATTNVDNVDKRAASVKDVLNAGWNKGVKPGT 228

QY 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDKGLVTG 298
DB 229 TGSENVDFVHTYDTVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDKGLVTG 288

QY 299 KKGENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSCTNVTFA 358
DB 289 KKGENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSCTNVTFA 348

QY 359 SGKGTATVSKDDOGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 418
DB 349 SGKGTATVSKDDOGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 408

QY 419 SKGKMDETVINAGNNTIETRNKNIDDIATSMTPQFSSVSLGAGADAPTLVSDDKGLNNG 478
DB 409 SKGKMDETVINAGNNTIETRNKNIDDIATSMTPQFSSVSLGAGADAPTLVSDDKGLNNG 468

QY 479 GSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNANRINDVNGNARAGIAQAIATAGLV 538
DB 469 GSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNANRINDVNGNARAGIAQAIATAGLV 528

QY 539 QAYLPKSKMMAIGGGTYLGEAGYAIYSSISDGNWIIKGTASGNSRGHFGASASVGYO 598
DB 529 QAYLPKSKMMAIGGGTYLGEAGYAIYSSISDGNWIIKGTASGNSRGHFGTSASVGYO 588

QY 599 W 599
DB 589 W 589

RESULT 14

US-09-669-974-19
: Sequence 19, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: PRIOR FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 19
: LENGTH: 589
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-19

Query Match 88.08; Score 2694; DB 4; Length 589;
Best Local Similarity 89.78; Pred. No. 4.6e-204;
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;

Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATLALLFATVQANATDEDEEEL 60
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATLALLSATSQANATDDEDEEL 60

Qy 61 EPVVSALVLOFMIDKEGNGENESTGNGSIYDNNHTLHGATVTLKAGDNLIKQNTN 120
Db 61 ESARSALVLOFMIDKEGNGEISTGDIWSIYDDNHTLHGATVTLKAGDNLIKQ--- 117

Qy 121 KNTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 180
Db 118 -----SGKDTYSLKKELDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170

Qy 181 DTVHLNGIGSTLDTLLNTGATTNVDNVTDDKKRAASVKDVLNAGNWKGVKPGTT 240
Db 171 DPTVHLNGIGSTLDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNWKGVKGTST 228

Qy 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKONGKRTVEVKIGAKTSVKEKDKLVTG 298
Db 229 TCQSENVDVFTYDTVEFLSADTKTTTVNVESKONGKRTVEVKIGAKTSVKEKDKLVTG 288

Qy 299 KGKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKPEFVTSGTNTVFA 358
Db 289 KGKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKPEFVTSGTNTVFA 348

Qy 359 SGKGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSP 418
Db 349 SGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSP 408

Qy 419 SKGKMDETVNIAGNNEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDDKGALNV 478
Db 409 SKGKMDETVNIAGNNEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDDEGALNV 468

Qy 479 GSKDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDNVNAGNARAGTAQAATAGL 538
Db 469 GSKDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDNVNAGNARAGTAQAATAGL 528

Qy 539 VQAYLPKGSMMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGY 598
Db 529 AQAYLPKGSMMMAIGGGTYLGEAGYAGYSSISDTCNWIKGTASGNSRGHFGTSASVGY 588

Qy 599 W 599

Db 589 W 589

RESULT 15

US-09-377-155-21
: Sequence 21, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 21
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 87.78; Score 2685; DB 4; Length 591;
Best Local Similarity 89.4%; Pred. No. 2.4e-203;
Matches 538; Conservative 16; Mismatches 34; Indels 14; Gaps 4;

Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATLALLFATVQANATDEDEEEL 59
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATLALLFATVQASANNEQEDEL 60

Qy 60 -LEPVRSALVLOFMIDKEGNGENEST-GNIGWSIYDNNHTLHGATVTLKAGDNLIKQ 117
Db 61 YLDPQRTVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITTLKAGDNLIKQ 120

Qy 118 NTNKNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 177
Db 121 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170

Qy 178 TNGDTTVHLNGIGSTLDTLLNTGATTNVDNVTDDKKRAASVKDVLNAGNWKGVKVP 237
Db 171 TNGDTTVHLNGIGSTLDTLLNTGATTNVDNVTDDKKRAASVKDVLNAGNWKGVKVP 230

Qy 238 GTTASDNVDVHTYDTVEFLSADTKTTTVNVESKONGKRTVEVKIGAKTSVKEKDKLVT 297
Db 231 GTTASDNVDVHTYDTVEFLSADTKTTTVNVESKONGKRTVEVKIGAKTSVKEKDKLVT 290

Qy 298 KGKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKPEFVTSGTNTVFA 357
Db 291 KGKGENGSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKPEFVTSGTNTVFA 350

Qy 358 ASGKGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVS 417
Db 351 ASGKGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVS 410

Qy 418 PSKGMDETIVNIAGNNEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDDKGALN 477
Db 411 PSKGMDETIVNIAGNNEITRNKNIDATSMTPQFSSVSLGAGADAPTLVSDG--DALN 469

Qy 478 VGSRDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDNVNAGNARAGTAQAATAG 537
Db 470 VGSRDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDNVNAGNARAGTAQAATAG 529

Qy 538 LVQAYLPKGSMMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGY 597
Db 530 LVQAYLPKGSMMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGY 589

Qy 598 QW 599

Món Jul 8 07:47:54 2002

us-09-771-382-6.std.ra1

Page 9

Db 590 QW 591

Search completed: July 3, 2002, 08:10:21
Job time: 533 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:25 ; Search time 95.27 seconds
(without alignments)
604.151 Million cell updates/sec

Title: US-09-771-382-6
Perfect score: 3060
Sequence: 1 MNKIYRIWNSALNAWAVS.....TASGNSRGFCASASVGVQW 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2685	87.7	591	2	G81133	adhesin NMB0992 fi
2	2587.5	84.6	592	2	A81888	probable surface p
3	601.5	19.7	298	2	I64138	adhesin homolog Hi
4	410.5	13.4	1190	2	A82615	surface protein XF
5	407	13.3	1107	2	AC0976	probable autotrans
6	406.5	13.3	2059	2	D82671	surface protein XF
7	369.5	12.1	1588	2	A86036	probable adhesin Z
8	369.5	12.1	1588	2	H91188	probable adhesin E
9	341	11.1	658	2	AC0110	probable surface p
10	264.5	8.6	1004	2	H82672	surface-exposed ou
11	241	7.9	2249	2	A41477	190K surface antig
12	240	7.8	1091	2	G64964	hypothetical prote
13	231	7.5	4919	2	T31105	hypothetical prote
14	228	7.5	949	2	D90803	Aida-I adhesin-lik
15	228	7.5	1005	2	H85611	probable adhesin-z
16	228	7.5	1325	2	A64905	ydek protein - Esc
17	225.5	7.4	1286	2	S28634	adhesin AIDA-I pre
18	221.5	7.2	1910	2	AF0394	probable adhesin h
19	221.5	7.2	2021	2	A97859	190-KDa cell surfa
20	217.5	7.1	2551	2	B98047	hypothetical prote
21	215	7.0	3705	2	AD0123	probable autotrans
22	213.5	7.0	1487	2	AG2560	hypothetical prote
23	213	7.0	1029	2	T30852	outer membrane pro
24	213	7.0	3013	2	AB0480	probable invasiv y
25	211	6.9	1109	2	A56143	surface-array prot
26	210	6.9	1536	2	A43855	high-molecular-wei
27	206	6.7	1477	2	B43855	high-molecular-wei
28	204.5	6.7	1343	2	D85724	hypothetical prote
29	203.5	6.7	1343	2	E90893	hypothetical prote

30	203	6.6	5291	2	F90696	hypothetical prote
31	202.5	6.6	936	2	I40711	sapB protein - Cam
32	202.5	6.6	4336	2	AH2515	hypothetical prote
33	201.5	6.6	893	2	A37284	surface-array prot
34	201.5	6.6	1635	2	A10452	hemolysin [impor
35	200	6.5	1645	2	JN0896	crystalline surfac
36	199.5	6.5	1655	2	E97835	hypothetical prote
37	199.5	6.5	3029	2	S76109	hypothetical prote
38	199	6.5	961	2	AD0548	puative autotransp
39	197.5	6.5	2020	2	C48399	ABC-type transport
40	197	6.4	1366	2	S57664	Iga-specific metal
41	197	6.4	2514	2	F81045	hemagglutinin/hemo
42	196.5	6.4	585	2	F90961	flagellin [impor
43	195.5	6.4	585	2	F85809	hypothetical prote
44	194.5	6.4	5188	2	B85547	probable RTX famli
45	193.5	6.3	365	2	AB3486	cell surface prote

ALIGNMENTS

RESULT 1

G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match	87.7%	Score 2685;	DB 2;	Length 591;
Best Local Similarity	89.4%	Pred. No. 1.9e-129;		
Matches 538;	Conservative 16;	Mismatches 34;	Indels 14;	Gaps 4;
Qy 1	MNKIYRIWNSALNAWAVVSELTRNHTKRASATVKTAVLATLLFPATVQANATDEDEEE- 59			
Db 1	MNKIYRIWNSALNAWAVVSELTRNHTKRASATVKTAVLATLLFPATVQASANNNEEQEEDL 60			
Qy 60	-LEPVRSALVLOFMIDKEGNGENEST-GNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQ 117			
Db 61	YLDPVQRTAVLVIVNSDKETGEKVEENSDWAVFNEKGVLTAAREITLKAGDNLKIKQ 120			
Qy 118	NTMKNENTNDSSFTYSYLUKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAG 177			
Db 121	-----NGNFYTSYLUKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAG 170			
Qy 178	TNGDTTVHLNGIGSTLDTLLNTGATTNTVNDNVTDKKRAASVKDVLNAGNINIGVKP 237			
Db 171	TNGDTTVHLNGIGSTLDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGNINIGVKP 230			
Qy 238	GTTFASDNVDFVHTYDVEFLSADTKTTTVNVEKDKNGKRTPEVKIGAKTSVIKEKDGKLVLT 297			
Db 231	GTTFASDNVDFVHTYDVEFLSADTKTTTVNVEKDKNGKRTPEVKIGAKTSVIKEKDGKLVLT 290			
Qy 298	GKGGKNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTNVTF 357			
Db 291	GKDKGNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFTETVSGTNVTF 350			
Qy 358	ASGKGTTATVSKDDQGNITVKYDVNVGDALNVNLQNSGNWLDKAVAGSSGKVGISGNVS 417			

Db 351 ASGGTTATVSKDDQGNITVYDVGALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410
Qy 418 PSKGMDETWINAGNNIEITRNKKNIDIAATSMPTQFSSVSLGAGADAPTLVSDDKGALN 477
Db 411 PSKGMDETWINAGNNIEITRNKKNIDIAATSMPTQFSSVSLGAGADAPTLVSDDKGALN 470
Qy 478 VGSKDANKPVRITNVAPGVKGGDTNVAQLKGVAGNLRNIDNDGNARAGIAQAIATAG 537
Db 470 VGSKDANKPVRITNVAPGVKGGDTNVAQLKGVAGNLRNIDNDGNARAGIAQAIATAG 530
Qy 538 LVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGY 597
Db 530 LVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGY 590
Qy 598 QW 599
Db 590 QW 591

RESULT 2
A81888
adhesin surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.
A:Reference number: A81775; MUID:20222556
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A:Experimental source: serogroup A, strain 22491
C:Genetics:
A:Gene: NMA1200

Query Match 84.6%; Score 2587.5; DB 2; Length 592;
Best Local Similarity 88.0%; Pred. No. 1.8e-124;
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

Qy 1 MNKRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
Db 1 MNKRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
Qy 61 EPPVRSALVLOFMIDKCEGNGENSTGNIGWSIYYDNDHNTLHG-ATVTLKAGDNLKIKQNT 119
Db 61 ESVQRS-VVGSIQASMEGSGELET--ISLSMTNDSKEFEVDPIYVVTLLKAGDNLKIKQ-- 114
Qy 120 NKNNTNENTNDSFYSYSLKDLTDLTSVETEKLSFGANGKNVNIISDYKGLNFAKETAGTN 179
Db 115 --NTNENTNASSFTYSYSLKDLTGLINVEETEKLSFGANGKNVNIISDYKGLNFAKETAGTN 172
Qy 180 GDTTVHLNGIGSTLTDLLNTGATTNTVNDNVTDDKKRAASVKDVLNAGNIRKGVKPGT 239
Db 173 GDTTVHLNGIGSTLTDLLAGSASHVDAGNOST--HYTRAASIKDVLNAGNIRKGVKPGT 230
Qy 240 TA--SDNVDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGAKTSVIERKDGKLV 297
Db 231 TTGQSNVDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGAKTSVIERKDGKLV 290
Qy 298 GKGKNGSSDDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFETVSGTNVTF 357
Db 291 GKGKNGSSDDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFETVSGTNVTF 350
Qy 358 ASGGTTATVSKDDQGNITVYDVGALNVNQLNSGWNLDKAVAGSSGKVISGNVS 417
Db 351 ASGGTTATVSKDDQGNITVYDVGALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410

Qy 418 PSKGMDETWINAGNNIEITRNKKNIDIAATSMPTQFSSVSLGAGADAPTLVSDDKGALN 477
Db 411 PSKGMDETWINAGNNIEITRNKKNIDIAATSMPTQFSSVSLGAGADAPTLVSDDKGALN 470
Qy 478 VGSKDANKPVRITNVAPGVKGGDTNVAQLKGVAGNLRNIDNDGNARAGIAQAIATAG 537
Db 471 VGSKDANKPVRITNVAPGVKGGDTNVAQLKGVAGNLRNIDNDGNARAGIAQAIATAG 530
Qy 538 LVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGY 597
Db 531 LVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGRHFGASASVGY 590
Qy 598 QW 599
Db 591 QW 592

RESULT 3
I64138
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TRIGR>
A:Cross-references: GB:U32846; GB:LA2023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 19.7%; Score 601.5; DB 2; Length 298;
Best Local Similarity 44.2%; Pred. No. 7.8e-24;
Matches 148; Conservative 37; Mismatches 85; Indels 65; Gaps 9;

Qy 1 MNKRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOA-----N 50
Db 1 MNKIFKVIWNVVTTQTVVSVSELTRAHTKRTSATVATVATVLSATVLSATVQAINDAAGTFFVKVQ 60
Qy 51 ATDEDEEEELPVPVRSALVLOFMIDKCEGNGENSTGNIGWSIYYDNDHNTLHGATVTLKAG 110
Db 61 STEDDIEDS-----AATKDON-----KNOALKAGDTLTLKAG 92
Qy 111 DNLKIKONTNKNNTNENTNDSFYSYSLKDLTDLTSVETEKLSFGAN-----GNKVNIT 163
Db 93 KNLKAKL-----DQGGKSVTFALAKDLVDKTAKVSDTLTIGNTPAAGGATPKVSIT 144
Qy 164 SDFKGLNFAKETAGTNGDTTVHLNGIGSTLTDLLNTGATTNTVNDNVTDDKKRAASVK 223
Db 145 STADGLKLAK---GTNGDGTAVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTRAATIK 200
Qy 224 DVLNAGNIRKGVKPGTTFASDNVDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGA 283
Db 201 DVLNAGNIRKGVKPGTTFASDNVDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGA 280
Qy 284 KTSVIERKDGKLVTKR-----GKGENGS-STDE 310
Db 261 KTSVIERKDGKLVTKR-----GKGENGS-STDE 295

RESULT 4
A82615
surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <STM>
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN001
A:Experimental source: strain 945c
R:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H.
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1981

Query Match 13.4%; Score 410.5; DB 2; Length 1190;
Best Local Similarity 24.8%; Pred. No. 2.4e-13;
Matches 163; Conservative 88; Mismatches 206; Indels 201; Gaps 27;
QY 84 STGNCWSYI--YDHNHNLHGATVTLKAGD-NLKIKQNTNNTNNTNDSFTY--SLK 137
DB 592 STASKGNLLASGANSNVVPGESVDLKNKSDGNLLITKT-----DSNDVTFNLTALK 645
QY 138 KD--LTDLSVTEKLSFGAN-----GNK--VNI---TSDTK 167
DB 646 VSLTGTGNTAMTGDVTVGSGNLTGLTVDPVTSVSSGISAGNOKITNVAAGTADTD 705
QY 168 GLNFA-----KETAG----- 177
DB 706 AVNFSQQAQVSSTASKGNLLASGANSNVVPGESVDLKNKNTDGNIVISKESGNDVLFNL 765
QY 178 -----TNGDTTVHLNGISGTLTDLTLLNTGATNTVNTDNDKRAASVKKDLVNA 228
DB 766 SSSLKLDKLTVDGVTMTNGV-----TVGSGVTLGSMGLVITDGPVTSSTSGI-----NA 814
QY 229 G-WNIKGVKPGTTASDNVDF-----VHTYDTVEFLSADTKTTTVNVESKDN 273
DB 815 GSKITNVAAGTADTDVAVNLSQLNTAMAGSGAKSVHYIYTD---GGTGGNVNGDGATG 871
QY 274 GKRTVEYKIGAKTSVIEKDKGLVTKGKGENG--SSTDEGEGLVTAKEVIDAVNKAGWRMK 332
DB 872 TRSIAVGVGTASA-----EGATAVGSAAASCKGSTAIGNAVASADGSGVALGD--CAKDG 926
QY 333 TTFANGQTQADKFETVTSNTVTSAGKGTATVSKDDQGNITVYKIDVNVGDALNVNQL 392
DB 927 ARGAESYTGKISGLQNTVTVSGVDSKGETRTVS-----NVADAKEAT--DAVNLRL 979
QY 393 ----QNSGWNLDKSAVAGSGKVISGNVSPSGKMDVTNINAGNIEITRNGKNIDIAI 448
DB 980 DRVAQDANRYVDNKIESLSEGGTF-----VKVNSLNN-----SAT 1014
QY 449 SMTPOFSSVSLGAGADA-----PTLSVDDKGL--NVSCKDANK 485
DB 1015 PIAAGVDATAIGVATASGADSIAMGNKASASADNAVAGNHSVADRANTVSVGSAGSER 1074
QY 486 PVRTNVAQVKGEDVTNVAQKGVAGNINNRIDNVGNAR-----AGIAQATATAGLVOA 541
DB 1075 --QVTNVAAGTADTDVAVNVSQNLQGLITAKQYTDGVVGSILRRDITDGGVAAATATANLPOA 1132
QY 542 YLPCKSMALGGTGYGEAGYAGYSSISDGGNWLKGTASGNRSGHFGASASVGVQW 599

DB 1133 YIPGRMNTSVGVSSYRGQSAIAVGVSSVSESGRWVFKFSGSANTRSQVIGAGVGVQW 1130
RESULT 5
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fair
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:gl6504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 13.3%; Score 407; DB 2; Length 1107;
Best Local Similarity 22.1%; Pred. No. 3.3e-13;
Matches 188; Conservative 116; Mismatches 255; Indels 290; Gaps 32;
QY 27 TKRASATVKTAVLATLILFATVOANATDEDEEEL-----EPVVRSAVLVQLQFMIDKEGEN 82
DB 273 TFSASRNGSASKITNLAAGTLAADSTDAVNGSOLYETNOKVDQNTSAI---ADINTSITN 329
QY 83 ESTGNCIGWYIYDNNHNLHGATVTLK-----AGD-----NLKIKONTN 120
DB 330 LSSDNLNWNETNFSASGSSSTNNKITNVAAGELSEESTDAVNGSOLFETNEKVDQNTT 389
QY 121 ---KNTNENTNDSSFTYSLKKDLTDL--TSV-----ETEKLSFGAN--GNKNVITS 164
DB 390 DIAANTNTITQNSTAIENLTNVSIDNTSITGLTDNALLWDEDTGAFSAHSGSTSKITN 449
QY 165 DTKGLNFAKETAGTNG---DITVHLNGISGTLTDLTLLNTGATNTVNTDNDKRAA 220
DB 450 VAAGALSESDDAVNGSOLYETNOKVDQNTSAID--INT-SITNLGTDALSWDDEGAF 506
QY 221 SVKDLVNLNAGNWKGVKPGTTASDNVDFVH---TYDT-----VEFLSADTKTTVN 267
DB 507 SASHGTSKGTNKTNNVAAGEIASDSDTAINGSOLYETNMLISQYNESISQLAGTSETYIT 566
QY 268 -----VESKDNKGRTEVKIGAKTSVIEKDKGLVTKG---KGENGSSDTDEG----- 311
DB 567 ENGTGVKYRTINDNGLEGQDAYATNGATAVGYDAVASAGCIALQGNSSSSTEGSIALG 626
QY 312 -----EGLV-----TAKEVIDAVNKA-----GWRMKTITFANGQTG 342
DB 627 SGSTSNRAITTGIRETSATSDGVVIGYNTDRELLGALSGLTGDGSEYRQITNVADG--SE 684
QY 343 ADKFETVTSNTVTSAGKGTATVSKDDQGNIT-----VKYDVMV 383
DB 685 AQDAVTVRLQNAIGA---VTTPTKYHYHANSTEEDSLAVGTDLSLAMGAKTIVNADAGI 740
QY 384 GDALNVNQLQN--SGWNLDKSAVAGSGKVISGNVSP----- 418
DB 741 GIGLNTLVNADALNGIAIGSNARANHANSTAMGNGSOTTRGAQTDYATNMDTPQNSVGE 800
QY 419 -SKGKMD---ETVNIAGN-----NIEITRNGKNI----- 444
DB 801 FSYGSEGGORQITNVAAGSADTDVAVNVGQLKVTDQVSRNTQSITNLNTQVSNLDTFRVTN 860
QY 445 -----DIATSMTPQF-----SSVSLCAGADAP-----TLSV--DDKG 474

Db 861 IENGIGDIVTGTGKYFKTNTDGADANAQAQADSVAGSGSTAAASNSVALGTNSVADEAN 920
Qy 475 ALNYSKSDANKPVRITNVAPGKEDGTNVNAQLK-----GSSTDEGEGLVTAKEVIDAVNKA 327
Db 921 TVSVGSSTQOR--RITNVAAGVNNVTDVAVNAQLKASEAGSVRYETNADGSVNYSVLNLGD 978
Qy 509 -----GVAQ-----NLRNDRNDVGNARAGIA 530
Db 979 GSGGTTTRIGNVSAAVNDTDVAVNAQLKRSVEANTYTDQKMGEMNSKIKGIENKMSGGIA 1038
Qy 531 QAIATAGLVQAYLPCKSMMAIGGTYRGEAGYAGYSSISDGGNWLKGTASGNSRGHFG 590
Db 1039 SAMAWGLPQAYAPGANNTSITAGCTFNGESAIVAGSVMSSEGGWYKLGQTSNSQGDYS 1098
Qy 591 ASASGYQW 599
Db 1099 AAGAGFQW 1107
RESULT 6
D82671
surface protein xfl529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-2059 <SIM>
A:Cross-references: GB:AE003982; GB:AE003849; MID:g9106554; PIDN:AAF84338.1; GSPDB:GN001
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.V.; Sawasak
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XFl529

Query Match 13.3%; Score 406.5; DB 2; Length 2059;
Best Local Similarity 25.5%; Pred. No. 7.8e-13;
Matches 170; Conservative 93; Mismatches 219; Indels 185; Gaps 32;
Qy 89 GWSIYYDNH--TLHGATVTLKAGD-NLKIKQNTK-----NTNENTNDSSFTY----SL 136
Db 1422 GWTLTASGANGSKVSGGTVDLKNLTGNTGLTISKSDSNDVVFNLSDELKESITVGNLTQ 1481
Qy 137 KKDLTDLTS---VTEKLSFGANGKNVITSDTKGLNFAKETA---GTNGDTTVHLNGI 189
Db 1482 DKDGVKSSNVLLDSNELVITSHSSTSSVKTLANGESVNVRTVVVNGDVNIDVVVNDL 1541
Qy 190 -----GSTTDLTLNLTGA---TTNVT-----NDNVTDDKKRAASVKDVLNAGWNI----- 232
Db 1542 GLSIVGASLTLSGINAGSHKITNVTAGTDTDAVNFSQLK---SVSEAVDKGWTLTASG 1598
Qy 233 ----KGKPGCTTASDNDV-----FVHTYDTVEFLSADTK-----TTTVNVESKDNG 274
Db 1599 ANGSKVYSGGTVDLKNLTGNTGLTISKSDSNDVVFNLSKDFKDVETAGTAVNTDGVKVG 1658

Qy 275 KRTEVKIGAKTSVIEKDKGLVTKGKGEN-----GSSTDEGEGLVTAKEVIDAVNKA 327
Db 1659 --SDVSLGAMCLFTANGSPVYATSGFNAGDKVISHVAVGMADTDVAVNSQLKQAVQSVTVK 1716
Qy 328 GWRMKTTT-----ANGQTGQ---ADKFETVTSGTNV-----TFASGKGT--- 364
Db 1717 ATRYSTNDGTOGGTGDGATGSKAIAAGVGTQASGEAAAVSGAAASGKGTALGR 1776
Qy 365 -ATVSKD-----DQG-----NITVKYD-----VNVG----- 384
Db 1777 NATASDGSVALGDKGGRGAESYTGKYSGVQNVNTVGTVSVGDAAKAGETRSTSNVADA 1836
Qy 385 ----DALNVNQL-----QNSGNWLD-----KAVAGSSGKVISGNSVSPSKGMD 424
Db 1837 KEAMDAVNLRLQDAVAKSNLQTDMMRHEINNIEDVFKITKDSASSVKG----- 1886
Qy 425 ETVNINA---GNNTIEITRN-----GKNIDTATSMTPQFSSVSLGAGADAPLTSVDDKAL 476
Db 1887 --MGVNMAIGTNAAVSGTESVALGKNTNVSAD-----NAVAIGNGSA-----DRANSV 1934
Qy 477 NVGSKDANKPVRITNVAPGKEDGTNVNAQLKGVNAQLNLRNDRNDVGNAR-----AGTAAQ 532
Db 1935 SVSGGSGSER--QVTNVAAGTADTDVAVNSQLNOGLITAKQYTDGMVGNLRRRETSGGVAA 1992
Qy 533 IATAGLVQAYLPCKSMMAIGGTYRGEAGYAGYSSISDGGNWLKGTASGNSRGHFGAS 592
Db 1993 IATANLPQAYVQGRGTMVSGVSSVQGGOSATAVGVSAGSHWVFKFSGSANTRSHVGVG 2052
Qy 593 ASVGYQW 599
Db 2053 AGVGYQW 2059
RESULT 7
A86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; MID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 25029

Query Match 12.1%; Score 369.5; DB 2; Length 1588;
Best Local Similarity 24.7%; Pred. No. 4.2e-11;
Matches 164; Conservative 97; Mismatches 259; Indels 143; Gaps 26;
Qy 49 ANATDEDEEELPVRKSVLQFMIDKEGNG-----ENES-----TGNIGWSIYYDN 96
Db 957 ANAEYNNVGDAIDLDNAL----LWDETANGAGAVNASHDGKASITTNVANGSISDS 1012
Qy 97 HNTLHGATVTLKAGDNLKIKONTNKNENTNDSSFTYSLKKDLTDLTSVET--EKLSEF- 153
Db 1013 TDAVNSQLN---ATNMIEQNT--QIINLAGNTDAIY--IQENGAGINVRTNDGDLAFN 1067
Qy 154 -----GANGKNVITSDTKGLNFAKETAAGTNGDTTVHLNGISLTTLTLLNTGA--TTNVT 207
Db 1068 DASAQGVGATAIGYNSVAKGDSVAIOGGSVDVDTGIALGSSSVSRVIAKGSRDTSIT 1127
Qy 208 NDNV-----TDDKKRAASVKD-----VLNAGWNTKGVKPGTASDNDVF----- 247

Db 1128 ENGVIYDITDGGELGALSIGDDGKYROIIN-----VADGSEAHDAVTVRQLQNAIG 1180
QY 248 -VHTYDTVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIEK-----DGKLV 296
Db 1181 AVATPTKTFHANSTEEDSLAVGT-----DSLAMGAKTIVNGDKIGIGYGAYVDANAL 1234
QY 297 TKGKGE-----NGSSTDEGGLVTAKEVIDAVNKGWRMKTITANGQ-----339
Db 1235 NGIAIGSNAQVIHVSIAIGNGSTTTTGAQTNTYATNMDAPQNSVGEFSGSADGQRIIT 1294
QY 340 ---TGQADKFETVSTNTVTFASGKGTATTATVSKDDGDNIT-----VKYDVNV 383
Db 1295 NVAAGSAD-----TDAVNV--GOLKVTDAQVSONTO--SITNLDNRVTNLSRVNTIENGI 1346
QY 384 GDAL-----NVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKM---DETVDNIN 430
Db 1347 GDIVTTGSKYKFTNTDGDVDSAQGKDSVAIGSGSIAAADNSVALGTGVSATTEENTISVG 1406
QY 431 AGNIEITRN---GKNIDIASMTPOFSSVSLGAGADAPTLSVDDKGALNVGSKDANKPV 487
Db 1407 SSTNQRRIITNVAAGKNATDAVNVAQLKSEAGGVRYDTKADGSIDYSNITLGGNGG-TT 1465
QY 488 RTNVAPEGVEGDVTNVAOLKGVAQ-----NLNRRIDNVGNARAGIAQAIATA 536
Db 1466 RISNVSAGVNNNDVNVYAQLKQSVQETKQYTDQRMVEMDNKLSKTESKSGGIASAMAMT 1525
QY 537 GLVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNIIKGTAGNSRGHFGASASVG 596
Db 1526 GLPQAVTPGASMASIGGGTYNGESAVALGSMVSNRVRVYKLOGSTNSQGEYSAAALGAG 1585
QY 597 YQW 599
Db 1586 IQW 1588

RESULT 8
H91188
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4480

Query Match 12.1%; Score 369.5; DB 2; Length 1588;
Best Local Similarity 24.7%; Pred. No. 4.2e-11;
Matches 164; Conservative 97; Mismatches 259; Indels 143; Gaps 26;
QY 49 ANATDEEEELPEPVRSALVQFMIDKENG-----ENES-----TCNIGWSIYYDN 96
Db 957 ANAEYNVGDALDLDNAL----LWDETANGAGAYNASHDGKASIIINVANGSISEDS 1012
QY 97 HNTLHGATVTLKAGDNLKIQTQNTKNTNENTNDSSTYSLLKDLTLTSVET--EKLSP- 153
Db 1013 TDVANGSOLN--ATNMTEQNT-QIINLAGNTDATY-IQENGAGINVTYRTNDDGLAFN 1067
QY 154 ----GANGKNYITSDTKGLFAKETAGTNGDTTVHLANGIGSTLDTLLNTCA-TTNT 207
Db 1068 DASAQGVGATAGYNSVANGDSVAIGQGSYSDVTGIALGSSSVSRVIAKGRDTSIT 1127
QY 208 NDNV-----TDDKKRAASVKD-----VLNAGWNKIGVKPGTTASDNVDF-----247

Db 1128 ENGVIYDITDGGELGALSIGDDGKYROIIN-----VADGSEAHDAVTVRQLQNAIG 1180
QY 248 -VHTYDTVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIEK-----DGKLV 296
Db 1181 AVATPTKTFHANSTEEDSLAVGT-----DSLAMGAKTIVNGDKIGIGYGAYVDANAL 1234
QY 297 TKGKGE-----NGSSTDEGGLVTAKEVIDAVNKGWRMKTITANGQ-----339
Db 1235 NGIAIGSNAQVIHVSIAIGNGSTTTTGAQTNTYATNMDAPQNSVGEFSGSADGQRIIT 1294
QY 340 ---TGQADKFETVSTNTVTFASGKGTATTATVSKDDGDNIT-----VKYDVNV 383
Db 1295 NVAAGSAD-----TDAVNV--GOLKVTDAQVSONTO--SITNLDNRVTNLSRVNTIENGI 1346
QY 384 GDAL-----NVNQLNSGNWLDKAVAGSSGKVISGNVSPSKGKM---DETVDNIN 430
Db 1347 GDIVTTGSKYKFTNTDGDVDSAQGKDSVAIGSGSIAAADNSVALGTGVSATTEENTISVG 1406
QY 431 AGNIEITRN---GKNIDIASMTPOFSSVSLGAGADAPTLSVDDKGALNVGSKDANKPV 487
Db 1407 SSTNQRRIITNVAAGKNATDAVNVAQLKSEAGGVRYDTKADGSIDYSNITLGGNGG-TT 1465
QY 488 RTNVAPEGVEGDVTNVAOLKGVAQ-----NLNRRIDNVGNARAGIAQAIATA 536
Db 1466 RISNVSAGVNNNDVNVYAQLKQSVQETKQYTDQRMVEMDNKLSKTESKSGGIASAMAMT 1525
QY 537 GLVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNIIKGTAGNSRGHFGASASVG 596
Db 1526 GLPQAVTPGASMASIGGGTYNGESAVALGSMVSNRVRVYKLOGSTNSQGEYSAAALGAG 1585
QY 597 YQW 599
Db 1586 IQW 1588

RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bartel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 11.1%; Score 341; DB 2; Length 658;
Best Local Similarity 24.7%; Pred. No. 3.8e-10;
Matches 124; Conservative 70; Mismatches 204; Indels 104; Gaps 17;
QY 149 EKLFGANGKNYITSDTKGLNFAKETAGTNG-----DTTVHLNGIGSTLTD 195
Db 210 QSLALGAGA---VTQANSIALGAASINTVGAQSSYSAYALTAPQASVCELIGITAGLN 265
QY 196 TLLNTGATTNVTNDNYT-----DDKKRAASVKDVLNAGWNKIGVKPGTTASDNVDF 247
Db 266 RKITGVAAGSASSDAVNVAQLTAVGQVQONTANITSLGGRVTTIEGSMASIAMGGVKY 325
QY 248 VHTYDT-VFELSADTKTTTVNVESKNGKRT-----EVKIGAKTSVIEKDKLVTGK 300
Db 326 FHANSTQPSVASGTSNVAIGPASLASGNAALASGAGAVAIG--DGAASADSGVAIGQ 383

Qy 301 KGENSGSTDBEGCLVTAKEVIDAVNKAGWRMKTTTANGQTGGADKFEETVTSGTNVTFASG 360
 :||| : | : : ||| :
Dd 384 SGDNRGVENYIG-----KYNSASTSSG-----TVSVGNTAT---- 416
 :||| : | : : ||| :
Qy 361 KGFTATVSXDDQCNIIVKVVDNVGDALNVLNQSLGWNLDSKAVAGSSGVISGNVSPSK 420
 :||| : | : : ||| :
Dd 417 -GETRTSVNAVDC-----LQATDAVNLRQLDGL- IAAISVVVNNVSGLGQ 458
 :||| : | : : ||| :
Qy 421 GKMDETVINIAGNNII-EITRNGKNIDI--ATSMTPOFSSVSLGAGADAPTLS----- 469
 :||| : | : : ||| :
Dd 459 NGTDGMFOVQNVNSSGLAKPSATGSATGANSTAFCSGSAKAATAANSAAALCANS 518
 :||| : | : : ||| :
Qy 470 -VDKGALANVGSDKANPKPVRIITWAPCVKEGDVTINVAQLKGYAQN-----LNNRIDNVGCN 524
 :|||| : | : : |||| :
Dd 519 VADRANSVSYGVSNGER--OITWNPAQTGTDAVFNDOLKSIASNOTNAYNTRQRYSELKOD 576
 :|||| : | : : |||| :
Qy 525 AR-----AGIAQAATACLAGLVAYLPKGSMMAIIGCTTYRGEAGYAIGYSISI SDGGNWII 577
 :||| : | : : |||| :
Dd 577 LRKQNSVLRSAGIASMSMASLTOPYTS GSSNTTI GAASYRQSALS LGVSSI SDSGRHWS 636
 :||| : | : : |||| :
Qy 578 KGTAGSNGSRGHFGCASVGVYG 599
 :||| : | : : |||| :
Dd 637 KLQASSNTQGDFGIGVGVG YQOW 658 .

RESULT 10

C82672

Surface-exposed outer membrane protein Xf1516 [imported] - *Xylella fastidiosa* (strain 9a)

C;Species: *Xylella fastidiosa*

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: C82672

R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequences

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A;Reference number: AB2515; MUID:20365717

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: C82672

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1004 <SIM>

A:Cross-references: GB:AE003981; GB:AEO03849; MID:g9106543; PIDN:AAF84325.1; GSPDB:CN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A.

Brites, M.R.S.; Bueno, M.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.

as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuranae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeiral, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; Miracca, E.C.; Miyaki, C.Y.;

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira

M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vittore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1516

Db 120 FSKAFAPNATALGVNSVTSQANNVVALGSNST-----VSGVNSVALGAGSMA 167
QY 158 NKNVITSDTKGLNFAKETAGTNGDVTTVHLNGIGSTLTDLLNTGATTNTNDNVTDKKK 217
Db 168 SELNVISVGGG-----DGTGPAVRRIVNVG---DGIGNDNAVKNKSLDGVTSVND 216
QY 218 RAASVKDVL-----NAGWNKGVKPGTTA--SDNVDFVHTVTEF----- 256
Db 217 VAASVKTIALTNTQVSSVASASGKESTAIGSQAQAVDN-----TVAFGGRATANA 268
QY 257 -----LSADT-----KTTTVNVESKD-----NGKRTVEKIGAKTSVIEK 291
Db 269 VGASALGDFDSHAKGINSTTVGTQSVSLGQGVSLGYSFVGEGSFNGLALGSNSLVLLQ 328
QY 292 DGKLVTKG---KGENGSSDDEGEL--VTAKEVI-----DAYNKAGWRMKTITAN 337
Db 329 VDSVALGSGSMASEPNVSVSGDGLRGPVRRIRIVNVGDIGNNDAYKNKSOLDGVTVASVN 388
QY 338 GQTQADKFEIV--TSGTNTVTFASGKTKTAT--VSKDQGNITVKYDVNVGDALNVNQLON 394
Db 389 DVASVKNIAQAIIQTIGSGVASVSGDSTAAGASQAAGDSSIA---LGARSANAIGS 444
QY 395 SGWNLD-----SKAVAGSSGKVISGNVSPSKCKMETVINAGNNIETRNCKNDIA 447
Db 445 SALGVGDHALGANSTALGGQSTAISEGTSLG---YNSFVGOSATNGIALGSN----- 494
QY 448 TSMTPQPSYSSVLGAGADAPTLSDVKALNVGSKD--ANKPV--RITNVAPCKREGDVTNV 504
Db 495 -AIVSGVNSVALGAGSVASELNV-----ISVGGDGTGTPAVRRIVNVGDIGNNDVANK 548
QY 505 AQLKGVAQNLN-----RIDNVDGNAR---AGIAQAI---ATAGLVOAYLPKSMMAIG--- 552
Db 549 SOLDGVTVASVNDVAASKVIQGTIIQTIGSGVASAIGKDSATGASQAQAVGSSVALGTGA 608
QY 553 -----GGTYRGEAGYAIGYSSISDGGNWIK-----CTASGNSRGH 588
Db 609 TANAIGSSVLGVDSSRRARGINSTALGROSNAIGDGSVSLGFSFVRQSGEHGVALGTDAVG 668
QY 589 FGA-SASVGY 597
Db 669 SGKDSIALGY 678

RESULT 11
A14177
190K surface antigen precursor - Rickettsia rickettsii
C:Species: Rickettsia rickettsii
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 08-Oct-1999
C:Accession: A14177
R:Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.
Infect. Immun. 58, 2760-2769, 1990
A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated,
A:Reference number: A14177; MUID:90354033
A:Accession: A14177
A:Molecule type: DNA
A:Residues: 1-2249 <AND>
A:Cross-references: GB:M31227; NID:g152465; PIDN:AAA26380.1; PID:g152466
A:Note: the authors translated the codon GAT for residue 430 as Gly, and CAA for resi
C:Keywords: surface antigen; tandem repeat
C:1-20/Domain: signal sequence (uncleaved) status predicted <SIGU>

4

Db 763 TLTNANAVITGAIIDNTGDNVGVNLNGLSQTVDIG-----NTNSL--ATISVGAG 814
QY 111 ----DNLKIKQNTKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDT 166
Db 815 TATLGGAIVKATTKLTNA-----ASVLT-----LTNANAVITGAVDNTTGGDNVGV--- 861
QY 167 KGLNFAKETAGTNGDTTVHLNGIGSTPLDTLNTGATNTVNDNV---TDDKKKRAASVK 223
Db 862 --LNLNGLSQTVDG-----IGNTSLATISVGAGTATLGGAIVKATTKLTNAASVL 912
QY 224 DVNLNAGNNIKGVKPGCTTASDNVDVFTVDFEFLSADTKTT---TVNVESKD---NG-- 274
Db 913 TLTNANAVITGAIIDNTGDNVGVNLNGLSQTVDIGTNTSLATISVGAGTATLGGAIV 972
QY 275 -KRTVEVKIGAKTSVKEKDKLVG---KKGKNGSSSTDEGEGLVTAK-----EVIDAVN 325
Db 973 IKATTKLTDAASAVKFTNPVVVGTGAIIDNTGNANNGIVFTGNSTVTVGNVNTNALATVN 1032
QY 326 KA-----GWRMKTFTTAN-----GOTQADKFETVTSGTNVTTFASGKGT 364
Db 1033 VGAGLLQVGGVVKANTINLTDNASAVTFTNPVVVGTGAIIDNTGNANNGI-VTFTGNSTVT 1091
QY 365 ATVSXDDQGNITVKVDVNVGDAL-----NVN-----QLQNS 395
Db 1092 GNV-----GNTNALATVNVGAGLLQVGGVVKANTINLTDNASAVTFTNPVVVGTGAI 1146
QY 396 GWNLDKAVAGSGGKVISGNVSPSKGMDETVNIAGNIEITRNG-----KNIDIATSWT 451
Db 1147 G-NANNGIVTFTGNSTVTGDI-----GNTNALATVNVGAGITLQAGGSLAANNIDFGARST 1201
QY 452 POFSSVSLGAGADAP-----TISVDKDALNVGSKDANK-----PVRITNVAPG----- 495
Db 1202 LEFNGPLDGGRAIPYFYGAIANGNAILNVNTKLLTASHLTIGTVAEINIGAGNLFTI 1261
QY 496 -VKEGDTVNVQALKGVAQNLNRR-----INDVDGNARAGIAQAATAGLVQVAYLPG--- 545
Db 1262 DASVGDVTTILN-----AQINFRARDSVLVLSNLTG---VGVNILLAADLV---APGAD 1310
QY 546 KSMNATGGCTYRGEAGYATGYS--SISDGG 573
Db 1311 EGTVPENGVLNGLVNSVAGTARNIGDGG 1340

RESULT 12
G64964
hypothetical protein b2000 - Escherichia coli
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
C:Accession: G64964
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: G64964
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1091 <BLAT>
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g1788309;
A:Experimental source: strain K-12, substrain MG1655
A:Keywords: nucleotide binding; p-loop
F:683-690/Region: nucleotide-binding motif A (p-loop)

Query Match 7.8%; Score 240; DB 2; Length 1091;
Best Local Similarity 21.9%; Pred. No. 0.0001;
Matches 148; Conservative 80; Mismatches 249; Indels 200; Gaps 33;
QY 1 MNKIYRIIWNLSALNANVAVSELTRNTHKRASATVKTAVIATLLFATVQANATDEDEEEL 60
Db 57 LNTCYRLVNHNTGAFVAVASELARARGGVAVALSAAVTSL----- 100
QY 61 EPVRSALVQLQFMIDKEGNESTGICGSIYDNDHNT--LHGATVTLKAGDNLKIKON 118

Db 101 -PVLAADIIVVH-----PCEIVNGGTLA-----NHDNQIVFGTTNGMTISTGLEYPD 146
QY 119 TNKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTGLNFAKETAGT 178
Db 147 NEANTG-----GQVQDGGTANKTTVTSG--GLQ-RVNPGG 180
QY 179 NGDVTTVHLNGIGSTL-----TDTLLNTG-----ATTNVTNDVNTDDKKRAASVKDV 225
Db 181 VSDTVISAGS-GQSLQGRAVNTTLNGEQMHGEGATGTVINDK----- 224
QY 226 LNAGNNIKGVKPGCTTASDNVDVFTT-----YDTVEFLSADTKTTTVN-----VE 269
Db 225 --GMOV--VKPGTAVATDV--VNTGAEGGDAENGDTGQFVRGDAVRTTINKNGRQIVR 277
QY 270 SKDNGKRTVEKIGAKTSV-----IKEKDKGLVTGKCKGEN 304
Db 278 AEGTANTTVVYAGGDDTVHGHALDITLNGGYQVHNGGTSASDTVNVNSDGMQIVKNG-GVA 336
QY 305 GSSTDEGEGLVTAKEVIDAVN---KAGWRMKTFTTANGOTG--QADKFETVT-SGTNVVTF 358
Db 337 GNTTVNQKGRLOVDAGGTATNTVTLKOGGALVTSTAAVTGGINELGAFSVVEGRADNVLE 396
QY 359 SG-----KGTATVSK-DDQGNITVKVDVNVGDALNVQNLQNSGWNLSKAVAGSSGV 411
Db 397 NGRRLDVLGTGHTATNTRVDDGGTLDVR--NGGTATTVS-MGNGG-----VLLADSGAA 446
QY 412 ISGNVSPSK-----KMDETVNIAGNIEITRNGKNIDIATSWTPOFSSVSLGAGADAP 466
Db 447 VSTRSDGKAFSTGGQADALMLEKSSFTLNAG-----DTATDTTVNGGLTARGGTLAG 502
QY 467 TISVDKDALNVGSKDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNRRINDVDGNAR 526
Db 503 TITLNNGAILTSLGKTVN-----NDTLTIREGD-----ALQGGSLTNGSVSK-SGSGT 551
QY 527 AGIAQAIAATAGLVQVAYLPKGSMMMAIGGT-----YRGEAGYATGYS-----S 568
Db 552 LTVSNTTLTKQKAVNL--NEGTLTNDSTVTTDVIORGTALKLTGTVLNGAIDPTNVT 608
QY 569 ISDGGNWIIGKTASGNS 585
Db 609 LASGATWNPIDNATVQS 625

RESULT 13
T31105
hypothetical protein 2 - Haemophilus ducreyi
C:Species: Haemophilus ducreyi
C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T31105
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.
J. Bacteriol. 180, 6013-6022, 1998
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.
A:Reference number: Z20984; MUID:99030326
A:Accession: T31105
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-4919 <WAR>
A:Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1
C:Genetics:
A:Gene: lspA2

Query Match 7.5%; Score 231; DB 2; Length 4919;
Best Local Similarity 22.4%; Pred. No. 0.002;
Matches 173; Conservative 91; Mismatches 268; Indels 240; Gaps 37;
QY 1 MNKIY----RIIWN---ALNANV-AVSELTRNTHKRASATVKTAVLA-----T 41
Db 376 LNKVYADYVRVVKGKDELANNGQIHADQQQLILNATGHVKLNDGSSVSNLNLGIALNLT 435
QY 42 LLFATVQAN-----ATDEDEEELEPVRVSALVLIQ---FMIDKEGNESTGICGSIY 93

Db 436 LENATVSANNLSFRVNTDKLNNLSKVSARAADLQSGNLDKASVLAKHKTLLNISNDVS 495
Qy 94 YDNHTLHGATVTLKAGDNLIKQ-----NTKNNTENTNDSSFTYSLAKDLTDLTSV 146
Db 496 LNNOSKL-----SANNLAKKKVRDLNLSSELSANNLTNTSNITLK-----538
Qy 147 ETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDITTVHLN---GIGSTLTDITLLNTGAT 203
Db 539 --NKSKEFTAGNWTNLVNTNVT--LNNDSLAANNLTNLVTKVNTLNDASKLSANKLDELNVT 595
Qy 204 TNYTND-----NVTDDKKRAASVKDVLNAGWNKIKGVKPTTASDNDVF 247
Db 596 DNVTLNLSKSTLSAGELFKVKVKNVTNLNDSLAANNLSNASHNVTLLNKSLSAQRADI 655
Qy 248 ----VHTYDVTVEFL--SADFTKTTNVNVEKDKGRTEVKIGAKTSVKEKDKGLVTG---298
Db 656 KAVNLTLDITTELAKNLIDNSTIIT-----NNGTIAGIFANITTEKLNKEKALILABQN 711
Qy 299 -----RKGE-----NGSSTDEGEGLVTAKEVIDAVNKAQWRMKTTT 335
Db 712 LNFTVNGSHYENKGDIVSKDKATVTFESKNSDFTSNGSKLVNAQN-----QLKYNV 761
Qy 336 ANQGTQADKFE---TVTSGTNVTFE--SGKGTTA--TVSKDDQGNITVKYDVNVGDALNV--389
Db 762 NNFTISQDDITLIGNVTNLNASGFTNSGNTTIVKTLVDVGIQNFNTKGNLTIVGEDLHIK 821
Qy 390 --NOLNSG-----WNLDSKAVAGSSGKVI-----SGN-----415
Db 822 SKTKITNDGKLISLKNLISEADFINNGTULGIEALKIATKGNFTNKEKAILASNSLLD 881
Qy 416 VPSKGRKMETVN---INAGNIEITRNGK--NIDIATSMTPQFSSVSLGAGADAPTLVS 470
Db 882 LSVAEGK--KTFNCTIESGRNLNITNGAFNLVDNATIR-----SFGVLNITSTGNV 932
Qy 471 DDGALNVGSK--DANKPVRTNVAPG-----VKEGDVTN-----VAQLKGV 510
Db 933 SNNGTLSNERLNTISAANFTNESNGTVMSNGLNIIITAKOGNITMKNLIASROOLNTAV 992
Qy 511 AONLNNRDNVDGNARAGIAQAIATAGV-----QAVLPG-----545
Db 993 ADNITN-----DSNISNKIA-VLHSLGNLSLNSKDDQVYNLGEIYAGNINSVKAHQLKNDV 1046
Qy 546 KSMMAIGGTYRGAGYAIYSSIDSGNWIITKGTASGNSRGHFCASASVGY 597
Db 1047 KLMDGDTTKTKREGQASVKLYQAS-----NGHEGNDGSSGY 1082

RESULT 14
D90803
A: Aida-I adhesin-like protein [imported] - Escherichia coli (strain O157:H7, substrain RIM
C: Species: Escherichia coli
C: Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C: Accession: D90803
R: Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A: Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A: Reference number: A99629; MUID: 21156231; PMID: 11258796
A: Accession: D90803
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-949 <HAY>
A: Cross-references: GB:BA000007; PIDN: BAB34819.1; PID: q13360856; GSPDB: GN00154
A: Experimental source: strain O157:H7, substrain RIMD 0509952
C: Genetics:
A: Gene: ECs1396

Query Match 7.5% Score 228 DB 2 Length 949;
Best Local Similarity 22.0% Pred. No. 0.00034;
Matches 180; Conservative 102; Mismatches 270; Indels 268; Gaps 42;
Qy 1 MNKYRIIWSALNANWAVSELNRHTKRASATVKTAATLTLFATVQANATDEDEBEL 60

Db 5 LNTSYRLVWNHITGLTVVASELARSGRKAGVALSAAV---TSVPALAAK-----55
Qy 61 EPVYRSALVLOFMIDKEGNGENESTGNIGWSIYYDNH---NTLHCATVT--LKAQDNLKI 115
Db 56 --VVOA-----GE---TVNDGTLTNHDNQIVFGTANGMTISTGLEIGPD--S 95
Qy 116 KQNTN-----KNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGA---NGKNVNI 162
Db 96 EENTGGQIOWNGGTTAGNTVTTNGRVV-----LEGGTASDTVIRDDGGOSLGLAVNT 149
Qy 163 TSDTKGLNFAKETAGTNGDITTVHLNGI-----GSTLTDITLLNTGATTNVTNDVTDKKK 217
Db 150 TLNRRGEQWHE--GGVATGTIINRDYQSVKSGGLATGTIINTGAEGSPDSDNSYTGQV 208
Qy 218 RAASVKDVLN-----AG--WNKGVKPGTTASDNVDVH---TYD 252
Db 209 QGTAESTTINKNQRIILFSGGLARDTLIYAGDQSVHGRALNTLLNGGYQVYHRDGLALN 268
Qy 253 TV-----EFLSAD--TKTTTVNVEKDKGRTEVKIGAKTSVKEKDKGLVT-----297
Db 269 TVINEGGQVVKAGGAAGNTIN---QNGELRVHAGGEATVQNTGGLVSTAAATVI 324
Qy 298 -----GKKG---ENGSTDEGEGLVTAKEVID-----AVNKAQWRMKTTTAN 337
Db 325 GTNRLGNFTVENGRADGVVLESGRDLVLESHSAQNTLVDDGGLAVSAGKATSVITTS 384
Qy 338 QGTQADKFEITVSGTNVTFASGK-----GTTATVSKDDQ--GNITVKY 379
Db 385 GGALITADSGATV--EGTN---ASGKFSIDGTSGOASGLLENGSGFTVNAGGQAGNTTVGH 440
Qy 380 D-----VNVGDALNVNOLNSGNWLD-----SKAVAG 406
Db 441 RGTTLAAGSLSGRTQLSKCASVNLNGDVVSTGDIVNAGEIRFDNQTTNPAALSRAVAK 500
Qy 407 SSG-----KVISGNVSPSKGMDETVNI-----NAGN--NI 435
Db 501 SNSPVTFHKLTTNLTGQGGTINMRVRLDGSNASDQLVINGQATGKTWLAFTNVGNSNL 560
Qy 436 EITRNGKNIDI-----ATSMTPQFS--SVSLGACADAPTLSDDKGALNVGSKDANK---485
Db 561 GVATTGQIRVVDQAONGATTEEGAFALSRPLOAGAFNFTLNRDDEDEWYLRSENAIRAEV 620
Qy 486 PVRTINVAPG-----VKEGDVTNVAQLKGAQNLNNRI-----DNVDGNARAGIAQAI 533
Db 621 PLYTSMLTQAMDYDRILLAGSRSHQTVGNGENNSVRLSIOGHLGHDNNGIARGATPSS 680
Qy 534 ATAG-----LVQAYLPKSKMM-----AIG-----GGTYRGAGYAIYGVSS 568
Db 681 GSYGFVRLEGDLRLTEVAGMSLTGTGVYGAAGHSSVDVKDDGSRAGTVRDDAGSLGGYLN 740
Qy 569 I--SDGGNW---ILKGF-----ASGNSRGHFCASASVGYQW 599
Db 741 LVHTSSGLMADIVAQGTNRHSMKASSDNNDFRFR---GNGW 777

RESULT 15
H85611
probable adhesin 21211 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C: Species: Escherichia coli
C: Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C: Accession: H85611; B85663
R: Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A: Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A: Reference number: A85480; MUID: 21074935; PMID: 11206551
A: Accession: H85611
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-1005 <STO>
A: Cross-references: GB:AE005174; MID: g12514025; PIDN: AAG55356.1; GSPDB: GN00145; UWGP:
A: Experimental source: strain O157:H7, substrain EDL933

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FT SIGNAL 1 52
FT CHAIN 53 551
FT CHAIN 552 1039
FT VARIANT 2
FT VARIANT 41 42
FT VARIANT 46 46
FT VARIANT 157 157
FT VARIANT 188 188
FT VARIANT 303 305
FT VARIANT 320 320
FT VARIANT 372 372
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FT VARIANT 855 855
FT VARIANT 888 888
FT VARIANT 1025 1025
FT CONFLICT 61 63
SQ SEQUENCE 1039 AA; 106841 MW; 51700647C8DEBE0 CRC64;

ANTIGEN 43 ALPHA CHAIN.
ANTIGEN 43 BETA CHAIN.
K -> N (IN STRAIN ML 308-225).
SL -> FF (IN STRAIN ML 308-225).
T -> K (IN STRAIN ML 308-225).
W -> L (IN STRAIN ML 308-225).
V -> F (IN STRAIN ML 308-225).
ATN -> STI (IN STRAIN ML 308-225).
A -> T (IN STRAIN ML 308-225).
N -> Q (IN STRAIN ML 308-225).
E -> V (IN STRAIN ML 308-225).
S -> N (IN STRAIN ML 308-225).
H -> Y (IN STRAIN ML 308-225).
E -> K (IN STRAIN ML 308-225).
M -> T (IN STRAIN ML 308-225).
GHL -> SHF (IN STRAIN ML 308-225).
S -> P (IN STRAIN ML 308-225).
A -> V (IN STRAIN ML 308-225).
C -> S (IN STRAIN ML 308-225).
LNLVHTS -> MNLYNA (IN STRAIN ML 308-225).
OQT -> LGA (IN STRAIN ML 308-225).
S -> T (IN STRAIN ML 308-225).
Q -> L (IN STRAIN ML 308-225).
S -> I (IN STRAIN ML 308-225).
ETV -> TTT (IN REF. 5).

Query Match 7.8%; Score 240; DB 1; Length 1039;
Best Local Similarity 21.9%; Pred. No. 6.4e-05;
Matches 148; Conservative 80; Mismatches 249; Indels 200; Gaps 33;

QY 1 MKKVIIRIINSAWVSELTNRHTRKASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 5 LNTCYRLVNHMTGAFVVASSELARARGRGVAVALSLAATVSL----- 48
QY 61 EPVRSALQFWMIDKEGNCENSTGNIOWSIYDHNHT--LHGATVTLKAGDNLKIKON 118
DB 49 -PVLADIIVH-----PGETVNGGTLA-----NHDNQIVFGTTNGMTISTGLEYPD 94
QY 119 TNKNTNENTNDSTFYSLKDLTDLTSVETKLSFGANGKNVITSDTKRFAKETACT 178
DB 95 NEANTG-----GQWVDGCTANKTIVTSG--GLQ-RVNPGGS 128
QY 179 NGDITVHLNGIGSTL---TDILLNG-----ATTNTDNDVNTDDKKRAASVKDV 225
DB 129 VSDTVISAGG-GQSLQGRAVNTTLNGGEQMHGALATGTVINDK----- 172
QY 226 LNAGNLIKGVKPTWASDNVDFVHT-----YDTVEFLSADTKTTVN-----VE 269
DB 173 ---GQVQ--VKPGTATDTV--VNTGABGPDPAENGDTGQFVRGDAVRTINKNGRQIVR 225
QY 270 SKDNKRTRTEVKIGAKTSV-----IREKQKLVTKGKGKGN 304
DB 226 AECTANTTVYAGGQTVHGHALDTTLNGGYQYVHNGGTASTVYNSDQWQIVKNG-GVA 284
QY 305 GSSTDEGLVTAKEVIDAVN---KAGWRMKTMTTANGQTG--QADKFETVT-SGTNVTFEA 358
DB 285 GNTTVNQKRLQVDAGGTATNTLQGGALVTSTATVTGINRLGAFVSVEGKADNVILE 344
QY 359 SG-----KGTATVSK--DDQNTIVKYDVNVGDALNQLQNSGNLNSKAVAGSSGVK 411
DB 345 NGRRLDVLFGHTATNTRVDGGLTDVNR---NGGTATTVS-MNGNG-----VLLADSGAA 394
QY 412 ISGNVSPSK-----KMDDETWINAGNITEITRNKGNIDIAATSMTPQFSSVSLGACADAP 466
DB 395 VSGTSDGKAFSIGGGQADALMLEKSSFTLNAG-----DTATDTTVNGGLTFARGGTLAG 450
QY 467 TLSVDDKALNYSKDKANRPVIRTNVAPGVKEGDTVNTVAQLKGAQNLNLRIDNVDGNAR 526
DB 451 TTTLNNGAILTLGGKTVN-----NDTLTIREGD-----ALLOGGSLTGNGSVEK-SGSGT 499
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```
QY 527 AGIAQAIATAGLVQAVLPCKSMMAIGGGT-----YRGEAGVAGVYS-----S 568
DB 500 LRVSWTTLTKQAVNL---NEGTLTLDSTVTTDVIATQRTALKLTGSLVNGAIDPTNVT 556
QY 569 ISDGGNWIITKGTASGNS 585
DB 557 LASGATWNPIDNATVQS 573

RESULT 3
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051: P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORET).
GN YDEK OR ORFT OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -!- SIMILARITY: TO E-COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
DB EMBL; AE000248; AAC74583.1; -
DB EMBL; D90793; BAA15190.1; ALT_INIT.
DB EMBL; D90794; BAA15197.1; ALT_INIT.
```

DE Adhesin aidA-I precursor.
GN AIDA-I.
OS *Escherichia coli*.

[illegible]


```
QY 64 VRSALVQLQFMIDKEGN-----GENESTGNIGWSIYYDNHNTLHGATVTLKAG----- 110
Db 111 DNLKIKONTKNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTGLN 170
QY 594 GGAIKATKTTKLT-DNASAVTFTNPV-----VVTGADNTGNANN-GIVTFTGNST 642
Db 171 FAKETAGTNGDTHLACIGSTLDTLLNTGATTNTVNTDDBKKRAASVKDVLNAGW 230
Db 643 VTGIGNTNALATVNV-GAGIATLEGAVIKATTTLTN-----AASVLTLTNVA 691
QY 231 NIKGVKGTASDNDVDFVHTYDTVEFLSADTKTT-----TNVNV-----ESKDNG---KRTEVK 280
Db 692 VLTGAIDNTTGVNDVGNVLNGLALSQVGTGNTGNATLISVGAKGATLGGAVIKATTK 751
QY 281 IGAKTSVIKEKDKGLVYG-----KKGKENGSTDEGEGLVTKA-----EVIDAVNKA----- 327
Db 752 LTDNASAVTFTNPVVTGADNTGNANNGIATFTGDSVTGTGNTGNATLAVNNGVAGLLR 811
QY 328 --GWRMKTTTAN-----GOTGOADK-----FETVT---SGTN- 354
Db 812 VQGGVWSKNTLNTDNASAVTFTNPVVTGADNTGNANNGIATFTGDSVTGTGNTGNATL 871
QY 355 ---VTFASGKGT-----TATVSKDDQGNITVKYDVNVGDALNVQLONGWNLDSKA 403
Db 872 LATISVGAGKATLGAIIKATTKLTLDNASAVTFTNPVVTGAID-----NTG-NANNGI 925
QY 404 VAGSSGKVISGNVSPSKMDETNIAGNNEI--TRNGKNIDIANIWTPOFSSVSLGA 461
Db 926 VTFTGDSVTGTGNTGNAL--ATNVGAGVTLQAGSLDANNIDFGARSTLEFNGLDGG 983
QY 462 GADAP-----TLSVDOK-----GALNVGSKDANK-PVRI 490
Db 984 GNAIPYFKGAIANGNNAIENVTKLTAYHLTGTVAEINIGAGNLPADASAGDVTIL 1043
QY 491 N-----VAPGYKEGDV-----TNVAQ 506
Db 1044 NAQDIHFRALDSALVLSNLGTGVGNVILLAADLVAPGVDEGTVPVFDGNGVNLGNSVA- 1102
QY 507 LKGAQNLLN-----RIDNVGNARAGTAQATA-TAGLVQA 541
Db 1103 --GAARIGDVGNGKFNFTLLIYNAVITDDVNLEGIQNVLLNNADFTSTFAFAGTIQ- 1159
QY 542 YLPCKSMMAIGGTY-----RGEAGYAIYSSISDGGWIIKGTASGNSR 586
Db 1160 -----INDAYTTDANNGLNIPAGNIKFAHADRAQLILQNLSSGND 1200
```

RESULT 6

```
OMP_RICTY
ID OMPB_RICTY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
DE OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
ON NCBI_TaxId=785;
RX STRAIN=WILMINGTON;
RC MEDLINE=8224886;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RL surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
```

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RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=WILMINGTON;
RX MEDLINE=92114896; PubMed=1370573;
RT Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RX Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC
CC EMBL: L04661; AAB48987.1; -
CC InterPro: IPR003858; rOmpA_rOmpB.
CC Pfam: PF02708; rOmpA_rOmpB; 1.
CC Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 657 657 H -> N (IN REF. 2).
FT CONFLICT 842 842 H -> I (IN REF. 2).
FT CONFLICT 1071 1071 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;
Query Match 6.5%; Score 200; DB 1; Length 1645;
Best Local Similarity 21.1%; Pred. No. 0.01;
Matches 158; Conservative 86; Mismatches 256; Indels 248; Gaps 37;
QY 25 NHTKRASATV-----KTAVLATLLFAT---VQANATDE-----DEEEE 59
Db 40 NRTTNAATTVDGAGFDGTGAVNLDPVATNSVITANSNNNAITFTNPNGNLNSLFDNTANT 99
QY 60 LEPVVSALVQLQFM--IDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIQ 117
Db 100 LAVTINENTTLGFTVNTVKOGNFFNFITG-AGKSLTITGHGITAQAATTKSAQNVVSKV 158
QY 118 NTKNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTGLNFAKETAG 177
Db 159 NAGAAINDN-----DLSGVGSIDFTAAPSVLFEFLNLPFTT-----QEAPL 198
QY 178 TNGDTTTHLNCIGSLGTLTDLTLNTGATTNTVND--NVTDKKKRAASVKDVLNAGWNKGV 235
Db 199 TLGDNNAKIVNGANGIL-----NITNGFVKVSD---KTFAGIK-TINIGDN-OGL 242
QY 236 KPGTTASDNVDVHTYDTVEFLSADTKTTTVNVESKD-----NGKRTYVKI----- 281
Db 243 MFNTTP-----DAANALNLOGGNTINFNGRGTGKLVLSKNGNATEFNVTGSL 292
QY 282 GAKTSVIKEKD-----GKLVTKGKGK-----ENGSG-----STDEG-----EGLVTA 317
RL Gene 133:129-133(1993).
```


Db 293 GGNLKVIEFTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSDNGNAATISGQVYA 352

QY 318 KEVIDAVNAGWRKTTTANGOT-----GQADKETVTSCNTVTFASCKGTATV 367

Db 353 KDIV-----IQSANAGQVTFEHLVDVGLGGKTNFKTADSKVITITENASFGST--- 400

QY 368 SKDDQGNITVKYDVN-----VGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSP 418

Db 401 ---DFGNLAVQIVPNKILTGFIGDA-----KNGG-NTAGVIITFNANGTLVSGNTDP 450

QY 419 S-----KGKMDTVNI-----NAGNIEITRNKNIDIAITSMTPQSSVS 458

Db 451 NIVVTNIKATEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPVPNQPLVNNNA 509

QY 459 LGAGA---DAPTLSDVD---KGALNVGSKD---ANKPVRITNVAP-----GVKEG----- 499

Db 510 LAAGSITDGSALITGIDNGAVNAALQDITLANDASKILTLGSAANIIGANAGGAHFQA 569

QY 500 -----DVTNVAQLKGVAQN-----LNNRIDNVDGNAR----- 526

Db 570 NGCTIQLTSPONNLLVDFDLVDITDQGVVDASSLLNNQTLTNGSLGTIGANTKILGRF 629

QY 527 -AGIAQAIATAGLV-----QAYLPKSMMAITGGGTGTYRGEAGYAGYSS 568

Db 630 NVGSSKTIILNAGDVAINELVWMDGSVHLTHNTLITKTINAANOQKIIVAADPINTDTA 689

QY 569 ISDGGNWLKGTASGRHFGASASVG 596

Db 690 LADGTN--LGSAESPLSNTHFATKAANG 715

RESULT 7

OMP_RICCN STANDARD; PRT; 1655 AA.

AC OMP_RICCN 09XK45; 1655 AA.

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein) (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]. GNP OR RC1085.

OS Rickettsia conorii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI_TaxID=781;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Wallish 7;

RX MEDLINE=21442074; PubMed=11557893;

RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;

RA "Mechanisms of evolution in Rickettsia conorii and R. prowazekii." Science 293:2093-2098(2001).

RL [2]

RN SEQUENCE OF 33-1649 FROM N.A.

RP STRAIN=Indian tick typhus, and Malish 7;

RC MEDLINE=20393643; PubMed=10939649;

RA Roux V., Raoult D.;

RT "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB)." Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).

RN [3]

RP SEQUENCE OF 353-1655 FROM N.A.

RC STRAIN=Wallish 7;

RA Stenos J., Walker D.;

RT "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group." Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY SIMILARITY).

CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).

CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.

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CC EMBL; AE008659; AAL03623.1; -

DR EMBL; AF123721; AAF34124.1; -

DR EMBL; AF123726; AAF34129.1; -

DR EMBL; AF149110; AAF39533.1; -

DR InterPro; IPR003858; rOmpA_rOmpB.

DR Pfam; PF02708; rOmpA_rOmpB; 1.

KW Antigen; S-layer; Cell wall; Complete proteome.

FT CHAIN 1 1334 1655 120 KDA SURFACE-EXPOSED PROTEIN.

FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).

FT CONFLICT 353 354 KD -> GH (IN REF. 3).

FT CONFLICT 776 776 F -> S (IN REF. 3).

FT CONFLICT 1159 1159 E -> D (IN REF. 3).

FT CONFLICT 1177 1177 G -> S (IN REF. 3).

FT CONFLICT 1492 1492 H -> R (IN REF. 3).

FT SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

QY 95 DNHTL-----HGATVTLKAGDNLKIKONTNK-----NTNENTNDSSFTYSLKKDLTDTSV 146

Db 249 DNVNTLNQANGATITFNGTD-----GTGRLVLLSKNAATDFNVTGSLGGLKGIIEF 302

QY 147 ETE-----KLSTGA-----NGNKVNITSDTKGLNFAKETAGT 178

Db 303 NTVAVNGQLKANAGANAIVGTNGAGRAAGFVVDNGKVATIDGQVYAKDMVQISANA 362

QY 179 NGDTT-----VHLNGIGISTLDTLTLNTGATTNVTNDVNTDDKKRAASVKD---VLNAGWN 231

Db 363 VGQVNFPHIVDVGTDGTTAFKTAASKVAITQNSNFGTDFGNLAQAQIIVPNTLNGNFT 422

QY 232 IKGVKPGTTASDNVDFVHTYD---TVEFLSADTKTTTVN-----VESKDNG-----KRT 277

Db 423 GDASNPGNTAG-----VITFDANGTLASADANAVTNNTITAIEASGAGVQVLSGTHAA 477

QY 278 EVKIGAKTSVIKEDGKLVTK-----GKGENSSTDEGEGLVTAKEVIDAVNKGAGW 329

Db 478 ELRLGNAGSVFKLADGTVINGKVNQTLVAGLAAGATITLDGSATITG-----DIGNAGG- 532

QY 330 RMKTTTANGOTGQADKFETVT-----SGTNVTFASGKGTATTATVSKDDQGNITVKYD 380

Db 533 ---AALQGITLANDATKTLTLGANGIANGGTINFQANGGTIKLTS---TQNNIVVDFD 587

QY 381 V-----NYGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGM-DETVNTN-- 430

Db 588 LAIATDQTVGVVDASSLTNAQTLTINGKIGTVGANNTKLTGQFNIGSSKTVLSDGVDVAINEL 647

Query Match 6.5%; Score 199.5; DB 1; Length 1655;

Best Local Similarity 23.6%; Pred. No. 0.011;

Matches 141; Conservative 66; Mismatches 253; Indels 137; Gaps 29;

```
Qy 431 -AGNN--IEITRNKKNIDATSMTPQ-----FSSV-----SLGAGADAPTSLVDDKALNV 478
Db 648 VIGNGAVQFAHNYLIRTTNAAGQKIIENPVVNNNTTILATGTLNLS-ATNPLAEINF 706
Qy 479 GSKDANKPVRITNVPAGVKEGDVNTVAQLKGAQNALNNRIDNVG-NARAGIAQAIIATAG 537
Db 707 GSKGAANVDVTNKGKGNVL-YAINTTTDA---NVGSFIFNAGTNIVSG-----TVG 756
Qy 538 LVQ-----AYLPKSKMAIGCTYRGEAGYAIGYSSISDGGNWIKGTASGRSG 587
Db 757 GQGNKNTVALDNGTTVKELGNATFNGNTTIAAN-STLQIGGNVTADEVASADGTG 812

RESULT 8
YDBA_ECOLI
ID AC P33666; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasantaram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR
CC BETWEEN AMINO ACIDS 839 AND 840.
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CC -----
DR EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
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DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -, NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydba.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 6.5%; Score 197.5; DB 1; Length 2003;
Best Local Similarity 24.2%; Pred. No. 0.017;
Matches 167; Conservative 89; Mismatches 249; Indels 185; Gaps 42;

Qy 33 TVKTAVALTLFLFA-TVQANATDEDEEELEPVRVSALVLPQFMIDKEGNG-ENESTGNIGW 90
Db 151 TEKTLTIRDSVFTYTENADGTFISLQDSN---GRKATINLWQIDEANNVALEGSADGA 206
Qy 91 SIYYDNHNTLHGATVTLKAGDNLIKONTNKNNTNNDSSFTYSLKDLTDLTSVETEK 150
Db 207 TKWOYNHN--GELVI--TGDNATV--NNNGKTTVDGKDSGTG---EINGNNGKVIODGD 256
Qy 151 LSPGANGKNVNTSDT-----KG-----LNFAKETAGTNGDITVH 185
Db 257 LDVSGGGHGIDITGDSATVDNKGKMTVTVDPESMGIDGDKAIVNNEGESITITNGGTGTQ 316
Qy 186 LNG-----IGSTLTDTLLNTGATTN-----VTNDNVNDDKK 216
Db 317 INGDDATANNNGKTTVDGKDSGTGTEINGNNGKVIODGDLVSGGGHGIDITGDSATVD-N 375
Qy 217 KRAASVDKVLNAGNINIKVPGTGTVDVHYDYVFEFLSADTKTTTNNVNESKDNGK- 275
Db 376 KGTMTVTDPEISIGIQVDG-DQAVVNNEGESAITNGGTGTQINGDDATANNNGKTTVDGKD 434
Qy 276 --RFEVKIGAKTSVIKEDGKL-VTGKKGK---ENGSTDEGEGLVTAKE-----VIDA 323
Db 435 STGTEI-AGNNGKVI--ODGDLVSGGGHGIDITGDSATVDNKGKMTVTVDPEISIGIQIDG 491
Qy 324 ---VNRKAGRMKTTTANGQTGOADKPFETVSGTNVTTFASGKGTATVSKDD-----QGN 374
Db 492 DQAVNNEG---ESTITNGGTG-----TOINGNDAT-ANNSGKTTVDGKDSGTGKIAGN 541
Qy 375 ITVYDYVNVGDALNV-----NOLQNSGN--LDSC-----AVAGSGKVISGNVSPSKGM 423
Db 542 IGI---VNLGSLVLTGGAHGVENIGDNGTVNNGKDIIVSDTSGTGLVINGEGATVSN TG 598
Qy 424 DETVNIAGNNIETRNKKNIDATSM-TPOFSS-VSLGAGADAPTSLVDD-----KG 474
Db 599 DVNVSV-NEATGFSITTSNGKVSAGSMQVGFSTGVDLNGNNSVTLAAKDLKVVGQKAT 657
Qy 475 ALNVGSKDANKPVRIT-----NVA-----PGV-----KEGDVTNVAQLKGA 511
Db 658 GINV-SGDAN-TVNITGNVLVDKDTADNAAEYFDPSPGVGINVYSDNNVTLDGKLT VVS 715
Qy 512 QN-LNNRIDNV-DGNARAGIAQAIIATAGLV-----QAYLPKSKMAIGGCTY 556
Db 716 DSEVTSRQSNLFDGSAE-----KTSGLVIGDGTNNMNGGLELIGEKNALADGSQVT 768
Qy 557 RGEAGYAI-----GYSSISDGGNWIIGK 579
Db 769 SLRTGYSTYSVIVVSGESSVYVLNGDITISG 798

RESULT 9
SLAP_CAMFE
ID SLAP_CAMFE STANDARD; PRT; 933 AA.
AC P35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
GN SAPA.
OS Campylobacter fetus.
```

OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=196;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=84-32 / 23D;
RX MEDLINE=90354448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
structure";
RL J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RN ERRATUM.
RP MEDLINE=91035477; PubMed=2229082;
RX Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CRITICAL FOR VIRULENCE.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
S-LAYER WITH HEXAGONAL SYMMETRY.
CC -----
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CC -----
DR EMBL; J05577; AAA23032.1; -
KW Cell wall; S-layer.
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match 6.4%; Score 196.5; DB 1; Length 933;
Best Local Similarity 22.7%; Pred. No. 0.0078;
Matches 141; Conservative 74; Mismatches 249; Indels 157; Gaps 29;

QY 78 GCNENEST-----GNICWSIYYDHNHILHGATVTLKAGDNLIKON---TNKNTN-ENTND 129
DB 222 GNCNTKSTLAFEDKTRWSVL--GRDTFLNAIFTAIRAAALTDQAEILTKRRTNVENIN- 278
QY 130 SFTYSLKKDLT---DLTSVETELKSGANGKNVITSD-TKGLNFAKETAGT----- 178
DB 279 -----IISDLETSGDFVNGYKGVNGLDIVSFATDASKSVNV--ETTGTITTAFTAA 330
QY 179 -----NGDITVHLNGIGSTLTDTLLNTGATTNVNDVNTDDKKRAAS 221
DB 331 GTGKVDVWAGKISALTADSRSTSVNLATNDTITLSANAATSVNLKORQAKD-----AT 384
QY 222 VKDVLNAGNIVKVGPGT---TASDNVDFVH-----TYDTEVEFLSA-D 260
DB 385 ITSAMOQKYNNRNRNRIATITTSATAVENLTVKHATVNALNGMDKLTATVTLDNAALTAAD 444
QY 261 TKT-TTVN-VESKDNG-----KREVEKIGAKTSVKEK-----DGKL 295
DB 445 IKSASTLNLINSVNGPKHLYSKRRYCKFKRAAAKVKLNTTAATDQTVTLKANATDNL 504
QY 296 VTGKGGKSGSDEGE---LVTAKEVIDAVNKAGWRMKTTTAN-----GQTGOADK 345
DB 505 EFDSATAKTTSVATSGSGKTLVKGAEVETLVN-----IDTTAFNALQSVSFCGTGGGK 559
QY 346 FETVTSGTNVTFASGKGTATVSK--DDOQNTIVKYDVNVGDALNVQNLQNSGNWLD 403
DB 560 F-SVKTGTGDDKLEFVGTTLTEGVSVDAPGNDTIAMKSAALTSANFTMIKNIEVAILSDA 618
QY 404 VAG---SSGKVISGNSPSKGMDETVNINAGNNIETRNKKNIDATSMTPFSSVSLG 460
DB 619 VATADUSSSAFKNSVIITTKAADTTLTINKQVI-----NFTAADAGSVKLITVKNL 671
QY 461 AGADAPTLSDVDDKALNVGSKDANKPVRITNVAPGVKEGD-----VTNVAQL--- 507

DB 672 ---DVTALMIVVKIVLDDAAAKD-----TNIALGTAADKALVIDTGTIETLNTISLVKA 721
QY 508 ---KGVAQNLNNRIDNVGNARAGIAQATATAGLVQAYLPKSKMAIGGGTYGEAGYAI 564
DB 722 TSPETTANTVNAKLTDTVTSIIIDGMQITLGHAGTAGTDYSKVSMDASA-----LKAGLTF 777
QY 565 GYSSISDGGNWIIGKTASGNS 585
DB 778 DASAITLGNATIKGGSGADS 798
RESULT 10
HLVA_SERMA
ID HLVA_SERMA STANDARD; PRT; 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia
marcescens";
RL J. Bacteriol. 170:3177-3188(1988).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
REQUIRES SHLB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
CC -----
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CC -----
DR EMBL; M22618; AAA50323.1; -
DR PIR; A28182; A28182.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 30
FT CHAIN 31 1608 HEMOLYSIN.
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.2%; Score 189.5; DB 1; Length 1608;
Best Local Similarity 22.3%; Pred. No. 0.033;
Matches 138; Conservative 68; Mismatches 217; Indels 195; Gaps 29;

QY 78 GCNENESTGN---IGWSIYYDHNHNL-----HGATVT-----LKAG-----DN 112
DB 544 GGDGNKNNRRREISHASELTSGGTURLNQOQGVITIGSKARGQKGEVATHGGLRLIN 603
QY 113 L-----KIKONTNKNNTN-----ENTNDSSTYSLKKDLTDLTSVETEL-----SFG 154
DB 604 ALSTTVDKIDARTGAFNITSSSHKADNSVQSSTASLAKSD-TNLTIVSHKADADVIGSQV 662
QY 155 ANGNKNVITSDTKGLNFAKETAGTNGD---TTVHLNGIGSTLTDTLLNTGATTNVNDNV 211
DB 663 ASGGELSVESKTCGNINVKAAERQONIDEQKALTALTVNGYAKEAGDKQYRAGRLIETHRDSE 722

```
QY 212 TDDKKRAAS-----VKDLNAGNNIKGVKFGTTASDNDVDFVHTYDTVEFLSAD 260
   : : : : :
Db 723 KTTTENSASSLSGGSVKLKAEKDVTFSGSKLVADKGDASVSGN-----KVSFLAAD 774
   : : : : :
QY 261 TKTTTAVNESKDNKRTEVKIKAKTSVKEKDGKLVTKGKGGENGSSDDEGEGLVTAKEV 320
   : : : : :
Db 775 DKTAS-NTE-----QTKIGG-----GFYITG----- 794

QY 321 IDAVNKAGWRMKTATTANGOTQADKEETVTSCTNVTASGKGTATTATVSKDDQGNITVKYD 380
   : : : : :
Db 795 --GIDKLGSGAEGYENKKT--QAQSSKAITSGSDV-----KGNLT----- 831

QY 381 VNVGDALNVNQLNSGWNLDKAVAGSGSKVVISGNVSPSKGMDETVNIAGNNIEITRN 440
   : : : : :
Db 832 INARDKLTQOQAQHSVGGAYQENAGVDHLAAADTASTTTTKTDGVNI----- 880

QY 441 GKNIDTATSMTPQPSFSSVLGAGADPTLSVDDKG-----ALNVGSKDANKPVRIRN-- 491
   : : : : :
Db 881 GANVDYSAVTRPRVERAVGKAAKLDA-TGVINDIGGIGAPNVGLDIGAQQSGSEKRSSSQ 939

QY 492 -VAPGVKGDV-----TNVAOLKGVAONLN-----NRIDNVGDNARAG 528
   : : : : :
Db 940 AVWSVQAGSIDINAKGEVRQGTQYQASKG-AVNLTAHSRSEAAANRQEQSRDTR-- 996

QY 529 IAQATATAGLVQAYLPKSKMMAIG-----GGTYRGEAGYAIGYSISDSGNW----- 575
   : : : : :
Db 997 -----GSAG-VRVYTTTGSDLTVDAKGGGTQRSNSASQAVTSIDAANGINNVKKDA 1050

QY 576 IIKGTASNSRGHPGASA 593
   : : : : :
Db 1051 IYQGTALNGRGRKTAUNA 1068

RESULT 11
HLXA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMa.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMa
CC REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMa
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC EMBL; M30186; AAA25657.1; -.
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.1%; Score 187.5; DB 1; Length 1577;
Best Local Similarity 20.2%; Pred. No. 0.04; 225; Indels 161; Gaps 27;
Matches 119; Conservative 84; Mismatches 225; Indels 161; Gaps 27;

QY 73 MIDKEGGENESTGNI-----GWSYVDNH--NTLHGATVT----- 106
   : : : : :
Db 435 LVEKESSENGKNNHHSRLSEGSWS---NSHQETETLKASELTAGKDLGLDAQGSITAQG 491

QY 107 --LKAGDNLKI--KONTNKNNTNENTSSFT-----YSLKKDLTDITSV 146
   : : : : :
Db 492 AKLHANENVLVNAKDNLNLNVOKTNDKTVDNVMVGGIGGGQNNNNQQVSHATQL 551

QY 147 ETEKLSFGANGKNYNIIT-SDTKGLNFAKETAGTNGDTTVHLNGIGSLTDTLLNTGATTN 205
   : : : : :
Db 552 TADGQLLEAADNNVNIITGSQVKG--NQGAFVKTQGDVVVID--NALSETISKIDERTGTAFN 609

QY 206 VTNDNVTDKKRAASVKDVLN-----AGWNKIKGVKPGTTASDNDVDFVHTYDTVEFLS 258
   : : : : :
Db 610 ITRKSHKNETNKQSTGSELISDAQLTVVSGNDVNVIGSLIKSADKLG-IHSLGDIINVKS 668

QY 259 ADTKTTTVNVESKDNKRTEVYKIGAKTSVKEKDGKLVTKGKGGENGSSDDEGEGLVTAK 318
   : : : : :
Db 669 AQ-----QVTKIDDEKTSLAITGH-----AK 689

QY 319 EVIDAVNKAGWRMKTATTANGOTQADKEETVTSCTNVTASGKGTATTATVS--KDDQGNIT 376
   : : : : :
Db 690 EVEDKQYSAGFHIHTTNKNTSTETEQANSTISGANVDLQANKDVTFRAGSLKTTAGNAS 749

QY 377 VKYDVNVGDALNVNQLNSGWNLDKAVAGSGSKVVISGNVSPSKGMDETVNIAGNNIE 436
   : : : : :
Db 750 ITGD-NVAFVSTENKQTD--NTDTTISGGFS---YTGVDKVGSKADFYD-KQHTQTE 802

QY 437 ITRN-GKNIDIATSMTPQFSVSLGAGA-----DAPTLVDDK-----GALN 477
   : : : : :
Db 803 VTKNRGSGTEVAGDLTITANKDLLHEGASHVEGRYQESGENIQHIAVNDSETSKTDSL 862

QY 478 VG-----SKDANKPVR-----ITNAPGVKEGDDVTNVAQLKGVAQLNNRIDNDVG 523
   : : : : :
Db 863 VGIDVGNLDYSGVTKPVKKAIEDGVNTTRPG--NTDILTCKVTARDATAIANLAN-LSNLE- 919

QY 524 NARAGIAQAATATAGLVQAYLPKSKMMAIGGTGYRGEAGYAIGYSISDGS 572
   : : : : :
Db 920 TPNVGVEVGIK-----GGGSQQSQSDSQAVSTISINAG 951

RESULT 12
ICEN_XANCT STANDARD; PRT; 1567 AA.
ID ICEN_XANCT
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
```

RT Xanthomonas campestris pv. translucens.";
 RL Mol. Gen. Genet. 223:163-166(1990).
 CC -!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.
 CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).
 CC -!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
 CC -!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
 CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
 CC FAMILY.
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 CC
 CC EMBL: X52970; CAA37140.1; -
 DR PIR: S11672; S11672.
 DR HSSP: P06620; I1INA.
 DR InterPro: IPR000258; Ice_nucleatn.
 DR Pfam: PF00818; Ice_nucleation; 81.
 DR PRINTS: PR00327; ICNUCLEATN.
 DR PROSITE: PS00314; ICE_NUCLEATION; 57.
 KW Ice nucleation; Repeat; Outer membrane.
 SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;
 Query Match 6.1%; Score 185.5; DB 1; Length 1567;
 Best Local Similarity 19.8%; Pred. No. 0.05;
 Matches 124; Conservative 94; Mismatches 279; Indels 129; Gaps 23;
 QY 20 SELTRNHRKRASATVKTAVLATLFLATVQANATDEDEEELEPVRSALVLOF---MIDK 76
 Db 712 SDVTAGYSGTGTAGADSTLIAG-YGSTQTSQSD-----SSLTAGYSGTQTAR 757
 QY 77 EGNGENESTGNTGWSYIYDNHNTLHGATVTLKAGDNMLKIKQNTNKNNTNNDSSSTYSL 136
 Db 758 KGSVDTAGYSGTGCTA-----GADSTLIAGY-----STQTSQSDSSLTAGY 798
 -QY 137 KRDLT-----DLTSVFETKLSFGA-----NGKNVITSDTKLNFKE---- 174
 Db 799 GSTQTRARKSDITAGYSGTGTAGADSTLIAGYSGTQTSQSDSSLTAGYSGTQTAREGSDV 858
 QY 175 -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATNTVNDVNDKRAASVKDVL 226
 Db 859 TAGYSGTGTAGADSTLIAGYSGTQTAGSDSSLTAGYSGTQTARKGSD-----V 906
 QY 227 NAGWNITKGVKPGTASNDVDFVHYDTVFLSADTKTTNNVNESKDKGRKTEVIGAKTS 286
 Db 907 TAGYSGTG-----TAGADSTLIAGYSGTQTSQSDSSLTAGYSGTQTARKGSDMTAGYSGT 961
 QY 287 VIKEDKGLVTKGKNGESSDDECEGLTAKEVIDAVNKAHGRMKTTTANGQTQADKF 346
 Db 962 GTAGADSTLIAGYSGTQTSQSDSSLTAGYSGTQTAGSDSSLTAGYSGTQTAREGSDV 1007
 QY 347 ETVTSGTNTVTFASGKGTATVSKDDOGNITVKYDVNVGDALNVNQLNSGWNLDLSKAVAG 406
 Db 1008 SYGTAGADSTLIAGYSGTQTAGSD--SSLTAGY-----GSTQTRAQSDVTAGYSGTGTAG 1061
 QY 407 SSGKVITSGNVSPSKGMDVETVNIAGNNTIEITRNGKNIDTATSMTPQFSVSLGADAP 466
 Db 1062 ADSTLIAGYSGTQTAGSDSSLTAGYSGT-QTAGRQSDI-----TAGYSGTGT-AGADSS 1113
 QY 467 TLSVDDKGLNVLGSKDANKPVRTVNVAPGVKEGDTVNVLAQLKGVQANLNINRINDVGNAR 526
 Db 1114 LIA--GYGSTQTAGYSDNLTAGYSGTQTAGSDSSLTAGYSGTSTAGHSDSSLTAGYSGTQT 1171
 QY 527 AGIAQAIATA-GLVQAYLPKSKSMAIGGGGTGRGEAGY----AIGYSSISDGG--NWIIG 579

Db 1172 AGVNSILTTGYSGTQTQAESSSLTAGYSGT--STAGYDSTLTLAGYSGTQTAKYKSTLTAG 1229
 QY 580 TASGNSRGRH-----FGASASVGYQ 598
 Db 1230 YGSNSTAGHSSLIAGYSGTQTAGYE 1255
 RESULT 13
 OMPB_RICRI
 ID OMPB_RICRI STANDARD; PRT: 1654 AA.
 AC Q53047;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (römpB)
 DE (römp B) [Contains: 120 kDa surface-exposed protein (Surface protein
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB.
 OS Rickettsia rickettsii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsieae; Rickettsia.
 OX NCBI_TaxID=783;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=92167802; PubMed=1724278;
 RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;
 RT "The 120 kilodalton outer membrane protein (römp B) of Rickettsia
 RT rickettsii is encoded by an unusually long open reading frame:
 RT evidence for protein processing from a large precursor.";
 RL Mol. Microbiol. 5:2361-2370(1991).
 RN [2]
 RP SEQUENCE OF 279-1654 FROM N.A.
 RC STRAIN=R;
 RX MEDLINE=90136087; PubMed=2515418;
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
 RT "Cloning, expression and sequence analysis of the gene encoding the
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
 RL Mol. Microbiol. 3:1579-1586(1989).
 CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
 CC LAYER WITH HEXAGONAL SYMMETRY.
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
 CC
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 CC
 CC EMBL: X16353; CAA34403.1; -
 DR InterPro: IPR003858; römpA_römpB.
 DR Pfam: PF02708; römpA_römpB; 1.
 KW Antigen; S-layer; Cell wall.
 FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
 FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
 FT DOMAIN 1181 1188 POLY-THR.
 SQ SEQUENCE 1654 AA; 168184 MW; D/AB70FB7087F618 CRC64;
 Query Match 6.1%; Score 185.5; DB 1; Length 1654;
 Best Local Similarity 22.9%; Pred. No. 0.053;
 Matches 178; Conservative 83; Mismatches 264; Indels 251; Gaps 44;
 QY 7 ITWNSALNVAWVSELTR-----NHTKRASATVKTAVLATLFLATVQANAT 52
 Db 92 LLLNTANNLAVTVSEDTTLGFTITVNVHNSFNLNAG---KTLTITGGVTAQAAT 148

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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:45 ; Search time 168.02 Seconds
(without alignments)
616.736 Million cell updates/sec

Title: US-09-771-382-6
Perfect score: 3060
Sequence: 1 MNYIRIINWALNAWAVS.....TASNSRGHGASASGVQW 599

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3060	100.0	599	2	Q9JPR8	Q9jpr8 neisseria m
2	2832.5	92.6	598	2	Q9JPR9	Q9jpr9 neisseria m
3	2830.5	92.5	598	2	Q9JPT0	Q9jpt0 neisseria m
4	2824.5	92.3	598	2	Q9JPS0	Q9jps0 neisseria m
5	2821.5	92.2	598	2	Q9JQY5	Q9jqy5 neisseria m
6	2802.5	91.6	594	2	Q9JPH7	Q9jph7 neisseria m
7	2792	91.2	595	2	Q9JPH0	Q9jph0 neisseria m
8	2781.5	90.9	600	2	Q9JPS6	Q9jps6 neisseria m
9	2776.5	90.7	594	2	Q9JPI3	Q9jpi3 neisseria m
10	2772.5	90.6	594	2	Q9JPS2	Q9jps2 neisseria m
11	2768.5	90.5	590	2	Q9JPS3	Q9jps3 neisseria m
12	2762.5	90.3	594	2	Q9JQY4	Q9jqy4 neisseria m
13	2737.5	89.5	592	2	Q9JPS9	Q9jps9 neisseria m
14	2710	88.6	589	2	Q9JPI0	Q9jpi0 neisseria m
15	2709	88.5	599	2	Q9JPS8	Q9jps8 neisseria m
16	2699.5	88.2	592	2	Q9JQY2	Q9jqy2 neisseria m

17	2694	88.0	589	2	Q93QY1	Q93qy1 neisseria m
18	2685	87.7	591	16	Q9JRI8	Q9jri8 neisseria m
19	2681	87.6	591	2	Q9JPS7	Q9jps7 neisseria m
20	2676.5	87.5	598	2	Q9JPR7	Q9jpr7 neisseria m
21	2676	87.5	591	2	Q9JQY3	Q9jqy3 neisseria m
22	2663.5	87.0	526	2	Q9JPS4	Q9jps4 neisseria m
23	2663.5	87.0	592	2	Q9AQF0	Q9aqf0 neisseria m
24	2660.5	86.9	600	2	Q9JPS5	Q9jps5 neisseria m
25	2651.5	86.7	530	2	Q9JPS1	Q9jps1 neisseria m
26	2587.5	84.6	592	16	Q9JQW4	Q9jqw4 neisseria m
27	1271	41.5	2353	2	P71401	P71401 haemophilus
28	1070.5	35.0	1098	2	Q48152	Q48152 haemophilus
29	455.5	14.9	1299	16	Q9F3X6	Q9f3x6 pasteurella
30	410.5	13.4	1190	16	Q9PC04	Q9pc04 xylella fas
31	407	13.3	1107	2	Q9F2D8	Q9f2d8 salmonella
32	406.5	13.3	2059	16	Q9PD50	Q9pd50 xylella fas
33	361.5	11.8	2712	16	Q9F3X5	Q9f3x5 pasteurella
34	264.5	8.6	1004	16	Q9PD63	Q9pd63 xylella fas
35	256	8.4	1291	16	Q92KQ7	Q92kq7 rhizobium m
36	252.5	8.3	1953	16	Q98HJ2	Q98hj2 rhizobium l
37	240	7.8	1039	2	Q9L6T7	Q9l6t7 escherichia
38	237	7.7	1039	2	Q9L6T8	Q9l6t8 escherichia
39	236	7.7	2276	2	Q93TY6	Q93ty6 staphylococ
40	234.5	7.7	873	2	Q9L960	Q9l960 moraxella c
41	234.5	7.7	1040	2	Q9AL50	Q9al50 shigella fl
42	233.5	7.6	3930	16	Q98E20	Q98e20 rhizobium l
43	233	7.6	989	2	Q9XD84	Q9xd84 escherichia
44	231	7.5	4919	2	Q9ZHL0	Q9zhl0 haemophilus
45	227	7.4	1265	2	Q9FDA0	Q9fda0 xanthomonas

ALIGNMENTS

RESULT 1

Q9JPR8	PRELIMINARY;	PRT;	599 AA.
ID	Q9JPR8		
AC	Q9JPR8;		
DC	01-OCT-2000 (TREMREL. 15, Created)		
DT	01-OCT-2000 (TREMREL. 15, Last sequence update)		
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).		
GN	GNA992 OR NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RP	STRAIN=NGH38;		
RX	MEDLINE=20175756; PubMed=10710308; -		
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=H38;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RL	membrane protein of Neisseria meningitidis."		
DR	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF226383; AAF42532.1; -		
DR	EMBL; AF157608; AAK68869.1; -		
SQ	SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;		

Query Match 100.0%; Score 3060; DB 2; Length 599;

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Best Local Similarity 100.0%; Pred. No. 6.3e-121;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVALATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVALATLLFATVQANATDEDEEEL 60
QY 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
Db 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
QY 121 KNTNENTNDSFYSYLSKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYLSKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
QY 181 DTTVHLNGIGSTLTDLLNTGATTTNNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
Db 181 DTTVHLNGIGSTLTDLLNTGATTTNNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
Db 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
QY 301 KGENGSTDEGGLVTAKEVIDAVNAGWRMKTTTANGOTGQADKFETVTSNTVTFASG 360
Db 301 KGENGSTDEGGLVTAKEVIDAVNAGWRMKTTTANGOTGQADKFETVTSNTVTFASG 360
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
QY 421 GKMDETVINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
QY 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLLNNDVGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLLNNDVGNARAGIAQAATATAGLVQ 540
QY 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYQW 599
Db 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYQW 599

RESULT 2
Q9JPR9 PRELIMINARY; PRT; 598 AA.
ID Q9JPR9
AC Q9JPR9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hurd E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1;
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 92.6%; Score 2832.5; DB 2; Length 598;
Best Local Similarity 93.0%; Pred. No. 2.1e-111;
Matches 557; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVALATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVALATLLFATVQANATD-DDDLYL 59
QY 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
Db 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 119
QY 121 KNTNENTNDSFYSYLSKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYLSKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 179
QY 181 DTTVHLNGIGSTLTDLLNTGATTTNNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
Db 181 DTTVHLNGIGSTLTDLLNTGATTTNNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 239
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
Db 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 299
QY 301 KGENGSTDEGGLVTAKEVIDAVNAGWRMKTTTANGOTGQADKFETVTSNTVTFASG 360
Db 301 KGENGSTDEGGLVTAKEVIDAVNAGWRMKTTTANGOTGQADKFETVTSNTVTFASG 359
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419
QY 421 GKMDETVINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 479
QY 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLLNNDVGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLLNNDVGNARAGIAQAATATAGLVQ 539
QY 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYQW 599
Db 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYQW 598

RESULT 3
Q9JPT0 PRELIMINARY; PRT; 598 AA.
ID Q9JPT0
AC Q9JPT0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hurd E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
```


RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RL membrane protein of *Neisseria meningitidis*."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157603; AAK68864.1; -.
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 92.2%; Score 2821.5; DB 2; Length 598;
Best Local Similarity 92.7%; Pred. No. 6e-111;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 EPVVSALVLFQFMDKEGGENESTGNIGWSIYYDNTLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVQRTAVLSFRSDKEGTEGKEDSNVAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 120 ENTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDKKRAASVKDVLNAGWNIKGVKPGTT 240
Db 180 DPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIKGVKPGTT 239
QY 241 ASDNVDFVHTYDTEFLSADTKTTTVVNESKDNKREVKIGAKTSVIKEKDGKLVTKGK 300
Db 240 ASDNVDFVHTYDTEFLSADTKTTTVVNESKDNKREVKIGAKTSVIKEKDGKLVTKGK 299
QY 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVTSCTNVTASG 360
Db 300 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVTSCTNVTASG 359
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 420
Db 360 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 419
QY 421 GKMDETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKGLNNGVS 480
Db 420 GKMDETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKGLNNGVS 479
QY 481 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLVQ 540
Db 480 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLAQ 539
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTASGNSRGRHFGASASVGYQW 599
Db 540 AYLPGKSMMAIGGTYRGEAGYAGYISISDGTGNWIKGTASGNSRGRHFGTSASVGYQW 598

RESULT 6
QJPH7 PRELIMINARY; PRT; 594 AA.
AC QJPH7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198; AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT *Meningococcus* by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=B2198;
RC Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*."
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226368; AAF42517.1; -.
DR EMBL; AF226358; AAF42507.1; -.
DR EMBL; AF157604; AAK68865.1; -.
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 91.6%; Score 2802.5; DB 2; Length 594;
Best Local Similarity 92.5%; Pred. No. 3.7e-110;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 EPVVSALVLFQFMDKEGGENESTGNIGWSIYYDNTLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVQRTAVLSFRSDKEGTEGKEDSNVAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 117 -NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDKKRAASVKDVLNAGWNIKGVKPGTT 240
Db 176 DPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIKGVKPGTT 235
QY 241 ASDNVDFVHTYDTEFLSADTKTTTVVNESKDNKREVKIGAKTSVIKEKDGKLVTKGK 300
Db 236 ASDNVDFVHTYDTEFLSADTKTTTVVNESKDNKREVKIGAKTSVIKEKDGKLVTKGK 295
QY 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVTSCTNVTASG 360
Db 296 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVTSCTNVTASG 355
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 420
Db 356 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVSPSK 415
QY 421 GKMDETVINAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKGLNNGVS 480
Db 416 GKMDETVINAGNIEITRNKKNIDTATSMAPQFSSVSLGAGADAPTLSDVDKGLNNGVS 475
QY 481 KDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLVQ 540
Db 476 KDTNKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVGNARAGIAQAIATAGLVQ 535
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTASGNSRGRHFGASASVGYQW 599
Db 536 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTASGNSRGRHFGASASVGYQW 594

RESULT 7
QJPHO PRELIMINARY; PRT; 595 AA.
ID QJPHO
AC QJPHO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=528, AND 1000;
RX MEDLINE=2017556; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL; AF226356; AAF42505.1; -;
DR EMBL; AF226356; AAF42505.1; -;
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;

Query Match 91.2%; Score 2792; DB 2; Length 595;
Best Local Similarity 92.5%; Pred. No. 1e-109;
Matches 556; Conservative 15; Mismatches 22; Indels 8; Gaps 3;

QY 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
QY 61 EPVRSALVLFQMDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
DB 61 EPVRSALVLFQMDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQ--- 117
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKETAGTNG 180
DB 118 -NTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKKTAGTNG 176
QY 181 DTTVHLNGIGSTLTDLLNTGATTNTVNDVDDKKRAASVKDVLNAGNWKVPGTT 240
DB 177 DTTVHLNGIGSTLTDLLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNWKVPGTST 234
QY 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGKLVG 298
DB 235 TGSSENVDFVHTYDTVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGKLVG 294
QY 299 KKGKNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 358
DB 295 KKGKNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTNVTF 354
QY 359 SKGKGTATVSKDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSP 418
DB 355 SKGKGTATVSKDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVSP 414
QY 419 SKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNV 478
DB 415 SKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNV 474
QY 479 GSKDANKPVRITNVAPGVKEGDVTNVQAQLKGVAGNQLNNDVNDGNARAGIAQIAIATAGL 538
DB 475 GSKDANKPVRITNVAPGVKEGDVTNVQAQLKGVAGNQLNNDVNDGNARAGIAQIAIATAGL 534
QY 539 VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKTASGNSRHFHGASASVGYQ 598
DB 535 VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKTASGNSRHFHGASASVGYQ 594
QY 599 W 599
DB 595 W 595

RESULT 8
Q9JPS6

ID Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=2017556; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -;
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 90.9%; Score 2781.5; DB 2; Length 600;
Best Local Similarity 91.6%; Pred. No. 2.8e-109;
Matches 554; Conservative 12; Mismatches 28; Indels 11; Gaps 3;

QY 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQANA-----TDE 54
DB 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVKTAVLATLLFATVQASADNVQASADN 60
QY 55 DEEEELPPVRSALVLFQMDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLK 114
DB 61 EEEYLEPPVRSALVLFQMDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLK 120
QY 115 IKONTNKTNTENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKE 174
DB 121 IKQ-----NTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKE 176
QY 175 TAGTNGDITVHLNGIGSTLTDLLNTGATTNTVNDVDDKKRAASVKDVLNAGNWK 234
DB 177 TAGTNGDITVHLNGIGSTLTDLLNTGATTNTVNDVDDKKRAASVKDVLNAGNWK 236
QY 235 VKPGTTASDNVDVHTYDTVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGK 294
DB 237 VKPGTTASDNVDVHTYDTVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGK 296
QY 295 LVTKGKNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTN 354
DB 297 LVTKGKNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTN 356
QY 355 VTASGKGTATVSKDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAGSSGKVISG 414
DB 357 VTASGKGTATVSKDQGNITVKYDYNVGDALNVNQLNSGNLDSKAVAGSSGKVISG 416
QY 415 NVSPSKGMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDK 474
DB 417 NVSPSKGMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDK 475
QY 475 ALNVGSKDANKPVRITNVAPGVKEGDVTNVQAQLKGVAGNQLNNDVNDGNARAGIAQIA 534
DB 476 ALNVGSKDANKPVRITNVAPGVKEGDVTNVQAQLKGVAGNQLNNDVNDGNARAGIAQIA 535
QY 535 TAGLVQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKTASGNSRHFHGAS 594
DB 536 TAGLVQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKTASGNSRHFHGAS 595
QY 595 VGYOW 599

Db 596 VGYQW 600
|||||
RESULT 9
QJUP13 PRELIMINARY; PRT; 594 AA.
ID QJUP13
AC QJUP13
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, B2322;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226376; AAF42525.1; -;
DR EMBL; AF226369; AAF42518.1; -;
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D0D4B46 CRC64;

Query Match 90.7%; Score 2776.5; DB 2; Length 594;
Best Local Similarity 92.0%; Pred. No. 4.5e-109;
Matches 551; Conservative 12; Mismatches 31; Indels 5; Gaps 2;
QY 1 MNKIYRIWNSALNAWVAVSELTRNHHKRSATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 MNKIYRIWNSALNAWVAVSELTRNHHKRSATVKTAVLATLLFATVQASTTD-DDDLYL 59
QY 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKONTN 120
DB 60 EPVQRTAPVLSFHADSEGTGEKEVTEDSNNGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116
QY 121 KNTNENTNDSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
DB 117 -NTDENTNASSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 175
QY 181 DTTVHLNGIGSTLDTLLNTGATTNVDNVDKDKKRAASVKDVLNAGNINIKVPGT 240
DB 176 DTTVHLNGIGSTLDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGNINIKVPGT 235
QY 241 ASDNVDFVHTYDIVEFLSADTKTTTVNVEKONGKTEVIGAKTSVKEKDGKLVTKG 300
DB 236 ASDNVDFVHTYDIVEFLSADTKTTTVNVEKONGKTEVIGAKTSVKEKDGKLVTKGD 295
QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFEFTVSGTNVTFASG 360
DB 296 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFEFTVSGTKVTFASG 355
QY 361 KGTATVSKDDOGNITVKYDVNVGDALNVOLNSGWNLDKAVAGSSGKVISGNVSPSK 420
DB 356 NGTTATVSKDDOGNITVKYDVNVGDALNVOLNSGWNLDKAVAGSSGKVISGNVSPSK 415
QY 421 GKMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDKALNVGS 480
DB 416 GKMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDKALNVGS 475
QY 481 KDANKPVRITNAPGVKEGVDVTNVAQLKGVAQNLNHNVDNVDGNARAGIAQAATATAGLVQ 540
|||||

QY 481 KDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLVQ 540
Db 476 KDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLVQ 535
QY 541 AYLPCKSMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 599
Db 536 AYLPCKSMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 11
QJPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzia M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.
RT *Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.*;
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 90.5%; Score 2768.5; DB 2; Length 590;
Best Local Similarity 91.5%; Pred. No. 9.7e-109;
Matches 549; Conservative 14; Mismatches 26; Indels 11; Gaps 2;
QY 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVQANATDEDEEL 60
Db 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVQANATDEDEEL 60
QY 61 EPVRSALVLOFMIDKEGNGENEST-GNIGWSIYDNNHTLHGATVTLKAGDNLKIKQNT 119
Db 61 DPVQRTAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAGTITLKAGDNLKIKQ-- 118
QY 120 NKNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 179
Db 119 -----NGTNFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 170
QY 180 GDTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWNIKGVKPGT 239
Db 171 GDTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWNIKGVKPGT 230
QY 240 TASDNDVDFVHTYDTVEFLSADTKTTVNVESKDNKRTEVKIGAKTSVKEKDKGLVTGK 299
Db 231 TASDNDVDFVHTYDTVEFLSADTKTTVNVESKDNKRTEVKIGAKTSVKEKDKGLVTGK 290
QY 300 GKGNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTGOADKFEFTVSGTNVTFAS 359
Db 291 GKGNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTGOADKFEFTVSGTNVTFAS 350
QY 360 GKGTTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPS 419
Db 351 GKGTTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPS 410
QY 420 KGKMDETVNIAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDDKAGLVQ 479
Db 476 KDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLVQ 535

Db 411 KGKMDETVNIAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDDKAGLVQ 470
QY 480 SXDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLV 539
Db 471 SXDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLV 530
QY 540 QAYLPCKSMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 599
Db 531 QAYLPCKSMAIGGGTYRGEAGYAIGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 590

RESULT 12
Q93QV4
ID Q93QV4 PRELIMINARY; PRT; 594 AA.
AC Q93QV4;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG327;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT *Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157605; AAK68866.1; -.
SQ SEQUENCE 594 AA; 62297 MW; 9DDD49B04B3A8EA2 CRC64;

Query Match 90.3%; Score 2762.5; DB 2; Length 594;
Best Local Similarity 91.7%; Pred. No. 1.7e-108;
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;
QY 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVQANATDEDEEL 60
Db 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLFLFATVQASATTD-DDDLVL 59
QY 61 EPVRSALVLOFMIDKEGNGENESTGNIGWSIYDNNHTLHGATVTLKAGDNLKIKQNTN 120
Db 60 EPVQRTAVVLSFRSDEKGEKEVEDSNWGYFDFKKGVLTAGTITLKAGDNLKIKQ--- 116
QY 121 KNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 180
Db 117 -NTNENTNASSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKKTAE 175
QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWNIKGVKPGT 240
Db 176 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWNIKGVKPGT 235
QY 241 ASDNDVDFVHTYDTVEFLSADTKTTVNVESKDNKRTEVKIGAKTSVKEKDKGLVTGK 300
Db 236 ASDNDVDFVHTYDTVEFLSADTKTTVNVESKDNKRTEVKIGAKTSVKEKDKGLVTGK 295
QY 301 GKGNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTGOADKFEFTVSGTNVTFAS 360
Db 296 GKGNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTGOADKFEFTVSGTNVTFAS 355
QY 361 KGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 420
Db 356 KGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVSPSK 415
QY 421 KGKMDETVNIAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDDKAGLVQ 480
Db 416 KGKMDETVNIAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSVDDKAGLVQ 475
QY 481 KDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLVQ 540
Db 476 KDANKPVRITNAPGVKEGDTNVAQLKGAQNLRNIDVNDGNARAGIAQAIAATAGLVQ 535

QY 541 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 599
|||||
Db 536 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
|||||
RESULT 13
Q9JPS9 PRELIMINARY; PRT; 592 AA.
AC Q9JPS9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=860800;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL; AF226361; AAF42510.1; -;
SQ SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;

Query Match 89.5%; Score 2737.5; DB 2; Length 592;
Best Local Similarity 92.2%; Pred. No. 1.9e-107;
Matches 553; Conservative 9; Mismatches 29; Indels 9; Gaps 4;
QY 1 MNKIYRIWNSALNNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
|||||
Db 1 MNKIYRIWNSALNNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
|||||
QY 61 EPVYRSALVLFQFMIDKEGNGENESTGNIGWSIYYDDNHTLHG-ATVTLKAGDNLIKQNT 119
|||||
Db 61 ESVQRS-VVGSIQASMEGSGELET--ISLSMTNDSKEFVDPYIVVTLKAGDNLIKQ-- 114
|||||
QY 120 NKNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 179
|||||
Db 115 --NTNENTNASSFYSYSLKKDLTGLINVTETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 172
|||||
QY 180 GDTTVHLNGIGSTLDTLLNTGATNTNDVNTDDKKRAASVKDVLNAGNWKGVKPGT 239
|||||
Db 173 GDTTVHLNGIGSTLDTLLNTGATNTNDVNTDDKKRAASVKDVLNAGNWKGVKPGT 232
|||||
QY 240 TASDNVDFVHTYDVEFLSADTKTTTVNVEKDKGKRTVEKIGAKTSVIKEDKGLVTGK 299
|||||
Db 233 TASDNVDFVRYDIVEFLSADTKTTTVNVEKDKGKRTVEKIGAKTSVIKEDKGLVTGK 292
|||||
QY 300 KKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKFEETVTSNTVTFAS 359
|||||
Db 293 KKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKFEETVTSNTVTFAS 352
|||||
QY 360 KGCTTATVSKDDQGNITVYKDYVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPS 419
|||||
Db 353 KGCTTATVSKDDQGNITVYKDYVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSPS 412
|||||
QY 420 KGMDETVNINAGNNIETRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGLNVG 479
|||||
Db 413 KGMDETVNINAGNNIETRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGLNVG 472
|||||
QY 480 SKDANKPVRITNAPGVKEGDTVNTVAOLKGVAQNLLNRRIDNVGDNARAGIAQAATAGLV 539
|||||

Db 473 SKDANKPVRITNAPGVKEGDTVNTVAOLKGVAQNLLNRRIDNVGDNARAGIAQAATAGLV 532
|||||
QY 540 QAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 599
|||||
Db 533 QAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 592
|||||
RESULT 14
Q9JPI0 PRELIMINARY; PRT; 589 AA.
AC Q9JPI0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGP165; 90/18311, AND 93/4286;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.F., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42533.1; -;
DR EMBL; AF226362; AAF42511.1; -;
DR EMBL; AF226363; AAF42512.1; -;
SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match 88.6%; Score 2710; DB 2; Length 589;
Best Local Similarity 90.2%; Pred. No. 2.7e-106;
Matches 542; Conservative 13; Mismatches 32; Indels 14; Gaps 3;
QY 1 MNKIYRIWNSALNNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
|||||
Db 1 MNKIYRIWNSALNNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
|||||
QY 61 EPVYRSALVLFQFMIDKEGNGENESTGNIGWSIYYDDNHTLHGATVTLKAGDNLIKQNTN 120
|||||
Db 61 ESVYRSALVLFQFMIDKEGNGEIESTGIGWSIYYDDHNTLHGATVTLKAGDNLIKQ-- 117
|||||
QY 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 180
|||||
Db 118 -----SGKDFYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 170
|||||
QY 181 DTTVHLNGIGSTLDTLLNTGATNTNDVNTDDKKRAASVKDVLNAGNWKGVKPGT 240
|||||
Db 171 DPTVHLNGIGSTLDTLLNTGATNTNDVNTDDKKRAASVKDVLNAGNWKGVKPGT 228
|||||
QY 241 A--SDNVDFVHTYDVEFLSADTKTTTVNVEKDKGKRTVEKIGAKTSVIKEDKGLVTG 298
|||||
Db 229 TGQSENDFVRYDIVEFLSADTKTTTVNVEKDKGKRTVEKIGAKTSVIKEDKGLVTG 288
|||||
QY 299 KKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKFEETVTSNTVTFE 358
|||||
Db 289 KKGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGQADKFEETVTSNTVTFE 348
|||||
QY 359 SGKCTTATVSKDDQGNITVYKDYVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSP 418
|||||
Db 349 SGNCTTATVSKDDQGNITVYKDYVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVSP 408
|||||
QY 419 SKGMDETVNINAGNNIETRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGLNV 478
|||||


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|||||
Db 409 SKGKDETVNINAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNV 468
QY 479 GSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNINNRIDNVNAGIQAQIATAGL 538
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QY 539 VOAYLPKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFASASVGYQ 598
Db 529 AOAYLPKSMMAIGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRHFAGTSASVGYQ 588
QY 599 W 599
Db 589 W 589

RESULT 15
Q9JPS8
ID Q9JPS8 PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;
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Query Match 88.5%; Score 2709; DB 2; Length 599;
Best Local Similarity 89.7%; Pred. No. 3.le-106;
Matches 539; Conservative 17; Mismatches 41; Indels 4; Gaps 2;

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QY 121 KNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
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QY 181 DTTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTT 240
Db 181 DTTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNKGVKPGTT 238
QY 241 A--SDNVDVHTYDVVEFLSADTKTTNVNVEKSDNGKRTKVKIGAKTSVKEKDKGLVTG 298
Db 239 TCQSENVDVFTYDVEFLSADTKTTNVNVEKSDNGKRTKVKIGAKTSVKEKDKGLVTG 298
QY 299 KGKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVSGTNVTF 358
Db 299 KGKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVSGTNVTF 358
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QY 419 SKGKMDETVNIAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDDKALNV 478
Db 419 SKGKMDETVNIAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDDKALNV 478
QY 479 GSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNINNRIDNVNAGIQAQIATAGL 538
Db 479 GSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNINNRIDNVNAGIQAQIATAGL 538
QY 539 VOAYLPKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFASASVGYQ 598
Db 539 VOAYLPKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFASASVGYQ 598
QY 599 W 599
Db 599 W 599
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Search completed: July 3, 2002, 08:28:47
Job time: 1168 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:31:04 ; Search time 104.77 seconds

(without alignments)
633.980 Million cell updates/sec

Title: US-09-771-382-7

Perfect score: 3044

Sequence: 1 MNKYRIIWSALNAWVVS.....TASGNSRGFCASASVGYQW 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	3044	100.0	598 20	AA23742 A surface protein
2	3044	100.0	598 22	AAU06177 N. meningitidis H1
3	3021	99.2	598 20	AA23738 A surface protein
4	3021	99.2	598 22	AAU06178 N. meningitidis B2
5	2971	97.6	594 20	AA23739 A surface protein
6	2971	97.6	594 22	AAU06179 N. meningitidis B2
7	2855	93.8	594 20	AA23740 A surface protein
8	2855	93.8	594 22	AAU06174 BAS029 amino acid
9	2855	93.8	594 22	AAU06174 N. meningitidis EG
10	2824.5	92.8	599 20	AA23743 A surface protein
11	2824.5	92.8	599 22	AAU06176 N. meningitidis H3

12	2735.5	89.9	591 21	AA57045 BAS029 amino acid
13	2725.5	89.5	591 20	AA27202 Amino acid sequenc
14	2725.5	89.5	591 20	AA23746 A surface protein
15	2725.5	89.5	591 22	AAU06171 N. meningitidis PM
16	2718	89.3	592 20	AA23737 A surface protein
17	2706.5	88.9	591 20	AA23741 A surface protein
18	2706.5	88.9	591 22	AAU06175 N. meningitidis EG
19	2667	87.6	592 20	AA23744 A surface protein
20	2667	87.6	592 22	AAU06172 N. meningitidis H4
21	2610.5	85.8	589 20	AA23745 A surface protein
22	2610.5	85.8	589 22	AAU06173 N. meningitidis P2
23	2524	82.9	592 22	AAU06180 N. meningitidis Z2
24	2488	81.7	592 20	AA27203 Amino acid sequenc
25	2460.5	80.8	513 22	AAU06183 N. meningitidis H4
26	2427	79.7	512 22	AAU06182 N. meningitidis PM
27	2344	77.0	502 22	AAU06186 N. meningitidis PM
28	2234	73.4	604 22	AAU06181 N. meningitidis PM
29	2010.5	66.0	433 22	AAU06185 N. meningitidis PM
30	1864.5	61.3	407 22	AAU06184 N. meningitidis PM
31	1318.5	43.3	2353 17	AAU99393 Haemophilus adhesi
32	1292.5	42.5	2411 21	AA23860 Haemophilus influe
33	1078	35.4	1094 21	AA23858 Haemophilus influe
34	1057	34.7	1098 17	AA299392 Haemophilus influe
35	1041	34.2	245 20	AA27201 Amino acid sequenc
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37	1010.5	33.2	679 21	AA23855 Haemophilus influe
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40	712	23.4	1104 21	AA23856 Haemophilus influe
41	712	23.4	1104 21	AA23859 Haemophilus influe
42	597	19.3	116 21	AA37832 Neisseria conserv
43	416.5	13.7	2314 22	AA69136 M. catarrhalis les
44	393.5	12.9	2123 22	AAE00701 Moraxella catarrha
45	391.5	12.9	1992 17	AAW04505 Moraxella 200 kDa

ALIGNMENTS

RESULT 1

AA23742

ID AA23742 standard; Protein; 598 AA.

XX AC AA23742;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX DE Surface protein; surface glycoprotein; infection; vaccine;

KW Immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYQU) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI; 1999-418754/35.

XX DR N-PSDB; AA85794.

XX PT Neisseria meningitidis surface proteins useful for treating N.

XX PT meningitidis infections

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*

CC meningitidis which is approximately 62 kDa. The *N. meningitidis*

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of *N. meningitidis* infection in humans.

CC The *N. meningitidis* surface glycoproteins can also be used to

CC prevent or treat *N. meningitidis* infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

XX

SQ Sequence 598 AA;

Query Match 100.0%; Score 3044; DB 20; Length 598;

Best Local Similarity 100.0%; Pred. No. 1.2e-175;

Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKYRIIWNALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60

Db 1 mnkyriiwnsalnawvvsseitnrhtrkasatvatvatlflfatvqanaddddlyle 60

Qy 61 PVQRTAVVLSFRSKEGTGEKGFEDSNMAYVFDEKRVLKAGAITLKAGDNLKIKQNTNE 120

Db 61 pvqrtavvlsfrskegtgekedtsnmayvfdekrvllkagaitllkagdnllkikqntne 120

Qy 121 NTNENTNDSSFTYSLKRDLTDLTSETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180

Db 121 ntentndssftysllkrdltdltseteklsfgangknvnitsdtkglnfaketagtngd 180

Qy 181 PTVHLNGIGSTLTDLTNLGTATFNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240

Db 181 ptvhlngigstltdlntlgtatfntndvtddekkraasvkdvlngagwnkvgkpgtta 240

Qy 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNGKTEVKIGAKTSVKEKDKGLVTGKKG 300

Db 241 sdnvdfvrtvdtveflsadtktttnnveskdngkktevkiagaktsvikegdkglvtgkkg 300

Qy 301 DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEVTSGTKVTFASGN 360

Db 301 dengsstdegeglvtakevidavnkagwrmtttangotgoadkfevtsgtkvtfasgn 360

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Db 361 gttatvskddgntvkyvdvngdnlvnlqnsqwnldskavagssgkvtsgnvspskg 420

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Db 421 kmdevtninagnntietrnknidiatstmpqfssvslgagadaptilsvddegalnvgsk 480

Qy 481 DANKPVRTNVPAGVKEGDVTNVQALKGVAQNANLNRRIDNVGNRAGTAQAIATAGLAQA 540

Db 481 dankpvrtnvpagvkegdvtnvqalkgvaqnlnrridnvdgnragtaqaiataglaqa 540

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Db 541 ylpksmmaigggryrgagyagysyssidtgnvviikgtasgnsgrhfgasasvgyqw 598

RESULT 2

AAU06177

ID AAU06177 standard; Protein; 598 AA.

AC AAU06177;

XX 24-OCT-2001 (first entry)

DT

XX

DE *N. meningitidis* H15 surface antigen Naha polypeptide sequence.

XX

KW Surface antigen Naha; meningococcal disease; meningitis vaccine.

XX

OS *Neisseria meningitidis* strain H15.

XX PH Region Location/Qualifiers

FT 1..50 /label= C1

FT /note= "Conserved region 1"

FT 51..104 /label= V1

FT /note= "Variable region 1"

FT 105..116 /label= C2

FT /note= "Conserved region 2"

FT 117..130 /label= V2

FT /note= "Variable region 2"

FT 131..194 /label= C3

FT /note= "Conserved region 3"

FT 195..216 /label= V3

FT /note= "Variable region 3"

FT 217..235 /label= C4

FT /note= "Conserved region 4"

FT 236..242 /label= V4

FT /note= "Variable region 4"

FT 243..598 /label= C5

FT /note= "Conserved region 5"

XX WO200155182-A1.

PN

XX 02-AUG-2001.

PD

XX 25-JAN-2001; 2001WO-AU000069.

PF

XX 25-JAN-2000; 2000US-0177917.

PR

XX (UYQU) UNIV QUEENSLAND.

PA

XX Peak IRA, Jennings MP;

PI

XX WPI; 2001-488774/53.

DR

XX N-PSDB; AAS09167.

DR

XX New Naha surface antigen polypeptides and polynucleotides from

PT *Neisseria meningitidis*, useful in producing vaccines for treating or

PT preventing broad spectrum of *Neisseria meningitidis* -

XX

PS Claim 9; Fig 1; 91pp; English.

XX

CC The present invention relates to the isolation of novel *Neisseria*

CC meningitidis mutant polypeptides of the surface antigen Naha

CC (AAU06182-AAU06186). The modified or mutant Naha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of *N. meningitidis*, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of *N. meningitidis* strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Naha

CC from *N. meningitidis* strain H15 is 1 of 10 Naha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in

CC the present invention.

XX

SQ Sequence 598 AA;

Query Match 100.0%; Score 3044; DB 22; Length 598;

Best Local Similarity 100.0%; Pred. No. 1.2e-175;

Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVWSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
 Db 1 mnkiyriiwnlsalnawvwwseltrnhtkrasatvatvatltilfatvqanatdddlyle 60

QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120
 Db 61 pvertavvlsfrsdkegtgekedtsnwavyfdekrvllkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
 Db 121 ntntentndsfstyslkdldtldtsveteklsfgangknvntsdtkglnfaketagngd 180

QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
 Db 181 ptvhlingigstltdltllntgattntvntdndvtddekkraasvkdvlngagwnikgvkpgtta 240

QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTVEKIGAKTSVIKEDGKLVTKGK 300
 Db 241 sdnvdfvrtvdytveflsadtktttvnvesskdngkktveikigaktsvikekgklvtgk 300

QY 301 DENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSVTSKVTTFASGN 360
 Db 301 dengssstdegeglvtakevidavnkagwrmtnttngotgoadkfevtsvtskvttfasgn 360

QY 361 GTTATVSKDDQGNITVKYIDVNVGDALNVNQLONGSNWNLDSKAVAGSGKVISGNVSPSKG 420
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QY 421 KMDETVNINAGNIEITRNKKNIDIAISMTPPQFSSVSLGAGADAPTLISVDDGALNVGSK 480
 Db 421 kmdetvninagnieitrngknidiaismtpqfssvslgagadaptilsvddegalnvgsk 480

QY 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVNGNARAGIAQAIATAGLAQA 540
 Db 481 dankpvrntnvapgvkegdtvntvaqlkgvaqnlrnnidvngnarnaragiaqaiataglaqa 540

QY 541 YLPQKSMMAIGGGTYRGEAGYAIYSSISDGTGNWIKGTASGNSRHFASASVGYQW 598
 Db 541 ylpqksmmaigggtyrgeagyaigyssisdgtgnwviktasgnsrghfgasasvgyqw 598

RESULT 3

AAU06178
 ID AAU06178 standard; Protein; 598 AA.

AC AAU06178;

XX 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;
 KW immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9311132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

XX (UYQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-PSDB; AAX85790.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX Claim 1; Page 91-93; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.

CC The N. meningitidis surface glycoproteins can also be used to

CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides.

XX Sequence 598 AA;

Query Match 99.2%; Score 3021; DB 20; Length 598;

Best Local Similarity 99.3%; Pred. No. 2.8e-174;

Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Db 1 mnkiyriiwnlsalnawvwwseltrnhtkrasatvatvatltilfatvqanatdddlyle 60

QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120

Db 61 pvertavvlsfrsdkegtgekedtsnwavyfdekrvllkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180

Db 121 ntntentndsfstyslkdldtldtsveteklsfgangknvntsdtkglnfaketagngd 180

QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240

Db 181 ptvhlingigstltdltllntgattntvntdndvtddekkraasvkdvlngagwnikgvkpgtta 240

QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNGKKTVEKIGAKTSVIKEDGKLVTKGK 300

Db 241 sdnvdfvrtvdytveflsadtktttvnvesskdngkktveikigaktsvikekgklvtgk 300

QY 301 DENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSVTSKVTTFASGN 360

Db 301 dengssstdegeglvtakevidavnkagwrmtnttngotgoadkfevtsvtskvttfasgn 360

QY 361 GTTATVSKDDQGNITVKYIDVNVGDALNVNQLONGSNWNLDSKAVAGSGKVISGNVSPSKG 420

Db 361 gttatvskddqgnitvkiyidvnnvgdalnnvnlqngsnwpldsavagsgkvisgnvpskg 420

QY 421 KMDETVNINAGNIEITRNKKNIDIAISMTPPQFSSVSLGAGADAPTLISVDDGALNVGSK 480

Db 421 kmdetvninagnieitrngknidiaismtpqfssvslgagadaptilsvddegalnvgsk 480

QY 481 DANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDVNGNARAGIAQAIATAGLAQA 540

Db 481 dankpvrntnvapgvkegdtvntvaqlkgvaqnlrnnidvngnarnaragiaqaiataglaqa 540

QY 541 YLPQKSMMAIGGGTYRGEAGYAIYSSISDGTGNWIKGTASGNSRHFASASVGYQW 598

Db 541 ylpqksmmaigggtyrgeagyaigyssisdgtgnwviktasgnsrghfgasasvgyqw 598

RESULT 4

AAU06178

ID AAU06178 standard; Protein; 598 AA.

XX AC AAU06178;

XX 24-OCT-2001 (first entry)

XX N. meningitidis B210 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.


```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS
XX Claim 1; Page 95-97; 132pp; English.
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;

Query Match          97.6%; Score 2971; DB 20; Length 594;
Best Local Similarity 98.0%; Pred. No. 2.9e-171;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

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Dd 1 mkklyriiwnsalnavwvseitrnhtrkrasatvatvatltilfatvqanatdddlyle 60
QY 61 PVQRTAVVLSFSDKEGTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
Dd 61 pvrqtavvlsfisdkegtegtegsdsnwavfyfdekrvllkagaitlkagdnlkikqntne 120
QY 121 NTNENTNDSSFTYSKLDLTLSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNGD 180
Dd 121 ntentndssftyskldltlsveteklsfgangknvniitstdtkglnfaketagtngd 180
QY 177 ntentndssftyskldltlsveteklsfgangknvniitstdtkglnfaketagtngd 176
Dd 177 ntentndssftyskldltlsveteklsfgangknvniitstdtkglnfaketagtngd 176
QY 181 PTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
Dd 181 ptvhlngigstltdllntgatntvndvtddekraasvkdvlntagwnikgvkpgtta 240
QY 241 SDNVDFVRYDVFELSDTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKGK 300
Dd 241 sdnvdfvrydvfelstdtkttvnvnekdkngktevkiaktsvkekdgklvtgk 300
QY 237 sdnvdfvrydvfelstdtkttvnvnekdkngktevkiaktsvkekdgklvtgk 296
Dd 237 sdnvdfvrydvfelstdtkttvnvnekdkngktevkiaktsvkekdgklvtgk 296
QY 301 DENGSTDEGLVTAKEVIDAVNKGWRMKTGTANGQTQADKFTVTSGTKVTFASGN 360
Dd 301 dengstdeglvtakevidavnnkgwrmtgttangqtqadkftvtsgtkvtfasgn 360
QY 297 dengstdeglvtakevidavnnkgwrmtgttangqtqadkftvtsgtnvfask 356
Dd 297 dengstdeglvtakevidavnnkgwrmtgttangqtqadkftvtsgtnvfask 356
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Dd 361 gttatvskddqgnitvkvdyvnnvgdnlvnnqlnsgwnldskavagssgkvsgnvspskg 420
QY 357 gttatvskddqgnitvkvdyvnnvgdnlvnnqlnsgwnldskavagssgkvsgnvspskg 416
Dd 357 gttatvskddqgnitvkvdyvnnvgdnlvnnqlnsgwnldskavagssgkvsgnvspskg 416
QY 421 KNDFTVNIAGNIIETRNKIDATSTMTPOFSSVSLCAGADAPTLSDVDDGALNVGSK 480
Dd 421 kndftvniagniieitrnkaidatstmtpofssvslcagadaptlsvddgalnvsgk 480
QY 417 kndetvniagniieitrnkaidatstmapdfssvslgagadaptlsvddgalnvsgk 476
Dd 417 kndetvniagniieitrnkaidatstmapdfssvslgagadaptlsvddgalnvsgk 476
QY 481 DANKPVRITNPAGVKEGSDVTNVAQLKGVAQLNNRIDNVNAGNARAGIAQALATAGLAQA 540
Dd 481 dankpvrinpagvkegsdvtvnvaqlkgvaqlnnridnvvnagnaragialataglaqa 540
QY 477 dtnkpvrintnpagvkegsdvtvnaqlkgvaqlnnridnvvnagnaragialataglaqa 536
Dd 477 dtnkpvrintnpagvkegsdvtvnaqlkgvaqlnnridnvvnagnaragialataglaqa 536
QY 541 YLPGKSMMAIGGTVRGEAGYAGYSSISDGTNNWIKGPASGNSRGHFGASVGVQW 598
Dd 541 ylpgksmmaiggtvrggeagayagysisdgtnnwikgpasgnsrghfgasvgyqw 598
QY 537 ylpgksmmaiggtvrggeagayagysisdgtnnwikgpasgnsrghfgasvgyqw 594
Dd 537 ylpgksmmaiggtvrggeagayagysisdgtnnwikgpasgnsrghfgasvgyqw 594

RESULT 6
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX
AC AAU06179;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis Bz198 surface antigen Nhha polypeptide sequence.
```

```
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain Bz198.
OS
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09169.
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain Bz198 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 594 AA;
SQ
```

Query Match 97.6%; Score 2971; DB 22; Length 594;
Best Local Similarity 98.0%; Pred. No. 2.9e-171;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNAWVVVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvavatltilfatvqanatdddlyle 60
QY 61 PVQRTAVVLFRSDKEGTGEGTSDSNWAVYDEKRVLRKAGATTLKAGNLIKQNTNE 120
DB 61 pvqrtavvlfrsdegtgegtedsnwavyfdekrvllrkagatllkagnlikqntne 116
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 117 ntentndssftyslkkdltdltsveteklsfgangknvitsdtkglnfaketagntgd 176
QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVDEKRAASVKOVNLNAGWNIKGVPKPTTA 240
DB 177 ptvhlngigstltdlntgattntvndvtddekkraasvkdvlnagwnikgvpkptta 236
QY 241 SDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLVTCGKG 300
DB 237 sdnvdfvrtvdtveflsadtkttnvnveskdngkktvkiaktsvkekdglvtcgkg 296
QY 301 DENGSSDEGEGLVTAKEVIDAVNKAQWRMKTITTTANGOTGQADKFETVTSCTKVFASGN 360
DB 297 dengssdegeglvtakevidavnkagwrmttttangotgqadkfetvtsctkvnfaskg 356
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
DB 357 gttatvskddqgnitvkydvnvgdalnvnglqnsqwnldskavagssgkvisgnvspkg 416
QY 421 KMDETVNIAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSK 480
DB 417 kmdetvniagnnieitrngknidia tsmappqfssvslgagadapltlsvdegalnvgsk 476
QY 481 DANKPVRITNVAPGVKEGDVTNVQALKGVAQNLNRRIDNVDGNARAGIAQAIATAGLAQA 540
DB 477 dtnkpvrntnvapgvkegdvtnvaqlkgvaqnlrridnvdgnaragiaqaiataglvqa 536
QY 541 YLPKKSMAIAGGTYRGEAGYAGYSSISDTGNVVIKGTASGNSRGRHFGASASVGYQW 598
DB 537 ylpqksmaiaaggtyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw 594

RESULT 7
AAV23740
ID AAV23740 standard; Protein; 594 AA.
XX
AC AAV23740;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX

DR WPI; 1999-418754/35.
DR N-PSDB; AAX85792.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 100-101; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;

Query Match 93.8%; Score 2855; DB 20; Length 594;
Best Local Similarity 94.8%; Pred. No. 2.9e-164;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNAWVVVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvavatltilfatvqastdddlyle 60
QY 61 PVQRTAVVLFRSDKEGTGEGTSDSNWAVYDEKRVLRKAGATTLKAGNLIKQNTNE 120
DB 61 pvqrtavvlfrsdegtgegtedsnwavyfdekrvllrkagatllkagnlikqntne 120
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 121 ntne-----sftyslkkdltdltsveteklsfgangknvitsdtkglnfakktacngd 176
QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVDEKRAASVKOVNLNAGWNIKGVPKPTTA 240
DB 177 ptvhlngigstltdlntgattntvndvtddekkraasvkdvlnagwnikgvpkptta 236
QY 241 SDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKLVTCGKG 300
DB 237 sdnvdfvrtvdtveflsadtkttnvnveskdngkktvkiaktsvkekdglvtcgkd 296
QY 301 DENGSSDEGEGLVTAKEVIDAVNKAQWRMKTITTTANGOTGQADKFETVTSCTKVFASGN 360
DB 297 dengssdegeglvtakevidavnkagwrmttttangotgqadkfetvtsctkvnfaskg 356
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
DB 357 gttatvskddqgnitvkydvnvgdalnvnglqnsqwnldskavagssgkvisgnvspkg 416
QY 421 KMDETVNIAGNNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSK 480
DB 417 kmdetvniagnnieitrngknidia tsmppqfssvslgagadapltlsvdegalnvgsk 476
QY 481 DANKPVRITNVAPGVKEGDVTNVQALKGVAQNLNRRIDNVDGNARAGIAQAIATAGLAQA 540
DB 477 dtnkpvrntnvapgvkegdvtnvaqlkgvaqnlrridnvdgnaraglaaiaataglvqa 536
QY 541 YLPKKSMAIAGGTYRGEAGYAGYSSISDTGNVVIKGTASGNSRGRHFGASASVGYQW 598
DB 537 ylpqksmaiaaggtyrgeagyaigyssisdggnwilkgtasgnsrghfgasasvgyqw 594

RESULT 8
AAV57044
ID AAV57044 standard; Protein; 594 AA.
XX
AC AAV57044;
XX
DT 21-FEB-2000 (first entry)

xx BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
xx
xx
xx BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
xx Infection; treatment; prevent; antibacterial drug.
xx
xx Nisseria meningitidis.
xx
xx
xx Key Location/Qualifiers
xx Misc-difference 104 /note= "Encoded by AATC"
xx
xx WO958683-A2.
xx
xx PD 18-NOV-1999.
xx
xx PF 07-MAY-1999; 99WO-EP03255.
xx
xx PR 13-MAY-1998; 98GB-0010276.
xx
xx (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
xx
xx Ruelle J;
xx
xx WPI; 2000-053103/04.
xx N-PSDB; AA239864.
xx
xx New polypeptide from neisseria meningitidis useful for diagnosis,
xx treatment or prevention of bacterial infections in mammal -
xx
xx Claim 4; Fig 2; 74pp; English.
xx
xx This is the Nisseria meningitidis BASB029 amino acid sequence from
xx serogroup B strain ATCC13090. The BASB029 protein is homologous to the
xx Haemophilus influenzae surface fibril (HSF) protein. The invention
xx relates to BASB029 polynucleotide sequences (AA239864-239865) and
xx polypeptide sequences (AA239864-239865) and their immunogenic fragments.
xx BASB029 polypeptides are useful in a method of diagnosing a Neisseria
xx meningitidis infection in a mammal. Compositions containing a Neisseria
xx polynucleotides and polypeptides are useful for generating an immune
xx response in an animal. A therapeutic composition comprising an antibody
xx directed against BASB029 is useful in treating humans with Neisseria
xx meningitidis disease. The polynucleotide is useful in the diagnosis of
xx the stage of infection, type of infection, susceptibility to an
xx infection which results from increased or decreased expression of the
xx polynucleotide, and for therapeutic or prophylactic purposes,
xx particularly genetic immunisation. Antibodies against BASB029
xx polynucleotides and polypeptides are also useful for treating infections
xx particularly bacterial infections. The protein is useful in the
xx screening and development of antibacterial drugs. Fused recombinant
xx protein is useful for the stimulation of the immune system of an organism
xx receiving the protein.
xx
xx SQ Sequence 594 AA;

Query Match 93.8%; Score 2855; DB 21; Length 594;
Best Local Similarity 94.6%; Pred. No. 2.9e-164;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVAVATVATLTLFATVQANATDDDLYLE 60
Db 1 mnkiyriiwsalnawvvsellnrhtkrasatvatvatvatllfatvqastdddlyle 60
QY 61 PVQRTAVVLSFRSDKEGTGKESGTESSNNAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
Db 61 pvqrtavvlsfrsdkegtgksgteessnnavyfdkkgvltagtitlkagdnlikqntne 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNPAKETAGTNGD 180
Db 121 ntne-----sstysllkkdltdltsvgeteklsfsangknvnitsdtkglnfakktatngd 176
QY 181 PTVHLNGIGSTLTDLTLNLTGATTVNTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240

Db 177 ttvhlngigstltdltnltgattvntndnvtddekkraasvkdvlngawnkvgkpgtta 236
QY 241 SDNVDFVRYDYVEFLSADTKTTTNNVESKDNGKKTEVKIGAKTSYIKEKDGKLVTKGKG 300
Db 237 sdnvdfvrydytveflsadtktttnnveskdngkrtvkvigaktsyikekdglvtgkdk 296
QY 301 DENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADKFEVTSGTKVTFASGN 360
Db 297 gendssstdekgeglvtakevidavnkagwrmttttangotgqadkfecvtsgtvntvfask 356
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSQWNLDSKAVAGSSGKVIISGNVSPSKG 420
Db 357 gttatvskddqgnitvmydvnvgdalnvnlqnsqwnldskavagsgkvisgnvpskg 416
QY 421 KMDETVNNAGNIEITRNCKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 417 kmdetvnnagnieitrncknidatmtptqfssvslgagadaptlsvddegalnvgsk 476
QY 481 DANKPVRITNVAPGVKEGVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLAQA 540
Db 477 dankpvrithvapgvegdvtnvaqlkgvaqnlmhlndvndgnaregiataglvqa 536
QY 541 YLPKCSMAIGGTYRGEAGYAIYSSISDPTGNWIKGTASGNSRHFASASVGYQW 598
Db 537 ylpkcsmaiggttyrgeagyaiyssisdgpnwikgtasgnsrghfgasasvgyqw 594

RESULT 9
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DT 24-Oct-2001 (first entry)
XX
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX

PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09164.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broad
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA;

Query Match 93.8%; Score 2855; DB 22; Length 594;
Best Local Similarity 94.6%; Pred. No. 2.9e-164;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDLYLE 60
Db 1 mnkyriiwsalnawvavseltrnhtkrasatvatavlatlilfatvqastdddlyle 60

Qy 61 PVQRTAVVLSFRSDEKGEKTEGDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
Db 61 pvqrtavvlsfrsdektegtesnwgvyfdkkgvltagtlkagdnlikkqntne 120

Qy 121 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
Db 121 ntntnndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagtngd 180

Qy 121 ntntnndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagtngd 176
Db 121 ntntnndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagtngd 176

Qy 181 PTVHLNGIGSTLTDTLLNTGATNTVNDVTDDEKKRAASVKDVLNAGWNIGVKPGPTA 240
Db 177 ttvhlngigstltdtllntgattntvndvtddekkraasvkdvlagnagwnikgvpqgta 236

Qy 241 SDNVDFVETVDFEFLSADTTTNNVESKDKGKTEVKIGAKTSVIEKDGKLVTKGK 300
Db 237 sdnvdfvetydfevltsadttnnnveskdngkrtevkigaktsviekdgklvtgkdk 296

Qy 301 DENGSSSTDEGEGVLTAKEVIDAVNKAQWRMKTITANGOTQADKPFETVTSKTVTFASGN 360
Db 297 gendsstdekgeglvtakevidavnkagwrmtttangotqadkfetvtsgnvtfasgk 356

Qy 361 GTTATVSKDDGNTVTKYDVNVGDALNVQNLQNSGWNILDSKAVAGSSGKVTSGNVSPSKG 420
Db 357 gttatvskddgntvmydvnvgdalnvqnlqnsqwnildskavagsgkvtsngvnspsk 416

Qy 421 KMDETVNLNAGNIEITFNGKNIDIAISMTPOFSSVSISGACADAPTLISVDDEGALNVCSK 480
Db 417 kmdecvnlagnieitfngknidiatismtpofssvsisgacadaptlisvdddegalnvcsk 476

Qy 481 DANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDVGNRAGIAQAIATAGLAQA 540
Db 477 dankpvrtnvapgvkegdvtnvaqlkgvaqnlhndvgnaragiataglaqlqa 536

Qy 541 YLPKSSMMAIGGGTYRGAGYAIGYSSISDTGNNVVIKTAGSNGSRGHFGASGVQYW 598
Db 537 ylpkssmmaigggtyrgeagyaigyssisdggnwllktagsgnsgrhfgasagvyqw 594

RESULT 10
AAV23743
ID AAY23743 standard; Protein; 599 AA.
XX
AC AAY23743;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAX85795.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 114-115; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 599 AA;

Query Match 92.8%; Score 2824.5; DB 20; Length 599;
Best Local Similarity 92.7%; Pred. No. 2e-162;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59
Db 1 mnkyriiwsalnawvavseltrnhtkrasatvatavlatlilfatvqanadede 60

Qy 60 EPVQRTAVVLSFRSDEKGEKTEGDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119
Db 61 epvrsalvlqfmidkeggenestgnigwsiydnhtlbgatvltkagdnlikqntn 120

Qy 120 ENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 179
Db 121 knntentndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagntg 180

Db 421 gkmdetvnaagnnieitrngkndiatstmpqfssvslgagadaptilsvddkgalnvgs 480
Qy 480 KDANKPVRITNVAPGVKGGDVTNVAOLKGVACNLNRRIDNDGNARAGIAQAIATAGLAQ 539
Db 481 kdankpvrinvapgvkegdvtnvaqlkgvagnlnrindvgnaragiataglvq 540
Qy 540 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDPTGNMVIKGTASGNSRHFSGASVGYQW 598
Db 541 aylpgksmmaigggtyrgeagyaigyssisdggnwlikgtasgnrghfgsasvgyqw 599

RESULT 12
AA57045
ID AA57045 standard; Protein; 591 AA.
AC AA57045;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
XX
KW BASB029; Neisseria meningitidis; surface fibril protein; HSP; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGT"
XX
PN WO9958683-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI; 2000-053103/04.
DR N-PSDB; AAZ39865.
XX
PT New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal -
XX
PS Claim 4; Fig 2; 74pp; English.
XX
CC This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and
CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BasB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX Sequence 591 AA;
SQ

Query Match 89.9%; Score 2735.5; DB 21; Length 591;
Best Local Similarity 91.4%; Pred. No. 4.5e-157;
Matches 550; Conservative 9; Mismatches 28; Indels 15; Gaps 4;
Qy 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATAVATLATLLFATVQANATD---DDDL 57
Db 1 mnkiyriiwsalnawvavseltrnhtkrasatvktavlatllfatvqasannee 60
Qy 58 YLEPQRTAVVLSPRSDEKTEGTECT-EDSNWAVYFDEKRVLRKAGATILKAGDNLKIKQ 116
Db 61 yldpqrvtvavlivnsdkektegveednwavfyfdegvltareitllkagdnllkikq 120
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Db 121 -----ngsnftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketag 170
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Qy 237 GTTASDNVDVFTYDTVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIERKDGKLV 296
Db 231 gttasdnvdfvrtvdtveflsadtktttvneskdngkrtevkigaktsviekdgklvt 290
Qy 297 GKGDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGQTGOADKFETVTSKTVTF 356
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Qy 537 LAQAYLPKSMMAIGGGTYRGEAGYAGYSSISDPTGNMVIKGTASGNSRHFSGASVGY 596
Db 530 lvqaylpksmmaigggtyrgeagyaigyssisdggnwlikgtasgnrghfgsasvgy 589
Qy 597 QW 598
Db 590 qw 591

RESULT 13
AA57202
ID AA57202 standard; Protein; 591 AA.
XX
AC AA57202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;

KW bacterial infection; treatment.
XX Neisseria meningitidis.
OS WO9936544-A2.
PN 22-JUL-1999.
XX 14-JAN-1999; 99WO-IB00103.
XX 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX WPI; 1999-444400/37.
DR N-PSDB; AAX99124.
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AAY27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA;

Query Match 89.5%; Score 2725.5; DB 20; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.8e-156;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

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DB 61 yldpvqrtvavlivnsdkegtgekeveensdwavfnekgvitareitlkagdnlikikq 120
QY 117 NTNENTNENTNDSFYSLSKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 176
DB 121 -----ngcnfyslskdltdltsvgtklsisangknvnitsdtkglnfaketag 170
QY 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVDKVLNAGNWKGVKP 236
DB 171 tngdptvhlngigstltdllntgattntvndntvtddekkraasvdkvlnagwnkvgkp 230
QY 237 GTTASNDFPVRYDVEFLSADTKTTTWNVESKDNKGKTEVKIGAKTSVIKEKDGKLYT 296
DB 231 gttasndfvrtydveflsadtktttwnveskdngkktvkekgaktsvikekgdklyt 290
QY 297 GKKGDENGSSTDEGEGLVTAKEVIDAVNKGAWPKTTTANGQTGQADKFTVTSKTVTF 356
DB 291 gkgdengsstdegeglvtakevidavnkagwrkmtttangqgtgqadkftvtsgnvtf 350
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DB 411 pskgkmdetvniagnniettrngknidiatsmtpfssvslgagadaptlsvdgd-aln 469

QY 477 VGSKDANKPVRIITNVAPGVKEGDTNVAOLKGAQNLNRRIDNVGNNARAGIAQAIATAG 536
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QY 537 LAQAYLPGRKSMAIGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRHFQASASVGY 596
DB 530 lvqaylpgksmaigggtyrgeagyaigyssisdggnwiikgtasngsrhfgasasvgy 589
QY 597 QW 598
DB 590 qw 591
RESULT 14
AAY23746
ID AAY23746 standard; Protein; 591 AA.
XX
AC AAY23746;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO99311132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85798.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 127-128; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 591 AA;

Query Match 89.5%; Score 2725.5; DB 20; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.8e-156;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

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DB 61 yldpvqrtvavlivnsdkegtgekeveensdwavfnekgvitareitlkagdnlikikq 120
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Db 530 lvqaylpkgsmmaiggttyrgeagyalgyssisdggnwlikgtsagnsrghfgasasvgy 589
QY 597 QW 598
Db 590 qw 591

RESULT 15
AAU06171
ID AAU06171 standard; Protein: 591 AA.
XX
AC AAU06171;
XX
DT 24-OCT-2001 (first entry)
XX
XX N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
KW Neisseria meningitidis strain PMC21.
XX
FH Key Location/Qualifiers
FT Peptide 1..51
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FT Region 1..50
FT FT /label= C1
FT FT /note= "Conserved region 1"
FT Region 51..108
FT FT /label= V1
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FT Protein 52..591
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FT FT /note= "Predicted mature protein, specifically claimed in claim 12"
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FT Region 230..236
FT FT /label= V4
FT FT /note= "Variable region 4"
FT Region 237..591
FT FT /label= C5
FT FT /note= "Conserved region 5"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI: 2001-488774/53.
XX
XX N-PSDB; AAS09161.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 591 AA;
SQ
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Query Match 89.5%; Score 2725.5; DB 22; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.8e-156;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

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GenCore version 4.5
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OM protein - protein search, using sw model

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 231628

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Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
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1	3044	100.0	598	4	US-09-377-155-13	Sequence 13, Appl
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3	3021	99.2	598	4	US-09-377-155-5	Sequence 5, Appl
4	3021	99.2	598	4	US-09-669-974-5	Sequence 5, Appl
5	2971	97.6	594	4	US-09-377-155-7	Sequence 7, Appl
6	2971	97.6	594	4	US-09-669-974-7	Sequence 7, Appl
7	2855	93.8	594	4	US-09-377-155-9	Sequence 9, Appl
8	2855	93.8	594	4	US-09-669-974-9	Sequence 9, Appl
9	2824.5	92.8	599	4	US-09-377-155-15	Sequence 15, Appl
10	2824.5	92.8	599	4	US-09-669-974-15	Sequence 15, Appl
11	2725.5	89.5	591	4	US-09-377-155-21	Sequence 21, Appl
12	2725.5	89.5	591	4	US-09-669-974-21	Sequence 21, Appl
13	2718	89.3	592	4	US-09-377-155-2	Sequence 2, Appl
14	2718	89.3	592	4	US-09-669-974-2	Sequence 2, Appl
15	2706.5	88.9	591	4	US-09-377-155-11	Sequence 11, Appl
16	2706.5	88.9	591	4	US-09-669-974-11	Sequence 11, Appl
17	2667	87.6	592	4	US-09-377-155-17	Sequence 17, Appl
18	2667	87.6	592	4	US-09-669-974-17	Sequence 17, Appl
19	2610.5	85.8	589	4	US-09-377-155-19	Sequence 19, Appl
20	2610.5	85.8	589	4	US-09-669-974-19	Sequence 19, Appl
21	1318.5	43.3	2353	4	US-09-377-155-33	Sequence 33, Appl
22	1318.5	43.3	2353	4	US-08-913-942-4	Sequence 4, Appl
23	1318.5	43.3	2353	4	US-09-669-974-33	Sequence 33, Appl
24	1317.5	43.3	2354	4	US-09-268-347-47	Sequence 47, Appl
25	1292.5	42.5	2411	4	US-09-268-347-36	Sequence 36, Appl
26	1251	41.1	607	1	US-08-409-995-6	Sequence 6, Appl
27	1251	41.1	607	3	US-08-685-467-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

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US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Ansell
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 97263
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: prt
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

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RESULT 2
US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
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US-09-669-974-13

Query Match 100.0%; Score 3044; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.9e-238;
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QY 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
QY 181 PTVHLNGIGSTLTDPLLTGATNTVNDVDEKRAASVKDVLNAGWNKGVKPGTTA 240
Db 181 PTVHLNGIGSTLTDPLLTGATNTVNDVDEKRAASVKDVLNAGWNKGVKPGTTA 240
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGRGK 300
Db 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGRGK 300
QY 301 DENGSTDEGGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEFVTSKVTTFASGN 360

Db 301 DENGSTDEGGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEFVTSKVTTFASGN 360
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSPSKG 420
Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSPSKG 420
QY 421 KMDETVNIAGNNEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 421 KMDETVNIAGNNEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 481 DANKPVRITNAPGVKEGDVTNVAOLKQVAQNLRNDRIDNVGNARAGIAQAATATAGLAQA 540
Db 481 DANKPVRITNAPGVKEGDVTNVAOLKQVAQNLRNDRIDNVGNARAGIAQAATATAGLAQA 540
QY 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598
Db 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598

RESULT 3
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 99.2%; Score 3021; DB 4; Length 598;
Best Local Similarity 99.3%; Pred. No. 3.6e-236;
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
QY 181 PTVHLNGIGSTLTDPLLTGATNTVNDVDEKRAASVKDVLNAGWNKGVKPGTTA 240
Db 181 PTVHLNGIGSTLTDPLLTGATNTVNDVDEKRAASVKDVLNAGWNKGVKPGTTA 240
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGRGK 300
Db 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIGAKTSVIREKDKLVTGRGK 300
QY 301 DENGSTDEGGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEFVTSKVTTFASGN 360
Db 301 DENGSTDEGGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKFEFVTSKVTTFASGN 360
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSPSKG 420

Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 421 KMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 421 KMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 481 DANKPVRITNVAPGVKEGDTVNVQAQLKGVAQNLNNRDNVDGNARAGIAQAIAATAGLAQA 540
Db 481 DANKPVRITNVAPGVKEGDTVNVQAQLKGVAQNLNNRDNVDGNARAGIAQAIAATAGLAQA 540
QY 541 YLPKSNMAIGGTYRGEAGYAGYSSISDTGNMWIKGTASGNSRGRHFGASASVGYQW 598
Db 541 YLPKSNMAIGGTYRGEAGYAGYSSISDTGNMWIKGTASGNSRGRHFGTSASVGYQW 598

RESULT 4
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 598
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match 99.2%; Score 3021; DB 4; Length 598;
Best Local Similarity 99.3%; Pred. No. 3.6e-236;
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MNKIYRIIWNLSALNNAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKISRIIWNLSALNNAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
Db 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
QY 181 PTVHLNIGISTLTDLLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKIKVKGPGTTA 240
Db 181 PTVHLNIGISTLTDLLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKIKVKGPGTTA 240
QY 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300
Db 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSKTVTFASGN 360
Db 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSKTVTFASGN 360
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420

Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 421 KMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 421 KMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 481 DANKPVRITNVAPGVKEGDTVNVQAQLKGVAQNLNNRDNVDGNARAGIAQAIAATAGLAQA 540
Db 481 DANKPVRITNVAPGVKEGDTVNVQAQLKGVAQNLNNRDNVDGNARAGIAQAIAATAGLAQA 540
QY 541 YLPKSNMAIGGTYRGEAGYAGYSSISDTGNMWIKGTASGNSRGRHFGASASVGYQW 598
Db 541 YLPKSNMAIGGTYRGEAGYAGYSSISDTGNMWIKGTASGNSRGRHFGTSASVGYQW 598

RESULT 5
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 97.6%; Score 2971; DB 4; Length 594;
Best Local Similarity 98.0%; Pred. No. 3.9e-232;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;
QY 1 MNKIYRIIWNLSALNNAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWNLSALNNAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
Db 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 117 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
QY 181 PTVHLNIGISTLTDLLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKIKVKGPGTTA 240
Db 177 PTVHLNIGISTLTDLLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKIKVKGPGTTA 236
QY 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300
Db 237 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 296
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSKTVTFASGN 360
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSKTVTFASGN 356
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 421 KMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

Db 417 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 476
QY 481 DANKPVRTITNAPGVKGGDVTNVAQLKGVAGNQLNRRIDNVGNARAGTAQAIAIATAGLAQA 540
Db 477 DTNKPVRTITNAPGVKGGDVTNVAQLKGVAGNQLNRRIDNVGNARAGTAQAIAIATAGLVQA 536
QY 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNVWIKGTASGNSRGHFGASASVGYOW 598
Db 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNVWIKGTASGNSRGHFGASASVGYOW 594

RESULT 6

US-09-669-974-7
: Sequence 7, Application US/09669974
: Patent No. 6331173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 7
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 97.68; Score 2971; DB 4; Length 594;
Best Local Similarity 98.08; Pred. No. 3.9e-232;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 116
QY 121 NTNENTNDSSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 117 NTNENTNDSSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
QY 181 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNIKGKPGTTA 240
Db 177 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNIKGKPGTTA 236
QY 241 SDNVDFVRTYDTVFLSADTKTTTVNVESKNGKTEVIGAKTSVKEKDGKLVTKGK 300
Db 237 SDNVDFVRTYDTVFLSADTKTTTVNVESKNGKTEVIGAKTSVKEKDGKLVTKGK 296
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEVTSCTKVTFSAGN 360
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEVTSCTKVTFSAGK 356
QY 361 GTTATVSKDDQGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 421 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 480
Db 417 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 476

Db 417 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 476
QY 481 DANKPVRTITNAPGVKGGDVTNVAQLKGVAGNQLNRRIDNVGNARAGTAQAIAIATAGLAQA 540
Db 477 DTNKPVRTITNAPGVKGGDVTNVAQLKGVAGNQLNRRIDNVGNARAGTAQAIAIATAGLVQA 536
QY 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNVWIKGTASGNSRGHFGASASVGYOW 598
Db 537 YLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNVWIKGTASGNSRGHFGASASVGYOW 594

RESULT 7

US-09-377-155-9
: Sequence 9, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 9
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 93.88; Score 2855; DB 4; Length 594;
Best Local Similarity 94.68; Pred. No. 9.3e-223;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
QY 121 NTNENTNDSSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 121 NTNA---SSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
QY 181 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNIKGKPGTTA 240
Db 177 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNIKGKPGTTA 236
QY 241 SDNVDFVRTYDTVFLSADTKTTTVNVESKNGKTEVIGAKTSVKEKDGKLVTKGK 300
Db 237 SDNVDFVRTYDTVFLSADTKTTTVNVESKNGKTEVIGAKTSVKEKDGKLVTKGK 296
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEVTSCTKVTFSAGN 360
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEVTSCTKVTFSAGK 356
QY 361 GTTATVSKDDQGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 421 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 480
Db 417 KMDETVINAGNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLTSSVDDGALNVGSK 476
QY 481 DANKPVRTITNAPGVKGGDVTNVAQLKGVAGNQLNRRIDNVGNARAGTAQAIAIATAGLAQA 540

Db 477 DANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 536
YQ 541 YLPKGSMAIIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFASASVGYQW 598
Db 537 YLPKGSMAIIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFASASVGYQW 594

RESULT 8

US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 93.8%; Score 2855; DB 4; Length 594;
Best Local Similarity 94.6%; Pred. No. 9.3e-223;
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;
YQ 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
YQ 61 PVQRTAVLSFRSDKEGTEGKEDTSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVQRTAVLSFRSDKEGTEGKEDTSNNGVYFDKGVLTAGTITLUKAGDNLKIKONTNE 120
YQ 121 NTNENTNDSSTFYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
Db 121 NTNA----SSFTYSLKKDLTDLTSVETEKLSFGANSKNVNIITSDTKGLNFAKTAETNGD 176
YQ 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
Db 177 TTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
YQ 241 SDNVDFVRTYDVFELSDTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGCK 300
Db 237 SDNVDFVRTYDVFELSDTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGDK 296
YQ 301 DENGSTDEGEGLVTAKEVIDAVNKGWMMKTTTANGQTQADKFETVTSKTFTVTFASGN 360
Db 297 GENDSTDKGEGLVTAKEVIDAVNKGWMMKTTTANGQTQADKFETVTSKTFTVTFASCK 356
YQ 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 420
Db 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 416
YQ 421 KMDETVINAGNNIETIRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 417 KMDETVINAGNNIETIRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
YQ 481 DANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 540
Db 481 DANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 540

Db 477 DANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 536
YQ 541 YLPKGSMAIIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFASASVGYQW 598
Db 537 YLPKGSMAIIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFASASVGYQW 594

RESULT 9

US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 92.8%; Score 2824.5; DB 4; Length 599;
Best Local Similarity 92.7%; Pred. No. 2.8e-220;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;
YQ 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59
Db 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60
YQ 60 EPQRTAVLSFRSDKEGTEGKEDTSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTN 119
Db 61 EPVRSALVQPMIDKEGNESTGICWISYVDNHNHTLHGATVTLKAGDNLKIKONTN 120
YQ 120 EYNTNENTNDSSTFYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 179
Db 121 KNTNENTNDSSTFYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
YQ 180 DPTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTT 239
Db 181 DPTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTT 240
YQ 240 ASDNVDFVRTYDVFELSDTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGKG 299
Db 241 ASDNVDFVRTYDVFELSDTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGKG 300
YQ 300 KDBNGSTDEGEGLVTAKEVIDAVNKGWMMKTTTANGQTQADKFETVTSKTFTVTFASG 359
Db 301 KDBNGSTDEGEGLVTAKEVIDAVNKGWMMKTTTANGQTQADKFETVTSKTFTVTFASG 360
YQ 360 NGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 419
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 420
YQ 420 GKMDETVINAGNNIETIRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNVGS 479
Db 421 GKMDETVINAGNNIETIRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNVGS 480
YQ 480 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 539
Db 481 KDANKPVRITNAPGVKEGDTNVAQLKGVAQNLNHNIDVNDGNARAGIAQAATATAGLVA 540
YQ 540 AYLPKGSMAIIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFASASVGYQW 598

Db 541 AYLPKSMMAICGGTYRGEAGYAICYSSISDGCNWIILKTASGNSRGHCASASVGYQW 599

RESULT 11

US-09-377-155-21

; Sequence 21, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; CURRENT FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 21

; LENGTH: 591

; TYPE: Prt

; ORGANISM: Neisseria meningitidis

US-09-377-155-21

[illegible]

Qy	1	MNKYRIIWSALNAWVVVSELTRNHTKRASATVATAVLATLLFAVPQANATDD---DD	56
Db	1	MNKYRIIWSALNAWVVVSELTRNHTKRASATVATAVLATLLFAVPQANANPRKDD	60
Qy	57	LYLPVQRTAVVLSFRSDKEGTEKECTED-SNWAYYFDEKRVLKAGATILKAGDNLKIK	115
Db	61	LYLPVQRTAVVLTNSDKEGTEKEKVEBSOWAYFYNEKGVLTAREITLLKAGDNLKIK	120
Qy	116	QNTNENTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA	175
Db	121	Q-----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA	170
Qy	176	GTNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGKV	235
Db	171	GTNGDPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGKV	230
Qy	236	PGTTASDNVDFVRTYDIVEFLSADTKTTNVNVEKDKNGKKEVKGAKTSVKEKDKGLV	295
Db	231	PGTTASDNVDFVRTYDIVEFLSADTKTTNVNVEKDKNGKKEVKGAKTSVKEKDKGLV	290
Qy	296	TGKCKDENGSTDEGELVTAKEVIDAVNKAGHRMKTTTTANGOTGOADFEIVTSGTKVT	355
Db	291	TGKCKDENGSTDEGELVTAKEVIDAVNKAGHRMKTTTTANGOTGOADFEIVTSGTNVT	350
Qy	356	FASGNGTTATVSKDDQGNITVYDVNVGDALNVQLONGSWNLDSKAVAGSGKVIISGNV	415
Db	351	FASGKGTATVSKDDQGNITVYDVNVGDALNVQLONGSWNLDSKAVAGSGKVIISGNV	410
Qy	416	SPSKCKMDETVMINAGNNIEITRNGKNIDIATSNTPQFSSVSLGACADAPTLISVDDEGAL	475
Db	411	SPSKCKMDETVMINAGNNIEITRNGKNIDIATSNTPQFSSVSLGACADAPTLISVDG-AL	469
Qy	476	NVGSKDANKPVRTITNVPAGYKGGDVTNVAQLKGVAONLNNRIDVNDGNARAGIAQAIATA	535
Db	470	NVGSKKONKPVRTITNVPAGYKGGDVTNVAQLKGVAONLNNRIDVNDGNARAGIAQAIATA	529
Qy	536	GLAQAYLPKGSMAIIGGTYRGEGAYGAYGSSISDGTGNVWIKGTASGNSRGHFASASVG	595

Db 530 GLVQAYLPCKSMMAIGGGTYRGEAGYATGYSISDGGNWIILKGTASGNSRGHFGASASVG 589
Qy 596 YQW 598
Db 590 YQW 592

RESULT 14
US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 89.3%; Score 2718; DB 4; Length 592;
Best Local Similarity 90.7%; Pred. No. 1.le-211;
Matches 547; Conservative 11; Mismatches 29; Indels 16; Gaps 4;
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDD---DD 56
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASANNRPKRD 60
Qy 57 LYLEPVQRTAVVLSFRSDEKTEGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 115
Db 61 LYLPVQRTAVVLSFRSDEKTEGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 120
Qy 116 QNTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 175
Db 121 Q-----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 170
Qy 176 GTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVK 235
Db 171 GTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVK 230
Qy 236 PGTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLV 295
Db 231 PGTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLV 290
Qy 296 TGKGDENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTQADKFFETVTSKT V 355
Db 291 TGKDGENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTQADKFFETVTSKT V 350
Qy 356 PASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSKAVAGSGKVISGNV 415
Db 351 PASGKGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSKAVAGSGKVISGNV 410
Qy 416 SPSGKMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVDEGAL 475
Db 411 SPSGKMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVGDG-AL 469
Qy 476 NVGSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGDNARAGIAQAIA 535

Db 470 NVGSKDANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGDNARAGIAQAIA 529
Qy 536 GLAQAYLPCKSMMAIGGGTYRGEAGYATGYSISDGGNWIILKGTASGNSRGHFGASASVG 595
Db 530 GLVQAYLPCKSMMAIGGGTYRGEAGYATGYSISDGGNWIILKGTASGNSRGHFGASASVG 589
Qy 596 YQW 598
Db 590 YQW 592

RESULT 15
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

Query Match 88.9%; Score 2706.5; DB 4; Length 591;
Best Local Similarity 90.5%; Pred. No. 9.5e-211;
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 MNEILLRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASANNBQEDDL 60
Qy 58 YLEPVQRTAVVLSFRSDEKTEGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 116
Db 61 YLDPVLRVAVLIVNSDKTEGEGTEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKIK 120
Qy 117 NTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 176
Db 121 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 170
Qy 177 TNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVK 236
Db 171 TNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIGVK 230
Qy 237 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLV 296
Db 231 GTTASDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLV 290
Qy 297 GKGDENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTQADKFFETVTSKT V 356
Db 291 GKDGENGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTQADKFFETVTSKT V 350
Qy 357 ASGNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSKAVAGSGKVISGNV 416
Db 351 ASGKGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSKAVAGSGKVISGNV 410
Qy 417 SPSKMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVDEGAL 476
Db 411 SPSKMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVGDG-AL 469
Qy 477 VGSKANKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLNRRIDNVGDNARAGIAQAIA 536


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|||||
Db 470 VGSKKDNKPVRTNVAPGVKEGDTNVAQLKGAQNLRIDNVDGNARAGIAQA1ATAG 529
QY 537 LAQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY 596
Db 530 LVOAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWI1KGTASGNSRGHFGASASVGY 589
QY 597 QW 598
|||
Db 590 QW 591
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Search completed: July 3, 2002, 08:37:08
Job time: 334 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:33:29 ; Search time 58.79 Seconds
(without alignments)
977.401 Million cell updates/sec

Title: US-09-771-382-7
Perfect score: 3044
Sequence: 1 MNKIYRIIWNLSALNAWVVS.....TASGNSRGHFGASASVGYQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2725.5	89.5	591	2 G81133	adhesin NMB0992 [i
2	2524	82.9	592	2 A81888	probable surface f
3	633	20.8	298	2 I64138	adhesin homolog HI
4	402	13.2	2059	2 D82671	surface protein XF
5	395	13.0	1107	2 AC0976	probable autotrans
6	382.5	12.6	1190	2 A82615	surface protein XF
7	368	12.1	1588	2 A86036	probable adhesin Z
8	368	12.1	1588	2 H91188	probable adhesin E
9	335	11.0	658	2 A80110	probable surface p
10	254	8.3	1004	2 C82672	surface-exposed ou
11	236	7.8	1091	2 G54964	hypothetical prote
12	222	7.3	949	2 D90803	Aida-I adhesin-lik
13	222	7.3	1005	2 H85611	probable adhesin Z
14	221.5	7.3	1910	2 AF0394	probable adhesin P
15	221	7.3	1018	2 H83135	probable adhesin h
16	220	7.2	1286	2 C82672	adhesin AIDA-I pre
17	215.5	7.1	4919	2 T31105	hypothetical prote
18	213.5	7.0	1325	2 A64905	ydek protein - Esc
19	213.5	7.0	3705	2 A80123	probable autotrans
20	213	7.0	1536	2 A43855	high-molecular-wei
21	211.5	6.9	1109	2 A56143	surface-array prot
22	210	6.9	1361	2 T03415	S-layer protein -
23	210	6.9	1608	2 A28182	hemolysin A - Serr
24	209	6.9	1417	2 A83080	hypothetical prote
25	207.5	6.8	961	2 A00548	puative autotransp
26	207	6.8	5291	2 F90696	hypothetical prote
27	206	6.8	2551	2 B90647	hypothetical prote
28	203	6.7	1327	2 B90674	Aida-I adhesin-lik
29	203	6.7	1349	2 E85524	probable beta-barr

ALIGNMENTS

RESULT 1

G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TE>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match	89.5%;	Score 2725.5;	DB 2;	Length 591;
Best Local Similarity	91.0%;	Pred. No. 1.8e-130;		
Matches 548;	Conservative 12;	Mismatches 27;	Indels 15;	Gaps 4;
Qy	1	MNKYRIIWNLSALNAWVVS	ELTRNHTKRASATVATVATLTLFATVQANATD---	DDDL 57
Db	1	MNKYRIIWNLSALNAWVVS	ELTRNHTKRASATVATVATLTLFATVQASANNEEQEEDL	60
Qy	58	YLEPQRTAVVLSPRSDEKGTGEKGTED-SNWAVYFDEKRVLKAGATLTLKAGDNLKIKQ		116
Db	61	YLDPQRTAVVLINSDREGTGEKEKVEENSOWAVYFNEKGLVTAREITLKAGDNLKIKQ		120
Qy	117	NTNENTNENTNDSPTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG		176
Db	121	-----NGTNFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG		170
Qy	177	TNGDPTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGCNWIKGVK		236
Db	171	TNGDPTVHLNGIGSTLTDLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGCNWIKGVK		230
Qy	237	GTTASDNVDFVRTYDTEVFLSADTKTTTVNVEKNGKKTVEKIGAKTSVIEKDGKLV		296
Db	231	GTTASDNVDFVRTYDTEVFLSADTKTTTVNVEKNGKKTVEKIGAKTSVIEKDGKLV		290
Qy	297	GKGDENGSSDDEGBGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKPEVTTVTSGTKVTF		356
Db	291	GKDKGENSSDDEGBGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKPEVTTVTSGTNVTFF		350
Qy	357	ASNGTGTATVSKDDQGNITVKYDVNVGDALNVNLQNSGNWLNDSRAVAGSSGKVTISGNVS		416

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <SIM>

A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorriy, H.; Facinani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

, F.G.; Nunes, L.R.; Oliveira, M.A.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1529

Query Match 13.2%; Score 402; DB 2; Length 2059;

Best Local Similarity 25.0%; Pred. No. 1.8e-12;

Matches 174; Conservative 100; Mismatches 215; Indels 208; Gaps 34;

QY 78 TGEKEDTSNNAVFDE-----KRVLKAGAITLKAGD-MLKTK 115

DB 1395 SGVTAGTEED-ANFSQLKSTSTAVDQGWTLTASGANGSKVSGGTVDLKNKTGDLNLTIS 1453

QY 116 Q--NTNE--NTNENTNDSSFTY----SLKDLTDLTIS----VETEKLSFGANGKVNITSD 164

DB 1454 KSGSDNDVVFNLSDELKESITVGNQTLQDKGVKSVNLLDSNELVITSHSSTSSVKTL 1513

QY 165 TKGILNFAKETA----GTNGDPTVHLNGI-----GSTLTDTLLNPGA--TTNVT-----N 207

DB 1514 ANGESVYNNVTVYVNGDGVNTDDVVYVNDLGLSIVGGASLTLSGINAGSHKITVNTAGTETD 1573

QY 208 DNVTDDEKKRAASVKDLNAGNII-----KGVPKPGTTASDNYD-----FVRTYDT 252

DB 1574 DAVNFSQLK---SVSEAVDKGWTLTASGANGSKVSGGTVDLKNKTGDNLAISKSGSDNDV 1630

QY 253 VBFLSADTK-----TTTVNYESKDNKKTEVKIGAKTSVKEKDKGLVTGKGKDN-- 303

DB 1631 VFNLSKDFKVDVETAGNTVVNTDGVKVG--SDVSLGAMGLFI--ANGPSVTASGFNAGDK 1686

QY 304 -----GSSDTGEGGLVTAKEVIDAVNKAGRMKTTTANGQTG-----QADKFETV 348

DB 1687 VISHVAVGMADTDVAVNSQLKQAVSVTVKATRYTSTDGGTGGNGYDGDGATGSKAIAA 1746

QY 349 TSSTKVT-----FASGNGTT-----ATVSKD-----DQG-----NITVKY 378

DB 1747 GVGTSAGGEEAAVSGAASGKGTSTAGRNIAIAGSVALGDGAKDGGRAESTYTKY 1806

QY 379 D-----VNVG-----DALNVNQL-----QNSGNLDS----- 400

DB 1807 SGVQNNVTGTVSGDAAKGETRSISNVADAKEAMDVNLRLDVAQKSNLQTDMDRHEI 1866

QY 401 -----KAVAGSSGKVISGNVSPSKGMDETNNINA-----GNNIETRN-----GKNIDI 445

DB 1867 NNIEDVFKITKGDSSASVAG-----MGVNAMAIGTNAAVSGTESVALGKNTNV 1914

QY 446 ATSMTPQFSSVSLGACADAPTLSVDDEGALNVGSKDNKAPVRLTNVAPGVKECDVTNVAQ 505

DB 1915 SAD-----NAVAIGNSVA-----DRANSVSGGSGSER--QVTNVAAGTADTDVAVNSQ 1962

QY 506 LKGVAQNLRNNDVNDGNAR-----AGIAQAIATAGLAQAYLPCKSMMAITGGGTYRGEAGY 561

RESULT 5

AC0976

probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0976

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

C:Genetics:

A:Gene: sapB

Query Match 13.0%; Score 395; DB 2; Length 1107;

Best Local Similarity 21.9%; Pred. No. 1.9e-12;

Matches 183; Conservative 116; Mismatches 259; Indels 278; Gaps 31;

QY 27 TKRASATVAT----AVIATLLFAT---VQANATDDDLLEVPQRTAVVLSFRSDEKGTG 79

DB 286 TNLAACTLAADSTDVANGSOLYETNQNQVDQNTSAIADINTSITLSSDNLNMTTNSFS 345

QY 80 EKEGTEDSNWAVFDEKRVLKAGAITLKAGD-----NLKIKQNTNE---NTNWT 126

DB 346 ASHGSSTTN-----KITNVAAGELSEESTDAVNGSOLFETNEKVDQNTDTIAANTTIT 399

QY 127 NDSSFTYSLKDLTDL--TSV-----ETEKLSFGAN--GNKNVITSDTKGLNFAKE 173

DB 400 QNSTAIENLTVSDINTSITGLTDNALLWDEDTGAFSANHGSGTSKIINVAAGALSIDS 459

QY 174 TAGTGNDPTVHLNGIGSTLTDTL--LNTGATTNVTNDVTDDEKKRAASVKDYVLNAGWNI 231

DB 460 TDAVNGSOLYETNQNQVDQNTSAIADINT--SITNLGTDALSWDDEGAFSASHGTSCTNKI 518

QY 232 KGVPKPGTTASDNDVDFV---RTYDT-----VEFLSADTKTTVN-----VESK 270

DB 519 TNVAAGEIASDSTDALINGSQLYETNMLISQYNESISQLAGDTSETYITENGTVGKVIRTN 578

QY 271 DNGKKE-----VKIGAKTSVKEK-----DGKLVTKGKNDN----- 303

DB 579 DNGLEQDDAYATNGATATVGVDAVASCAGCLALQNSSSSIEGSIAGSGSTNRAITWG 638

QY 304 ---GSSDTGEGGL---VTAKEVIDAVNKA----GWRMKTITTANGQTG----- 341

DB 639 IRETSATSDGVVIGYNTTDRILLGALSCTDGESYRQITNVADGSEADQAVTVRQLQNAI 698

QY 342 -----ADKFETVTSCTKVTFASGNGTTATVSKDDOGNTVYKDVNVGALNVNQLQN-- 393

DB 699 GAVTTTPTTKYKHANSTEDSLAVGTDLSLAKGAK-----TIVNADAGIGLNTFLVMADAI 753

QY 394 SGWNLDKSAVAGSSGVISGNVSP-----SKGKMD---ETV 426

DB 754 NGIAGSNRANHANSIANGNGSQTRGAQTDYATNMDTPQNSVGEFSVGSDEGQRIIT 813

QY 427 NINAGN-----NIEITRNGNI-----DIATSMIT 450

Db 814 NVAAGSADTDAVNVGQLKVTDAQVSRNTQSTITNLNTQVSNLDRVTNIENIGDIVTGS 873
Qy 451 PQF-----SSVSLGAGADAP-----TSLVDEDE-GALNVGSKDANKPV 486
Db 874 TKYFKTNTDGADANAQAGDSVAIGSGSITAAENSVALGTNSVADEANTVSGSSTQOR-- 931
Qy 487 RITVAPGVKGGDVNTVAQLK-----RITVAPGVKGGDVNTVAQLK-----507
Db 932 RITVAAAGVNTDAVNVAAQLKASEAGSVRYETNADGSGVNTSVLNLGDSGGTTRIGNVSA 991
Qy 508 -----GVAQ-----NLNRRIDNVNDRAGIAQAATATAGLAQAYL 542
Db 992 AVNTDVAVNTAQLKRSVEEANTYTDQKMGEMNSKIKIGENKMSGGIIASAMAGLPQAYA 1051
Qy 543 PGKSMIAIGGTYRGEAGYAGISISDTGNWVTKGTASGNSRHFSGASASVGYOW 598
Db 1052 PGANWTSIAGGTFGESVAIGSVMSSEGWVYKLGOTSNQSDYSAACAGCFQW 1107
RESULT 6
A82615
surface protein Xf1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <SIM>
A:Cross-references: GB:AE004017; GB:AE003849; MID:g9107083; PIDN:AAF84783.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
A:Genetics:
A:Gene: XF1981

Query Match 12.6%; Score 382.5; DB 2; Length 1190;
Best Local Similarity 24.6%; Pred. No. 8.7e-12;
Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;
Qy 47 VQANATDDLLLEPVORTAVVLSFRSDKECTGEGEDSNWAVYDEKRVLKAGAITL 106
Db 572 VAAGTADTDAVNSQLQ-----AVSTASKGNLLASGANSN-----VPGESVDL 618
Qy 107 KAGO-NLKIKONTNENTNDSFTY--SLKRD--LTDLTSVETKLSFGAN-----155
Db 619 KNSDGNLLTKTT-----DSNDVTFNLATALKVDSLTGTNTMTDGVTVGSNVLTGST 672
Qy 156 -----GNK--VNI-----TSDTKGLNFA-----171
Db 673 GLVITDGPSTSSGISAGNOKITVAAAGTADTDAVNFSQLQAVSSTASKGNLLASGANS 732
Qy 172 -----KETAGT-----NGDPTVHLNGIGS-----TLTDTLLNTGATT---NV 205
Db 733 SNVAPGESVDLKDGNITVSKESGNDVLFNLSSSLKLDKLTVDGTVMTTNGVTVGSGV 792

RESULT 7
A86036
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; MID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UMGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5029

Query Match 12.1%; Score 368; DB 2; Length 1588;
Best Local Similarity 24.9%; Pred. No. 6.8e-11;
Matches 171; Conservative 79; Mismatches 221; Indels 216; Gaps 28;
Qy 11 SALNAW-VVYSELTRNHTKRASATVATVATLTLFATVQANATDDLLLEPVORT---A 66
Db 1019 SOLNATNMIMEQNTQIINQLAGNTDATYIOEN--GAGINVYRTNDDGLAFNDASAOQVGA 1076
Qy 67 VLSFRSDKECTGEGEDSNWAV---YFD-----EKRVLKAG-----AIT- 105
Db 1077 TAIGYNSVAKG-----DSSVAIGOGSVDVDTGIALGSSSVSSRVIAKGRDTSITE 1128
Qy 106 -----LKAGDNLKIKONTNENTNDSFTYSLKLDL-----139
Db 1129 NGVVIGYDTTDELLGALSIGDGGKYRIINNVADGSEAHDAVTVRQLONAIGAVATTPTK 1188
Qy 140 -----TDLTSVETEKLSFGA-----NGNK-----VNITSDTKGLNFAKETAGTNGDPT 182

RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001)
C;Accession: AH0110
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Pridmore
delo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.;
den, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB00001; MUID:21470413; PMID:11586360
A;Accession: AH0110
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-658 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:gl5978974; GSPDB:GN000
C;Genetics:
A;Gene: YPO0902

[illegible]

C:Genetics:
A:Gene: Z1211; Z1651

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Query Match          7.3%; Score 222; DB 2; Length 1005;
Best Local Similarity 22.7%; Pred. No. 0.00089;
Matches 152; Conservative 89; Mismatches 263; Indels 166; Gaps 32;

QY 1 MNKIYRIIWNLSALNNAVYSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60
DB 61 LNTSYRLVWNHITGLVASELARSCKRAGAVALSAAV-----TSPALAAD----- 110
QY 61 PVORTAVILSFRSDKGTGKEGTEDSNNAVYDEKRVLKAGAITLKAGDNLIKONTNE 120
DB 111 -----KVQAGETVNDGT-----LTNHDNQIVFG-----TANGMTISTG--LELGPDS 153
QY 121 NTN-----EN-----TNDSSFTYSLKKDLTDLTSVETEKLSFGA-----NGKNVNTSDTKGLN 169
DB 154 NTGQWQIONGGIAGNTVTVTNGRVVLEGGTASDTVIRGGGOSLGLAVNTTLNRRGEQ 213
QY 170 FAK-----TACT-----NGDPTVHLNGIGSTLTDLTLLNTGATNTVNDVTDDEKKRAASVK 222
DB 214 WHEGGVATGIINRDGYQSVKSGLA---TGTIINTGABGGPDSNSYTGQK----- 263
QY 223 DVLNAGWNKGVKPGTASDNVDVRYT-----DTVEFLSADTK-----TTTVNVESKD 271
DB 264 -----VQGTAEATTINKGRQIILFSLGLARDTLIYAGGQSVHGRALNTTLN----- 310
QY 272 NGKKEVKIG-AKTSVKEKDKLVTKCKDENGSSSTDEGEGLVTAKEVIDAYNK-AGWR 329
DB 311 GGYQYVHRDGLALNTVINEGGVQVVRAGGAAGNTTINQNGELRVHAGGEATAVTQNTGGA 370
QY 330 MKTTTA-----NGOTQADKFETVTSKTKVTFASGNGTATVSKDDQGNITVK 377
DB 371 LVTSTATVIGTRNLGNFTVENGKADCV-VLESGRDLVLESHAQNTL-VDDGGLAVS 428
QY 378 YDYNVDGALNVQ/LQNSGNWLDKAVAGSKVYISGNVSPSKGMDTETVNNAGNIEIT 437
DB 429 AG---GKATSVT-ITSG-----ALTDGATVEGTNAGSKFSDIDTSGQASGLLIE-- 476
QY 438 RGNKNDIATSWTPQPSVSLGAGADPTLSVDDEGALNV-----GSKDANKPVRIITN 490
DB 477 -NG-----GSFTVNAGGQAGNTTVGHRGTLTLAAGGSLGRTQLSKGASMWL 522
QY 491 VAPVKEGQDVNTVAOLKGAQNLNNDVNGNARAGIAQAIATAG-----LAQAYLP 543
DB 523 NGDVSTGDIVNAGEI-----REFD-QTTPNALSRAVAKSNSPVTFHKLTTNLT 572
QY 544 GK-----SMAIGGGTYRGEAGYA---IGYSS---ISDTGNWVWIKGTASG 582
DB 573 GQGGTINMVRVLDGNSASDQLVINGGQATGKTWLAFTNVGNSNLGVATTGGIRVVDAQN 632
QY 583 NSRGHFCASA 592
DB 633 GATTEGAGA 642
```

RESULT 14
AF0394
Probable adhesin hmwa [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0394
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Parraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>

A:Cross-References: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN0175
C:Genetics:
A:Gene: hmwa

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Query Match          7.3%; Score 221.5; DB 2; Length 1910;
Best Local Similarity 22.2%; Pred. No. 0.0022;
Matches 160; Conservative 85; Mismatches 259; Indels 217; Gaps 34;

QY 14 NAMVYSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLEPVO-----R 64
DB 898 NATITANNISMN---GNITANDAVLNTFTLAKGDIKT---LTSPTKGLWFRNGGM 950
QY 65 TA---VVLSPRSDEKGTGKEGTEDSNNAVYDEKRVLKAGA-ITLKAGDNLIKONTN- 119
DB 951 TAANNILLVANSTSSGETVKINASSN-----KMNITAGKDISIITAG-NSKTATGPNI 1002
QY 120 --ENTVENINDSFTYSLKKDLTDLTSVETEKLSFGAGKNKVNITSDTKGLNFAKETAGT 177
DB 1003 NIENVLETNNGNFT-----TNGIITSWLGVNVVSANG---VDITSNSTG-----TGGI 1048
QY 178 NGDPTVHLNGIGSTLTDLTLLNTGATNTVNDVTDDEKKRAASVKOV-----LAAGWNKIG 233
DB 1049 VLDNTNLTIVGD-----INT-IVTNSSCKGIWIKSNSTLNSNKDITLVGSAGQN-EG 1100
QY 234 V--KPGTASDNVDVRYTVEFLSADTKTIVNVESKDKNGKKTEVKIG--AKTSVIKE 289
DB 1101 VTIQSSDASRN-----NISAQGNITLIGKMGSGQHSNLINLGNVSLTS----- 1145
QY 290 KDKLVTGKDKDENGSSSTDEGEGLVTAKEV-----IDAVNKAGWR 329
DB 1146 -----SGRNIDINGSAGTGDVYFTNVELNATAGNVSIYAETKTALSTSLNVLISLGN 1199
QY 330 MKTTTANG-OTGOADKFETVTSKTKVTFASGNGTATVSKDDQGNITVK----- 377
DB 1200 NSIKAQNGWLIGA--PNT-----TOGAGIGFRANSSLSVDGNIILKGETEGVATRK 1250
QY 378 ----YDYNVDGALNVQ/LQNSGNWLDKAVAG----- 405
DB 1251 GIDFYGANTLIIKGSQSLGKAGQDAGGNGISYTSIAKLTVNNNGSLKMEGRSTS 1310
QY 406 -----SSGKVISGNVSPSKGMD----- 423
DB 1311 GTGIFPSSNNTLVFNGDGTLLKSSVAGTGAISGVNNSTGPMTEIGISTDGAQVHL 1370
QY 424 -----ETVINAGN---NIEITRNKNIDIA-TSMTPOFSSVSLGA--GADAPTISV 469
DB 1371 FSAEHRIDRINVTGSSTHAELRISGNAAIVDTTLTKCSINGSGVKIDSLPGSSVVTSTV 1430
QY 470 DDEGALNVGSKDANKPVRIITNAPVKEGDVNTVAOLKGAQNLNNDVNGNARAG-- 527
DB 1431 LDNATLN-GSSSSGKGVETSDINGIHSSINGTTTGTGYCIDIGEN-SNVTGTSEADLL 1488
QY 528 IAAIATAGLAQAY-LPKSKMAIGGTYRGEAGYAIGYSS-ISDTGNWVWIKGTASGNSR 585
DB 1489 ILOGVATGTGTGTLKLNNDLSNTLSNASSAVDGIADITGPLANQGNVILGTASGSI 1548
QY 586 G 586
DB 1549 G 1549
```

RESULT 15
H83135
Probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: H83135
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337
A:Accession: H83135
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1018 <STO>
A:Cross-references: GB:AE004824; GB:AE004091; NID:g9950277; PIDN:AAG07469.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4082

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Query Match          7.3%; Score 221; DB 2; Length 1018;
Best Local Similarity 22.1%; Pred. No. 0.001;
Matches 150; Conservative 89; Mismatches 209; Indels 230; Gaps 32;

QY 1 MNKIYRIIWSALNANVVYSELTRNHTKRASATVATVATLTLFAIVQANATDDDDLLYLE 60
Db 1 MNKCYALVWNVVSGQWNVVSEGRRRGKPAKAAATASVLALJGATALAPA-----YAL 54
QY 61 PVORTAVLVSFRSDKEGTEGKEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 55 PSGGTVV-----GGSAN-----GEIHLGGNSLSVNOKYDK 85
QY 121 NTNENTNDSFTYSLKK----DLTDITSVETEKLSFCANGKNYNIITSDTKGLNFAKETAG 176
Db 86 LI---ANWDSFVAACGERVIFNPSSSIALNRV-IGTRASDIQGRIDANGQVF----- 135
QY 177 TNGDPTVHLNGIGSTLTDILLNTGATNV-----TNDNVTDDE-----KKRAASVKD 223
Db 136 -----LVNPNV-----LFGRGAQVNVGGLVASTLDTDAEFNGNSSRYRFTGPSTNG 183
QY 224 VLNAGWNIGVKPKPTTA-----SDN-----VDFVRTYDVFELSDTKT 262
Db 184 VLNHGGAITAAEGGSIALIGAQVDNRGTVLAQMGVGLGAGSDLTNFDGNKLLDIRVDA 243
QY 263 TTVNVESKONG----KKEVYKIGAKTS-----VKEKDKGLVTGKGKD 301
Db 244 GVANALASNGGLLKADGGRYLMAARTANALLNTVNSQGAIEARSLRGKNGRIVLDGGPD 303
QY 302 ENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITANGQT-----CQADKFEVTVSGTKVTF 357
Db 304 -----GKVMVGGALSANALNGP-----HGGTVEVRGQAVE---VALGTQVNTL 344
QY 358 SGNQTTAT--VSKDDQGNITVKYDVN---VGDALNVNQLQNSGMNLDKAVAGSSGKVIS 412
Db 345 ASNGLNGTWKIAD-----KIDVRPSAVSDGVTVHA-----DTLSRNLASTNIELVS 391
QY 413 GNVYPSKG--KMDETVINAGNNI-----EITRNGKNIDIAATMTPTQFSSVSLGAGADA 464
Db 392 -----TKGDLDLDSVNWASGNRLGLGSAADLTNGR-----LNASGAK 430
QY 465 PTLVDDEGALNVGSK-----DANKPVRI-----TNVAPGVKEGD 499
Db 431 AGLELKAEGAIDINDRIVLGGAGSALAMDAGEGHRVNGTASVSLAGANATYVSGYYTYV 490
QY 500 VTNVAOLKGVQAOLNRRIDNVGNRAGIAQATATAGLAQAYLPKGSMAIGG--GTYRG 557
Db 491 VQNLAQQLAKNKLDG--LYVLGNILGGSYYCTA-----LQSIGGPAGVFSG 536
QY 558 E---AGYAIGYSSISDTG 572
Db 537 TLDGLGNSIGLSISNTG 554
```

Search completed: July 3, 2002, 08:38:17
Job time: 288 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:14 ; Search time 29.79 Seconds
(without alignments)
777.250 Million cell updates/sec

Title: US-09-771-382-7
Perfect score: 3044
Sequence: 1 MNKIYRIIWSALNANVVS.....TASGNSRGHFGASASGVQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description
1	236	7.8	P39180 escherichia
2	220	7.2	Q03155 escherichia
3	213.5	7.0	P32051 escherichia
4	210	6.9	P15320 serratia ma
5	197	6.5	P15921 rickettsia
6	190	6.2	P16466 proteus mir
7	188	6.2	Q53047 r outer mem
8	187	6.1	Q9kka3 r outer mem
9	184.5	6.1	Q52657 rickettsia
10	183.5	6.0	P14914 rickettsia
11	183	6.0	P18127 ranthomonas
12	182.5	6.0	P33666 escherichia
13	182.5	6.0	Q07833 bacillus su
14	181.5	6.0	P34487 caenorhabdi
15	180	5.9	P52143 escherichia
16	180	5.9	P25927 salmonella
17	178.5	5.9	O06653 r outer mem
18	175	5.7	P06989 r outer mem
19	174.5	5.7	P35827 campylobact
20	171	5.6	Q08860 shigella fl
21	169.5	5.6	P38536 t amylopull
22	168	5.5	P37710 enterococcu
23	168	5.5	Q53020 r outer mem
24	167	5.5	P35825 bacillus st
25	166	5.5	Q48253 helicobacte
26	165.5	5.4	P45355 haemophilus
27	165	5.4	P35828 caulobacter
28	164.5	5.4	Q09624 caenorhabdi
29	163.5	5.4	P45354 haemophilus
30	163	5.4	P06176 salmonella
31	163	5.4	Q9PJY2 chlamydia m
32	162	5.3	FLIC_SALNA
33	162	5.3	Q06982 salmonella

34	162	5.3	1007	1	Y741_CHLMU
35	161	5.3	497	1	FLIC_ECOLI
36	161	5.3	504	1	FLIC_SALSE
37	161	5.3	1394	1	HAP_HAEIN
38	160	5.3	504	1	FLIC_SALDU
39	160	5.3	825	1	GUN3_BACS4
40	160	5.3	1702	1	IGA2_HAEIN
41	160	5.3	1770	1	PMPC_CHLTR
42	159.5	5.2	948	1	HP11_DEIRA
43	159.5	5.2	1200	1	ICEN_PSESV
44	159	5.2	1250	1	YFAL_ECOLI
45	159	5.2	1637	1	MRSP_STAAU

ALIGNMENTS

RESULT 1
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P39180; P76360; P75614; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nasimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubdaram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-Kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded


```
CC -----
DR EMBL: X65022; CAA46156.1; .
DR PIR: S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP ? 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match          7.2%; Score 220; DB 1; Length 1286;
Best Local Similarity 17.4%; Pred. No. 0.00091;
Matches 160; Conservative 106; Mismatches 290; Indels 362; Gaps 33;

QY 1 MNKIYRIWNSALNAWVYSELTRNH-----TKRASATVATA--VLATLLFATVOANA 51
DB 1 MNKAYSILNHSRQAWIVASELARGHGFVLAKNTLLVAVSTIGNAFVAINSGTVSSGG 60
QY 52 TDDDLYLEPVRTAVVLSFRSDKEGTGEKETE-----
DB 61 TVSSG-----ETQIVSYSGRCNSATVNSGGTQIVNNGGKTTATTVNSSGSONVGTSCA 113
QY 86 -----DSNNAVYFDEKVLKAGAIT--- 105
DB 114 TISTIVSGGIQIORSVGGVYASATNLSSGAQNTYINLGHASNTVIFSGNQOTIFSGGITDST 173
QY 106 -LKAGDNLIKIKO-NTNENTNENTNDSSFTYSLKDL-TDLSVETEKLSFGANGKNVIT 162
DB 174 NISSGQQRVSGGVASNTINSSGAQNLSEGAISTHISGGNQYISAGANATETIVN 233
QY 163 SDTKGLINFAKETAGTNGDPTVHLNG-----IGSLTDLTLN 198
DB 234 SG-----GFORVNSGAVATGTVLSGGTQNVSSGSAISTSVYNSGVQTVFAGATVDTTVN 289
QY 199 TGATNTVNDVTDDEKKRAASVKQVLNAG-----WNKIG----- 233
DB 290 SGGNQNISSGGIVSETTVNSVSGTQNIYSGGSALSANSQIIVNSRGTAINTLVSDGGYQ 349
QY 234 -VKPGTASDNDFVRTYDTVEFLSADTKTVTVNYESKDKGKTEVKIGAKTSVLIKE--K 290
DB 350 HIRNGIASGTIVNSGY-----VNISGGYAESTIINSGTLRVLSGDGYA 395
QY 291 DGKLVTKGKD--ENGSG-----STDEGEGLVTAKEVIDAVNKAG----- 327
DB 396 RGTILNNSGRENVSNGVSYNAINTGGNQYIYSDGEATAIVNTSGFORINSGGTAPVQ 455
QY 328 -----WRMKTITANGQ-----TG 340
DB 456 NSVVVTRTVSSAAKPFDAEYVSGGKQTVYLWRGIWYNFLTAVMSFPGTASGANVLSG 515
QY 341 QADKFTVTSQT-----KVTASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQ-- 392
DB 516 RUNAFAGNVVGTILNOBGRQYVYSGATATSTVGNNEGREGYVLSGGITDGTVLNSGGLQAV 575
QY 393 NSGWNLDKAVAGSSGKVT--SGNYSPSKGMDETWINAGN---NIEITRNGKNIDIAIT 447
DB 576 SSGKRASATVINEGGAQFYVDGGQVGTGNIKNGGIRVDSGSALNIALS--SGGNLFTST 634
QY 448 SMT-POFSSV-----SIGAGAD-----APTLSDVDEGALN- 476
DB 635 GATLPELTMAALSQNSHASNIVLENGGLLRVTSGGTATDTVNSAGRLRIDGGGTING 694
QY 477 -----VCSKDANKPVRTNAP----- 493
DB 695 TTTINADGIVAGTNTQNDGNFILNLAENYDFETELSGGVLVKDNTGIMTYAGTLTQAQG 754
QY 494 -GVKEG-----DVTNVAQLKGAQN-----LNNRIDNVGDGNARA 526
DB 755 VNVKNGGIIFDSAVNVADNAVQNVAYINISDOATINGSVNNNGSIVINNISI--INGNITN 812
QY 527 GIAQAIATAGLAQAYLPKGRSM-----MAIGGGT-----YRGEAGYAIYSSSI--- 568
DB 813 DADLSFGTAKLLSATVNGSLVNNKNILNPTKESAGNTLTVSNYTCGTPGSVLSLGGVLESG 872
```

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QY 569 --SDTGNVWIKGTASGNS 584
DB 873 DNSLTDRLVVKGNTSQGS 890

RESULT 3
YDEK_ECOLI STANDARD; PRT: 1325 AA.
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (OREF).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RC SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sabei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RC SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoj P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000248; AAC74583.1; .
DR EMBL: D90793; BAA15190.1; ALT_INIT.
DR EMBL: D90794; BAA15197.1; ALT_INIT.
DR EMBL: X73295; CAA51730.1; ALT_FRAME.
DR PIR: S34315; S34315.
DR EcoGene: EG11780; ydek.
DR PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
```

KW Hypothetical protein; Membrane; Lipoprotein; Signal;
KW Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHELICAL LIPOPROTEIN YDEK.
FT LIPID 19 13 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 N -> K (IN REF. 3).
FT CONFLICT 1317 M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 7.08; Score 213.5; DB 1; Length 1325;
Best Local Similarity 22.1%; Pred. No. 0.002;
Matches 147; Conservative 72; Mismatches 271; Indels 159; Gaps 28;

QY 1 MNRIYIWSALNAWVYVSELTRNHTKRASATVATATLFLFATVQANATDDDDLYLE 60
DB 1 MNRIYIWNCTLOVFOACSELFRACKTSTVNLRKSSGLTTFEURL 47
QY 61 PVQRTAVVLSFRSDKECTG---EKEGTEDSNWAVYFDEKRV--LKAGAITLKAGDNLKIK 115
DB 48 ---TLGVLLALSGSASCASLEVDNDQITNIDTDVAYDAYLVGWYGTGVNLILAGGNASLT 104
QY 116 QNT-----NENTNENTNDSFYSLKDLTDLTSVTEKLSFGANGKNYNI--TSDTKGL 168
DB 105 TITTSVIGANEDSGTYNVVLGGTWRL-----YDSGNARPLNVGQSGTGL 150
QY 169 N-----FAKETAGTNGDPTVHLNGIGSTLTDLTNTGATTNTVNDVTDDEKRA 218
DB 151 NIKQKHVDGGYLRGSGTGVTVNVEGEDSVLTTFELFG--SYGTGSLNITD----- 203
QY 219 ASVKDVLNAGNIIKGVKPGTASDNDVFRYDTVEFLSADTKTTTVNVESKONGKTEV 278
DB 204 -----KG-----YVTSIVA-----ILGYQAGSNGQVVVE 228
QY 279 KIGAKTSVIEKDGKLVTKGDKENGSTDEGEGLYTAKEVIDAVNKAGRMKTTTANGQ 338
DB 229 KGG---EWLKNNDSSIEFQIGNOGTGEATIREGLVTAENTIIGGNATG----IGTLNVQ 282
QY 339 TGOADKETVTSQTKVTFASNGGTATVSKDDQGNIVK--YD--VNVGDALN--VNOQLNS 394
DB 283 ----DQDSVITVRLYNGYFGNG---TVNISNGLINNKKEYSLVGVQDGHGVVNVTDKG 335
QY 395 GWNL-----DSKAVAGSGKVIISGNVSPSKMKMDETVNIAGN----- 432
DB 336 HWNPLRGGEAFRYIIGDAGDGLNVSSEKGVDSGIITAG---MKET---GTGNITVKDK 389
QY 433 NIETTRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNV-----GSKDANKPVR 487
DB 390 NSVITNLGTLNLDYDGHGEMNISNOGLVVSNGGSSLYGETGVGNVSITTGGMWEVKNVY 449
QY 488 ITNVAPGVKEGDVTNVLAQLKGVAQNLRNIDVNDGNARAGIAOIAIA---TAGLAQAAYLPG 544
DB 450 TTICVAGVGNLNTSDGG--KFVSONITFLDGKASGIGTGLNMDATSSFDVINGVNF--G 506
QY 545 KSMMAIGGGYRGEAGYAI-----GYSSISDTGNWIKGTASGNSR 585
DB 507 SGIVNVNNGATLNTSGYGFICGNAGSGIVNISDTSLSWNLK--TSSTNAQ 554

RESULT 4

HLVA_SERMA STANDARD; PRT; 1608 AA.
ID HLVA_SERMA
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
ON NCBI_TaxID=615;
RX [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia
marcescens.";
RL J. Bacteriol. 170:3177-3188(1988).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA
REQUIRES SHLB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
DR EMBL; M22618; AAA50323.1; -.
DR PIR; A28182; A28182.
KW Hemolysin; Toxin; Outer membrane; Signal.
FT SIGNAL 1 30 HEMOLYSIN.
FT CHAIN 31 1608
SQ SEQUENCE 1608 AA; 165078 MW; D869B476FE7DAD51 CRC64;

Query Match 6.9%; Score 210; DB 1; Length 1608;
Best Local Similarity 22.1%; Pred. No. 0.0036;
Matches 159; Conservative 89; Mismatches 275; Indels 196; Gaps 34;

QY 24 RNITKRASATVATVATLTL-----FATVQANATDDDDLYLE---PVQRTAVVLSFRSDK 75
DB 396 REQLQAGSVAAAGSAGKLISTOEDVKLLGANVSADRALSKAARDVHLAGLVEKDKSE 455
QY 76 EG--TGEKEGTEDSNWAVYFDEKRVLA-----GATLKAGDNLKIKONTNENTN 127
DB 456 RGYQRNITSSLTGRWS--NSDESELSKASELSEGLTLKAGRVNS--TGAKVHAQADLT 513
QY 128 ---DSSFTYSLKDLTDLTSVTEKLSFGANG---NRVNITSDTKGLNFAKETAGTNGDP 181
DB 514 IDADNQIOGVQK--TANAKAVRDDKTSWGGIGGDNKNN--SNRREISHASEL--TSGG-- 567
QY 182 TVHLNG--IGSTLTDTL--NTGATTNTVNDVTDDEKKRAASKVDVLA---GWNIKGV 234
DB 568 TRLNGQOGVTITGSKARGQKGEVTAHGLRID--NALSTTVDKIDARTGTAFNI--- 622
QY 235 KPGTTASDNDVFRYDTVEFLSADTKTTTVNVESKD--NGKKT---EVKIGAKTSVIKE 289
DB 623 ---TSSSHKADNSYQSSTASELSKSDTNLTIVSHKADADVIGSVASGSGELSVEKTNIV 679
QY 290 KDGKLVTKGCKDENGSTDEGEGLVT---AKEVIDAVNKAGWRM-----KTT----- 333
DB 680 KAA-----ERQNIDEQKALTIVNGYAKAGADQYRAGLRIEHTRDSEKTRTENS 730
QY 334 -----TANGOTQADKFETVTSKVTTFASNGTTA----- 364
DB 731 ASSLSGGSVKKAEDKDVTFSGKLVADKGDASVSGNKVSFLAADDKTFASNETQTKIGGGF 790
QY 365 -----TVSKDDQGNITVKYDVNVGVALNVQNLONS 394
DB 791 YVTGGIDKLGSGVEAGYENNKTAQSSKAITSGSDVKGNLT---INARDKLTQOQGAHS 846
QY 395 GWNLDKSAVAGSGKVIISGNVSPSKMKMDETVNIAGNNTIETRNKNIDATSMTPQS 454
DB 847 VGGAYQENAGVDHLAAADASTTKTKTDVGVNI-----GANVDYSATVRPVER 895
QY 455 SVSLGAGADAPTLSDVDEG-----ALNVGSKDANKPVRITN---VAPGVKEGDV----- 500


```
Db 896 AVGKAALDA-TGVINDIGGIGAPNVGLDIGAGGSSSEKSSSSQAVSSVQAGSIDINA 954
QY 501 -----TNAQLKGVANLN-----NRIDNVGNARAGIAQAATAGLAQAYL 542
Db 955 KGEVRDQGTQYQASK-AVNLTAHSRSEAAANRDEQSDRTGSGVRVYTTTGSDLTV 1013
QY 543 PKSMMAIGGGTYRGAGYAIGYSSISDTGNW-----VIKGTASGNSRSHFGASA 592
Db 1014 DAKG-----EGGTQRSSSSASQAVTGSIDAANGINNVKKDAIYQGTALNGRGRKTAVNA 1068

RESULT 5
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
RT repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP B FAMILY.
CC
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CC
CC -----
CC EMBL; M31227; AAA26380.1; -
CC PIR; A41477; A41477.
CC InterPro; IPR003858; rOmpA_rOmpB.
CC Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;
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Query Match 6.5%; Score 197; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. No. 0.023;
Matches 143; Conservative 71; Mismatches 261; Indels 166; Gaps 29;

QY 34 VATAVLATLLFATVOANATDDDDLYLEPQVORTAVVLISFRSDKEGTEKGEKSGTDSNNAVYF 93
Db 39 VATGVATNNNAFSSNNVGNNN--WNEITAAGV-----ANGTPAGGPONNNAFTY 86
QY 94 D-----EKRLKA-----GAI-----TLKAGDNLKIKQ 116
Db 87 GGDYTVTADAADRIKAIINVAGTTPVGLNITONTVVGSIITKGNLLPVLNAGKSLTNG 146
QY 117 NTNENTNENTSSFTYSLKDLTDLTSVETEKLSFGANG-----NKNVITS--DT 165
Db 147 NNAVAANHGFADAPDNY-----TGLGNIALG----GANAALIQAAPSKITLAGNIDG 196
QY 166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDLTLNTGATTNVTNDNV---TDDEKKRAASYK 222
Db 197 GGIIVTKTDAAINGT-----IGTNALATVNVGAGTATLGGAIVKATTKLTNAASVL 249
QY 223 DVLNAGWNKGVKPGT TASDNVDFVRTYDTVFELSDTKTT----TVNVESKD---NG-- 273
Db 250 TLTNANAVLTGAIDNTTGGDNVGLNLNGALSOVTDGIGNTSLATISVGAGTATLGGAV 309
QY 274 -RKTEVKIGAKTSVIKEKDKLVTG----KGDENGSTDEGEGLVTAK----EVIDAVN 324
Db 310 IKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGNTVTGNVGNNTALATVN 369
QY 325 KAGWRMKTITANGOTQOAKKFETVSGTKVTFASGNGTTATVSKDDQGNIT---VKYDVN 381
Db 370 VGAGLLQ---VQGGVVKANTINLTNDAASAVTFT--NPVVVTGAIDNTGNANNGIVTFTGN 424
QY 382 ---VGDALNVNOLNSGWNLDKAVAGSSGKVI SGNVSPSKGKMDVTNINA--GNNIEI 436
Db 425 STVTGIDGNTNALTATVNVGAGTATLGGAVIKATTKLTNAASVLTLT--NANAVLTGAIDN 483
QY 437 TRNGKNIDIAI-----SMTQPSVSSVLSGAGADAPTLSDVDEGALNVGSKDANK 484
Db 484 TTGSDNVGLNLNGALSOVTDGIGNTSLATISVGAG--TATLGGAVIKATTKLTDAAS 541
QY 485 PVRTINVAPEKGEDEVNVAQLKGVANLNLRIDNVGDNARA-----GIAQAIATAGLAQA 540
Db 542 AVKFTN--PVVVTGAIDNTG-----NANNGIVTFTGNTSTVTGDCIGNTSLAT----- 586
QY 541 YLPKGSMAITGGTYRGAGYAIGYSSISDTGNWIKGTAS 581
Db 587 -----ISVGAGT-----ATLGGAVIKATTK 606
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```
RESULT 6
HLVA_PROMI
ID HLVA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN hPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hPMA and hPMB) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
```

CC DEFINED.
CC -1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
CC REQUIRES HPMB FUNCTION.
CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC
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CC
CC EMBL; M30186; AAA25657.1; --
CC PIR; A35140; A35140.
CC Hemolysis; Toxin; Outer membrane; Signal.
CC SIGNAL 1 29
CC CHAIN 30 1577 HEMOLYSIN.
CC SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.2%; Score 190; DB 1; Length 1577;
Best Local Similarity 20.1%; Pred. No. 0.034;
Matches 142; Conservative 101; Mismatches 227; Indels 238; Gaps 35;
QY 23 TRNITKASATVATA-----VLAYLLFATVQANATDDDDLYLEPVQRTAVVLSF 71
DB 619 TNKQTSGLSELISDAQLTVSGNDVNVIGSLKSAKGLHGLSDGINVKSAAQVTKRIDDE 678
QY 72 RSDKEGTGEKEDSDNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNENTNENTDSSF 131
DB 679 KTSIAITGHAKVEDEKQYSAGF-----HITHTKNTKNTSTTEQANS 719
QY 132 TYS-----LKKDLT-----DL-----TSVETEKLKSGANGKVNITSDTKLNFAR 174
DB 720 TISGANVDLQANKDVTAGSLDKTTAGNATGDNVAFVSTENK-----KQT 766
QY 175 AGTNGDPTVH-----LNGIGS-----TLDTLLNTGATNTVND----- 208
DB 767 --DNTDTTISGGFSYTGVDKVGSKADFDYDKQHTQTEVTNKRGSQTEVAGDLTITANKD 824
QY 209 -----NVTDEKKRAASKVDVLNAGWNI-----KGV 234
DB 825 LLHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGNLDYSGVTPVKKAI 884
QY 235 KPG---TTASDNVDF---VRTYDVEFLSADTKTTTVNVESKDKNGKKTEVKIGAKTSVIK 288
DB 885 EDGVNTTKPGNNTDLTKKVTARDAIANLA-----NLSNLETTPNVGVEVIGKGG--SQQS 937
QY 289 EKDKGLVT---GKKG---DENGSTDEGEGLVTAKEVIDAVNKAQWKMKTITANGQTGQA 342
DB 938 QTDQAVSTISNAGKIDIDSNKLNKLDQGTHTYQSTQEGI-----SLTANTHTSEA 986
QY 343 --DRFEVTVSGTK----VTFASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGW 396
DB 987 TLDKHQHTFTHETKGGGIGVSTKGTSDITVAIKEGQTT-----DNALMETHKAKGSQF 1039
QY 397 --NLDSKAVAGSSGKVIISGNVSPSKMDTEVTNINAGNNIEITR-----NGK- 441
DB 1040 TSNAGDISINVENAHYEGAQFDAQKGR---TV-INAGGDLTLAQATDTHSESQSNVNGSA 1095
QY 442 NIDATSWTQFQSSVSLGACADPTL--SVDDGALNVGSKDANKPVKITVAPCVKCGDV 500
DB 1096 NLKVGTT--TPE--SKDYGGGFNAGTTHHSKEQTTAKVGTITGSQIELNAGHNLTLQ-- 1149
QY 501 TNVAOLKGVANLNLRID-----NVDGNARAGTQ-----ATATAGLAQAYL 542
DB 1150 THLSSEQDIALNATNKVDLQASASSEHTEKGNLSSGGVQAGFGKKMTDASSVNGL----- 1204

QY 543 PGKSMMAIG-----GGTYRGEAGYAIGYSSISDGTGNWIKGTA 580
DB 1205 -GSAQFAIGKQDEKSVSREGT-----INNSGNLTNGNS 1238
RESULT 7
OMPB_RICRI
ID OMPB_RICRI STANDARD; PRT; 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia
RT rickettsii is encoded by an unusually long open reading frame:
RT evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X16353; CAA34403.1; --
CC InterPro; IPR003858; rOmpA_rOmpB.
CC Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
FT SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.2%; Score 188; DB 1; Length 1654;
Best Local Similarity 21.9%; Pred. No. 0.045;
Matches 159; Conservative 85; Mismatches 285; Indels 198; Gaps 36;
QY 15 AWVVSELTNRHTKRA-----SATVATVATL-----LFATVQA-NATDDD 55
DB 181 ASTLVFNLNPTTQKAPLILGDNAVINGVNTLVNTGTFQVSNKSFATVKAINIADGQ 240
QY 56 DLYLEPVQRTAVVLSFSDKEGTEKEDSDNNAVYFDEKRVLKAGAITLKAGDNLK-- 113

Db 241 GIIFNTDANNANTLNAGGTT-TINFCTGDTGRLVLLSKHAAATNFNITSLGGNLKGV 299
QY 114 IKONT-----NENTNENTND-----SFTYSLKDKDLTDLTSVETEKLSFGANG 156
Db 300 IFENVAVDQGLTANAGANAVIGNNGRAGRAAGFVSVYD-----NG 341
QY 157 NKVNITSPTKGLNFAKETAGTAGTNGDPTV-HLNGIGSTLTDLTLLNTGATTVNTNDN--VTDD 213
Db 342 KVATIDGOVYAKDMVQSANATGQVNFRIHVDVGADGTTAFKTAASKVITITQDSNFGNFD 401
QY 214 EKKRAASVK--DVLNAGWNKIG--VKPGTASDNVDFVRYD---TVEFLSADTKTTTVN 266
Db 402 FGNLAQKIKVPNAITLTGNTGDSANPGNTAG-----VITFDANGTLESASADANAVYTN 456
QY 267 ---VESKDNG-----KKTETVKIGAKTSVIKEXDKLVTKG-----CKDENGSGT 307
Db 457 NITAIERSGAGVQVLSGTHAEELRLGNAGSIFKLDGTVINGKVNQVOTALVGGALAGTIT 516
QY 308 DECEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKTVTFASNGT-----362
Db 517 LOGSATITGD--IGNAGGAALQRITLAN-----DAKKTLLGGAIIIGAGGTIDLQA 568
QY 363 -----TATVSKDDGNTTVKYDV-----NVGDALNVNQLNSGWN-----LDSK 401
Db 569 NGGTIKLTST-----QNNIVVDLAIATDQTCVVVDASSLTNAQTILTINGKIGTIGANNK 623
QY 402 AVA-----GSSGKVIS-GNV-----SPSKGKMDTETVNLN 429
Db 624 TLGQFNIGSKTVLSNGVNAIVNELVIGNDGAVQFAHDTYLTITRTNNAAGOGKIIFNPVN 683
QY 430 AGNIEITRNKNIIDATSMTPQFSVSLGAGADAPTLSDVDEG-----ALNVGSKDANKP 485
Db 684 NGTTLAA---GTNIGSATNPLAEINFGSKGVNVD--VLNV-GEVNLXATNTITTDANVG 738
QY 486 VRI-----TNVAPGV---KEGDTVNVQALKG---VQNLNLRIDN-----VDGN 523
Db 739 SEFVNAGGTNIVSGTVGGQGNKFTVALENGTTVKFLGNATFNNGNTTAAANSTLQIGGN 798
QY 524 ARAGIAQAIATAGLAQAYLPKSKMAIGGTVRGEAGYAIYSSISDGTGNWIKGTASGN 583
Db 799 YTADCVASADGTGIVEFVNTGITVTL---NKQAPVNAKQITVSGPQNVVI--NEIGN 953
QY 584 SRGHFCA 590
Db 854 AGNHGCA 860
RESULT 8
ID OMPA_RICCN STANDARD; PRT: 2021 AA.
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
AC Q52670; Q52674;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (rOmpA) (rOmp A).
GN OMPA OR RCL273.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Malish 7;
RX MEDLINE=94171067; PubMed=8125327;
RA Croquet-Valdes P.A., Weiss K., Walker D.H.;
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia
RT conorii (Malish 7 strain).";
RL Gene 140:115-119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Malish 7;

RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
[3]
RP SEQUENCE OF 8-204 FROM N.A.
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;
RX MEDLINE=97015921; PubMed=8862558;
RA Roux V., Fournier P.E., Raoult D.;
RT "Differentiation of spotted fever group rickettsiae by sequencing and
RT analysis of restriction fragment length polymorphism of PCR-amplified
RT DNA of the gene encoding the protein rOmpA";
RL J. Clin. Microbiol. 34:2058-2065(1996).
[4]
RP SEQUENCE OF 953-2012 FROM N.A.
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;
RA Raoult D., Fournier P.E., Roux V.;
RT "Phylogenetic analysis of spotted fever group rickettsiae by study
RT of the outer surface protein rOmpA";
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC or send an email to license@sib-sib.ch).
CC
DR EMBL; U01028; AAA17405.1; -
DR EMBL; AE008674; AAL03811.1; -
DR EMBL; U43794; AAB49549.1; -
DR EMBL; U43798; AAB49550.1; -
DR EMBL; U43806; AAB49551.1; -
DR EMBL; U45244; AAB49556.1; -
DR EMBL; U46918; AAB49566.1; -
DR EMBL; U83440; AAC35179.1; -
DR EMBL; U83443; AAC35179.1; -
DR EMBL; U83448; AAC35184.1; -
DR EMBL; U83453; AAC35189.1; -
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
KW Complete proteome.
FT SIGNAL 1 38
FT CHAIN 39 2021
FT DOMAIN 238 946
FT DOMAIN 1424 1528
FT VARIANT 60 60
FT VARIANT 76 76
FT VARIANT 86 137
FT VARIANT 126 133
FT VARIANT 953 954
FT VARIANT 1245 1245
FT VARIANT 1308 1308
FT VARIANT 1877 1877
FT CONFLICT 10 10
FT CONFLICT 92 92
FT CONFLICT 126 126
FT CONFLICT 137 137
FT CONFLICT 157 157
FT CONFLICT 369 369
FT CONFLICT 374 388
FT CONFLICT 640 640
FT CONFLICT 1
FT N -> D (IN REF. 1).
FT N -> H (IN STRAIN MOROCCAN).
FT M -> I (IN STRAIN INDIAN TICK TYPHUS).
FT Q -> K (IN REF. 1).
FT I -> V (IN REF. 1).
FT V -> I (IN REF. 1).
FT T -> N (IN REF. 1).
FT G -> D (IN REF. 1).
FT IS -> VN (IN REF. 1).
FT KATLGAAIKATTK -> LLOVQGVVVKANTIN (IN
FT REF. 1).
FT N -> D (IN REF. 1).

```
FT CONFLICT 669 669 V -> I (IN REF. 1).
FT CONFLICT 793 793 N -> D (IN REF. 1).
FT CONFLICT 803 804 VN -> IS (IN REF. 1).
FT CONFLICT 809 823 LLRVGGVKSNTIN -> KATLGGAIIKATTK (IN REF. 1).
FT CONFLICT 898 898 D -> Y (IN REF. 1).
FT CONFLICT 908 908 P -> N (IN REF. 1).
FT CONFLICT 985 985 N -> K (IN REF. 1).
FT CONFLICT 1009 1009 L -> S (IN REF. 1).
FT CONFLICT 1013 1013 Y -> S (IN REF. 1).
FT CONFLICT 1182 1182 K -> Q (IN REF. 1).
FT CONFLICT 1314 1314 N -> Y (IN REF. 4).
FT CONFLICT 1451 1451 H -> N (IN REF. 1).
FT CONFLICT 1624 1624 G -> D (IN REF. 1).
FT CONFLICT 1628 1628 E -> G (IN REF. 1).
FT CONFLICT 1872 1872 A -> V (IN REF. 1).
FT CONFLICT 1875 1875 T -> P (IN REF. 1).
FT CONFLICT 1878 1879 MS -> LP (IN REF. 1).
FT CONFLICT 1936 1936 E -> A (IN REF. 1).
FT CONFLICT 1965 1970 MTAFLP -> ITPLS (IN REF. 1).
FT CONFLICT 1997 1997 G -> R (IN REF. 1).
SQ SEQUENCE 2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;

Query Match 6.1%; Score 187; DB 1; Length 2021;
Best Local Similarity 21.6%; Pred. No. 0.064;
Matches 176; Conservative 86; Mismatches 287; Indels 264; Gaps 40;

QY 10 NSALNANVVVSELTRN-HTKRASATVAT-AVLATLLFATVQANATDDDD-----LYLEPV 62
DB 415 NNGIVFTGDSVTGNTGNATLISVGAGKATLGGAIIKATTKLTNDASAVTFNPV 474
QY 63 QRTAV-----VLSFRSDKGEKTEKEDSSNAVVFDEKRVLKAGAI-----TLKA 108
DB 475 VVTAIDNTGNANNGIVFTGDSVTG-NIGNTNALATISVGAGKATLGGAIIKATTKL 533
QY 109 GDNLIKIKONTN-----ENT-NEN-----TNDSSFTYSL-KKDLTDLTSVETKLSF 152
DB 534 TDNASAVTFNPVVVTAIDNTGNANNGIVFTGDSVTGNTGNATLISVGAGKATL 593
QY 153 GA-----NGKNVITSDTKGLNFAKETAGTN-----GDPVHLNGIGSTLT 193
DB 594 GGAIKATTKLTNDASAVTFNPVVVTAIDNTGNANNGIVFTGDSVTGNTGN-IGNTNA 652
QY 194 DTLLNTGA-----TTVVNDNVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
DB 653 LATVNVGAGIATLEGAVIKATTKLTN-----AASVLTITNVNAVLTGAIDNTG 702
QY 241 SDNVDFVRYTDVFEFLSADTKTT-----TVNV---ESKDNG---KKTEVKIGAKTSVIEK 290
DB 703 VDNVGVNLNCGALSQVTGNTGNATLISVGAGKATLGGAIIKATTKLTNDASAVTF 762
QY 291 DGKLVG-----KGDENGSSTDEGEGLVTAK-----EVIDAVNKA-----GWRMKTTTA 335
DB 763 NPVVVTAIDNTGNANNGIATFTGDSVTGNTGNATLISVGAGLLRVGGVYKNTI 822
QY 336 N-----GOTGOADK-FETVTSKTKVFASGN-GTTATVS-----367
DB 823 NLTDNASAVTFNPVVVTAIDNTGNANNGIVFTGDSVTGNTGNATLISVGAGKA 882
QY 368 -----KDOGNITKYDYNVGDALNVNQLONGSNWLDKAVAGSGKVI 413
DB 883 TLGGAIKATTKLTNDASAVTFNPVVVTAID-----NTG-NANNGIVFTGDSVTG 936
QY 414 NVSPSKMDETNYINAGNIEI---TRNGKNIDATSWTQFSSVSLGAGADAP-----T 466
DB 937 NIGNTNAL--ATVNVGAGVTLQAGSLDANNIDFGARSTLEFNGPLDGGGNAIYPFKGA 994
QY 467 LSVDEGALNVGSK-----DANK-PVRIITN-----490
DB 995 IANGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVITLNAQDTHFRALD 1054
QY 491 -----VAPGVKEGDV-----TNVAQLKGVAQNLR 516
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DB 1055 SALVLSNLTVGVNINILLAADLVAPGVDEGTGVFVGGVNGNLNIGSNVA---GAARN-----1107
QY 517 IDNVGDNA-----RAGIAQAIATAGLAQAYLPKG---SMMAIGGTYVR-GEAGYAI 563
DB 1108 IGVGGNKNFLLLYNAVITDDVNLGIONVLLNNADFTSSTAFNAGTIQINDATYTI 1167
QY 564 -----GYSSISDGTGNWIKGTASGNSR 585
DB 1168 DANNGLNIPAGNIKFAHADQAQLILQNSSGND 1200

RESULT 9
OMP_RICCN
ID OMPB_RICCN STANDARD; PRT; 1655 AA.
AC Q9KKA3; Q9KK98; Q9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Orata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
[2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the gene coding the outer-membrane protein rOmpB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
[3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY SIMILARITY).
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A 5-LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DB EMBL; AE008659; AL03623.1; -
DB EMBL; AF123721; AAF34124.1; -
DB EMBL; AF123726; AAF34129.1; -
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DR EMBL: AFL149110; AAD39533.1; --
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.

KW Antigen; S-layer; Cell wall; Complete proteome.

FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.

FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.

FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 353 354 KD -> GH (IN REF. 3).
FT CONFLICT 776 776 F -> S (IN REF. 3).
FT CONFLICT 1159 1159 E -> D (IN REF. 3).
FT CONFLICT 1177 1177 G -> S (IN REF. 3).
FT CONFLICT 1492 1492 H -> R (IN REF. 3).
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 6.1%; Score 184.5; DB 1; Length 1655;
Best Local Similarity 22.1%; Pred. No. 0.067;
Matches 147; Conservative 76; Mismatches 292; Indels 149; Gaps 30;

QY 10 NSALNAVVVSELTNRHTKRASATATAVLATLLEFATVOANATDDDDLLLEPVQRTAVVL 69
DB 211 NGTLN-----VTFGKVSRSFATVNVIGDGGIMFNTDADNVNTLNQANGATI 263
QY 70 SFRSDKEGTGEKEDSDSNWVDFDKRLKAGAILKAGDNLK-----IKQ 116
DB 264 TF-----NGTDGRLVLLSNAATDENVTGSLGGNLKGLIEFTVAVNQLKA 313
QY 117 NTNEN-----TNTNTNDSS-FYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNF 170
DB 314 NAGANAAVICTNNGAGRAAGFVVSVD-----NGKVATIDQGVYAKDM 355
QY 171 AKETACTNGDPT---VHLNGTGSTLDTLLNTGATNTVNDVNDTDEKKRAASVKD--- 223
DB 356 VTQSANAVGOVFRHIVDGTGDTTAFKAASKVAITQNSFGTTDFGNLAAQIIVPNTM 415
QY 224 VLNAGNIRKGVPGTTASDNVDFRTYD---TVEFLSADTKTTTVN---VESKDMG--- 273
DB 416 TLNGNFTGDSNPGNTAG-----VTFDANGTLASASADANVAVTNNITAEASGAGVVQ 470
QY 274 ----KTEVKIGAKTSVIREKDGKLVTKG-----GKDENGSSDTDEGLVTAKEVID 321
DB 471 LSGTHAAELRLGNAGSVFKLADGTGVINGKVNQALYVGGALAAAGTITLDGSATITG---D 526
QY 322 AVNKAQRMKTTTANGOTQADKFEVTV-----SGTKVTFASGNGTTATVSKDDQG 372
DB 527 IGNAGG-----AALQGITLANDATKTLTGGANIIGANGGTINFGANGTIKLTS--TON 580
QY 373 NITVKYDV-----NVGDALNVQLNSQWNLDSKAVAGSGKVIISGNVSPSKGMK-DE 424
DB 581 NIVVDFDLAIAITDQGVVDASSLTNAQTITINGKITGVANKNTLQFNIGSKTVLSDG 640
QY 425 TVNIN---AGNN---IEITRNGKNIDIATSMTPQ-----FSSV-----SLGAGADAPTLSDV 470
DB 641 DVAINELVINGNAGVQFAHNTYLTITRNAAGOGKIIFNPVNNNTTLATGTNLGS-ATN 699
QY 471 DECALNVGSKDANKPVRIINVPAGVKEGDTVNVQAQLKVAQNLNLRIDNVDC-NARAGTIA 529
DB 700 PLAEINFGSKGANVDTVLNVGKGNL-YATNITTTDA-----NVGSPFIIFNAGGTNIYSG-- 753
QY 530 QALATAGLAQ-----AYLPKGSMAAIGGGTVRGEAGVAGYSSISDGTGNVVKTAGS 582
DB 754 ----TVGGQGGKFNFTVLDNGTTVFLGNATFNNGNTTAAAN-STLIQGNVYADPFVSA 808
QY 583 NSRG 586
DB 809 DGTG 812

RESULT 10

120K_RICRI STANDARD; PRT; 1300 AA.

AC P14914;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DE 01-MAR-2002 (Rel. 41, Last annotation update)

DE 120 kDa surface-exposed protein.

GN P120.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiella; Rickettsia.

OX NCBI_TaxID=783;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=R;

RX MEDLINE=90136087; PubMed=2515418;

RA Gilmore R.D. Jr., Joste N., McDonald G.A.;

RT "Cloning, expression and sequence analysis of the gene encoding the

RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";

RL Mol. Microbiol. 3:1579-1586(1989).

CC -!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS

CC -!- RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A

CC -!- S-LAYER WITH HEXAGONAL SYMMETRY.

CC -!- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES

CC -!- CONFERRING ANTIGENICITY TO THE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL: X16353; CAA34402.1; --

DR PIR; S07575; S07575.

DR InterPro: IPR003858; rOmpA_rOmpB.

DR Pfam: PF02708; rOmpA_rOmpB; 1.

KW Antigen; Glycoprotein; Cell wall; S-layer.

FT CARBOHYD 7 7 N-LINKED (POTENTIAL).

FT CARBOHYD 66 66 N-LINKED (POTENTIAL).

FT CARBOHYD 86 86 N-LINKED (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (POTENTIAL).

FT CARBOHYD 147 147 N-LINKED (POTENTIAL).

FT CARBOHYD 268 268 N-LINKED (POTENTIAL).

FT CARBOHYD 330 330 N-LINKED (POTENTIAL).

FT CARBOHYD 375 375 N-LINKED (POTENTIAL).

FT CARBOHYD 415 415 N-LINKED (POTENTIAL).

FT CARBOHYD 424 424 N-LINKED (POTENTIAL).

FT CARBOHYD 430 430 N-LINKED (POTENTIAL).

FT CARBOHYD 436 436 N-LINKED (POTENTIAL).

FT CARBOHYD 444 444 N-LINKED (POTENTIAL).

FT CARBOHYD 515 515 N-LINKED (POTENTIAL).

FT CARBOHYD 547 547 N-LINKED (POTENTIAL).

FT CARBOHYD 593 593 N-LINKED (POTENTIAL).

FT CARBOHYD 655 655 N-LINKED (POTENTIAL).

FT CARBOHYD 698 698 N-LINKED (POTENTIAL).

FT CARBOHYD 710 710 N-LINKED (POTENTIAL).

FT CARBOHYD 799 799 N-LINKED (POTENTIAL).

FT CARBOHYD 800 800 N-LINKED (POTENTIAL).

FT CARBOHYD 826 826 N-LINKED (POTENTIAL).

FT CARBOHYD 844 844 N-LINKED (POTENTIAL).

FT CARBOHYD 861 861 N-LINKED (POTENTIAL).

FT CARBOHYD 879 879 N-LINKED (POTENTIAL).

FT CARBOHYD 920 920 N-LINKED (POTENTIAL).

FT CARBOHYD 926 926 N-LINKED (POTENTIAL).

FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).

FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).

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FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).
FT CARBOHYD 1146 N-LINKED (POTENTIAL).
FT CARBOHYD 1211 1211 N-LINKED (POTENTIAL).
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

Query Match 6.0%; Score 183.5; DB 1; Length 1300;
Best Local Similarity 21.8%; Pred. No. 0.056;
Matches 161; Conservative 93; Mismatches 273; Indels 213; Gaps 37;

QY 30 ASATVATAVLATLFAVQAN--ATDDDLVLEVPQVAVL--SPRSDKEGTEKEGTE 85
DB 22 ADGTAFTKTAASKVTITQDSNFGNDFCNLAQAQIKVPNAITLTCNFTGCDASNPGNTAG-- 79

QY 86 DSMNAVYFDEKRVLKAGAILKAGDNLIKONTN--ENTNENTNDSSFTYSLKXDLRLDT 143
DB 80 ----VITFDANGTLESAS----ADANVAVTNNTAIEASGAGVVQLSGTHAAELRLGNAG 131

QY 144 SVETEKLSFGA--NGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTLDLTLNAGA 201
DB 132 SI--FKLAGDTVING-KVNQTA-----LVGGALAAGTITLDG-SATITGDIGNAG 178

QY 202 TTNVTNDNVTDDEKRAASVKVDLNAAGNKGKPGT-----TASDN---VDF 246
DB 179 AALQRTILANDAK-----KTLPLGGANLIGAGGGTIDLOANGGTTKLTSTQNNIVVDF 232

QY 247 ---VRTYDT-----VEFLSADTKTTTVNVESKDNGK-----KT-----E 277
DB 233 DLATADOTGVVDASSLTNAQTLTKINGKIGTIGANNKTLQGFNIGSSKTVLSNGVAIN 292

QY 278 VKIGAKTSVTEKDKGLVT-----GKKG-----DENGSTSD----- 308
DB 293 LVIGNDGAVOFAHDTYLTITRTTNAAGOKIIFNPVNVNGTTLAAGTNLGSATNPLAEINF 352

QY 309 --EGEGLVTAKEVIDANKAGWRMKTITAN-----GQTG--QADKFTVT 349
DB 353 GSKGVNVDTVLNVGEGVNLATNITTTDANVGSFVNAGTNIVSGVGGQGNKFTVA 412

QY 350 --SGTKVTF---ASNGGTTATVSKDD---QGNITVKVDVNVGDALNVNLQNSG---WNL 398
DB 413 LENGTTVKFLGNATFNCTTAA NSTLIQIGNYTDAC-VASADGTGIVEFVNTGPIVTL 471

QY 399 DSKA-----VAGSSKVIS--CNVSPSKMDTETVNI----- 428
DB 472 NKQAPVNALKQITVSGPNVINEIGNAGNHGAVDTTIAFENSLSGAVVFLPRGIPFN 531

QY 429 MAGNIEIT-----RNGKNIDIATSMT-----POFSSVSLGAGAD--- 463
DB 532 DAGTMPLTKSTVGNKTAQGFVPSVVVLGVDSVIADGQVIGQNNIVGLGSDNGII 591

QY 464 --APTLSV-----DDEGALNVGSKDANKPVRIITNVPAGVKEGDTNVAQLKGVQNLNN 515
DB 592 VNATTLVAGISTLNNQGTVTLSGVPNTPTGVYGLGTGIGASKFKQVT---FTTDYNN 647

QY 516 RIDNVGDNARAGIAQATATAGLAQAYLPKGSMAIGGTVRGEAGYAGYSSISDTCNVV 575
DB 648 LGNIATNATINDGVTVTTGGIAGIGDFGK--ITLGSVNGNGNVRFADGILSNSTS---M 702

QY 576 IKGTFASGNSRGHFCASASVG 595
DB 703 IGTTKANNGVITYLGNAPVG 722

RESULT 11
ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
```

```
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X56S;
RX MEDLINE-91080859; PubMed-2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
RT Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -I- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC -I- CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -I- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -I- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; X52970; CAA37140.1; -.
CC PIR; S11672; S11672.
CC HSSP; P06620; IINA.
CC InterPro; IPR000258; Ice_nucleatn.
CC Pfam; PF00818; Ice_nucleation; 81.
CC PRINTS; PR00327; ICENUCLEATN.
CC PROSITE; PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; CBB451D959ECAD63 CRC64;

Query Match 6.0%; Score 183; DB 1; Length 1567;
Best Local Similarity 20.2%; Pred. No. 0.074;
Matches 115; Conservative 83; Mismatches 274; Indels 98; Gaps 19;

QY 77 GTGKEGTEDSNAVYFDEKRVLKAGAILKAGDNLIKONTN-----ENTNENTNDSSF 131
DB 735 GSTQTSKSDSSLTAGYGTQTARKGSDVTAGYGTGTAGADSTLIAGYGTQTSGSDSL 794

QY 132 TYSLLKDLT-----DLTSVETEKLSFGA-----NGKNVITSDTKGLNFAKE 173
DB 795 TAGYGTQTARKGSDITAGYGTGTAGADSTLIAGYGTQTSGSDSLTAGYGTQTARE 854

QY 174 -----TAGTNGDPTVHLNGIGSTLT---DTLLATGATTVTNDVTDDEKRAASV 221
DB 855 GSDVTAGYGTGTAGADSTLIAGYGTQTAGSDSLTAGYGTGTARKGSD----- 905

QY 222 KDVNLNAGWNKGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIG 281
DB 906 ---VTAGYGTG---TAGADSTLIAGYGTQTSGSDSLTAGYGTGTARKGSDMTAG 957

QY 282 AKTSVIREKDGKLVTKGKDENGSSDTEGEGVLTAKEVIDAVNKGAWRMKTTTANGQTG 341
DB 958 YGSTGTAGADSTLIAGYGTQTSGS-----DSSLTAGYGTGTAREGSDVT 1003

QY 342 ADKEPTVTSCTKVTFASSNGTATVSKDDQGNITVKYDVNVGDALNVNOLNSGNLDSK 401
DB 1004 AGYGTGTAGADSTLIAGYGTQTAGSD---SSLTAGY-----GSTQTARQGSDDVTAGYST 1057

QY 402 AVAGSSGKVISGNVSPSKMDTETVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAG 461
DB 1058 GTAGADSTLIAGYGTQTAGSDSSLTAGYGT--QTARQGSDI-----TAGYGTGT--AG 1109
```

QY 462 ADAPTLVSDEGALNVGSKDANKPVRIITNVPFCVKEGVDVTVNAQLKGVANLNLRIDNVD 521
DB 1110 ADSSLIA--GYGTAGYDSNLTAGYGTQTARESSSLTAGYVGSPTAGHDSLLIAGYG 1167
QY 522 GNARAGIAQAIATA-GLAQAYLPKGSMAIAGGTYRGEAGY-----AIGYSSISDTG--NW 574
DB 1168 STQTAGYNSILTYGYSQTQTAQESSSLTAGYGT--STAGYDSTLTAGYGSTQTAGYKST 1225
QY 575 VIKGTASGNSRGH-----FGASASVGYQ 597
DB 1226 LTAGYGSNSTAGHESLIAGYGSTQIAGYE 1255

RESULT 12

YDBA_ECOLI
ID YDBA_ECOLI STANDARD: PRT: 2003 AA
AC P33666; P76087; P76088; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydba.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RA "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Samesi G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN-K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RA "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S.TYRIMURIUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC -----
DR EMBL; AF000237; AAC74483.1; ALT_SEQ.
DR EMBL; AF000237; AAC74487.1; ALT_SEQ.
DR EMBL; D50778; BAA15009.1; ALT_SEQ.

DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydba.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 6.0%; Score 182.5; DB 1; Length 2003;
Best Local Similarity 22.8%; Pred. No. 0.1;
Matches 158; Conservative 94; Mismatches 234; Indels 207; Gaps 42;

QY 54 DDDLXLEPVQRTAV-----VLSPRSDKEGTGEKGTSDS-----WAVYFDE----- 95
DB 143 NNDVILDKTEKTLTIRDSVFYTYTENADGT---ISLQDSNGRKATINLWQI--DEANNTVA 197
QY 96 -KRVLKAGAITLK-----AGDNLKIKONTNENTNENTNDSSFTYSLKDLTDLTSV 145
DB 198 LEGVSADGATKQYNHNGELVITGDNATV--NNGKTTVDGKDSGTCT--EINGNNGKVI 252
QY 146 ETEKLSFGANGKNVNTSDT-----KG-----LNFPAKETAGTNGD 180
DB 253 QDGLDLVSGGGHIDITGDSATVDNKGTTVTDPESMGIGIDGDKAIVNNEGESTITNG 312
QY 181 PTVHLNG-----IGSTLTDLTLLTGATTNTNDNVTD----- 213
DB 313 TGTQINGDDATANNNGKTTVDGKDSGTGTENGNGKVIQDGLDLVSGGGHIDITGDSAT 372
QY 214 -EKKRAASVKDVLNAGNINIKVPGTGTASDNDFVRYDTVEFLSADTKTTTNNVESKDN 272
DB 373 VDNKGTMTVTPESIGIQVDG--DOAVNNEGESAITNGTGTQINGDDATANNNGKTTVD 431
QY 273 GKK---TEVKIGAKTSVIEKDGKLVTT---GKKDKENG--SSTDGEGELVTAKE-----V 319
DB 432 GKDSGTGTEI--AGNNGKVI--QDGLDLVSGGGHIDITGDSATVDNKGTTMTVTPESIGIQ 488
QY 320 IDA-----VNKAGHRMKTTTANGOTGOADKPEVTSTGKTVTFASNGTTATVSKDD----- 370
DB 489 IDGDAQIAVNEG---ESTITNGGTG-----TOINGNDAT--ANNNGKTTVDGKDSGTGKI 538
QY 371 QGNTIKVYDVNGDALNV-----NOLQNSGWN---LDSK-----AVAGSSGKVIISGNVSPSK 419
DB 539 AGNIGI---VNLDSLTVTGGAGVENIGDNGTVNKNKGDIWVSDTGSIGVLINGEGATVS 595
QY 420 GKMDFTVINAGNIIETRNKNIDIATSM--TPQFSS--VSLGAGADAPTLVSDD----- 471
DB 596 NTGDVNVVS--NEATGFSITTSNGKVSLSAGSMQGVGDFSTGVDLNGNNSVTLAAKDLKVVGQ 654
QY 472 -EGALNVGSKDANKPVRIIT-----NVA-----PGV-----KEGDTVNTVAQLK 507
DB 655 KATGINV--SGDAN--TVNITGNVLVDKDKTADNAAEYFFDPDSVGINVGSDNNVTLDGKLT 712
QY 508 GVAQN--LNNRIDNV--DGNARAGIAQAIAATAGAAQLPAGKSMMAIGGTYRGEAGYAGY 565
DB 713 VVSDSEVTSRQSNLFDGSAE-----KTSGL-----VVIGDG----- 743
QY 566 SSISDFTGNVVIKGTASGNSRGHFGASASVGYOW 598
DB 744 NTVNMNGGLELICEKNALADGSQVTSILRTGYSY 776

RESULT 13
WAPA_BACSU
ID WAPA_BACSU STANDARD: PRT: 2334 AA.
AC Q07833;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE Wall-associated protein precursor.
GN WAPA OR N17G.
OS Bacillus subtilis.

QY 477 VGSKDNKPVRTITNVAAPGKESDVTNVAOLKGYAQNINRIDVDGNARAGIAQAIATAG 536
DB 470 VGSKKNNKPVRTITNVAAPGKESDVTNVAOLKGYAQNINRIDVDGNARAGIAQAIATAG 529
QY 537 LAQAVLPKSMMAIGGTYRGEAGVAIGYSSISDTGNMWYIKGTASGNSRHFASASVGY 596
DB 530 LVQAVLPKSMMAIGGTYRGEAGVAIGYSSISDGNMWIKGTASGNSRHFASASVGY 589
QY 597 QW 598
DB 590 QW 591
RESULT 15
ID 09JRI8 PRELIMINARY: PRT: 591 AA.
AC 09JRI8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHAH OUTER MEMBRANE
PROTEIN).
GN GNA992 OR NMB0992 OR NHAH.
OS Neisseria meningitidis, and
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci L., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF226375; AAF42524.1; -
DR EMBL: AE002450; AAF41395.1; -
DR EMBL: AE226367; AAF42516.1; -
DR EMBL: AF226370; AAF42519.1; -
DR EMBL: AF226374; AAF42523.1; -
DR EMBL: AF157611; AAK68872.1; -
DR TIGR: NMB0992; -
KW Complete proteome.
SQ SEQUENCE 591 AA; 62112 MW; 7c22f3cae7f73ec6 CRC64;

Query Match 89.5%; Score 2725.5; DB 16; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.1e-106;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;
QY 1 MNKIYRIIMSALNAVVSSELRNHTKRASATVATVATLLFATVQANATD---DDLL 57
DB 1 MNKIYRIIMSALNAVVSSELRNHTKRASATVATVATLLFATVQANNEQEDLL 60
QY 58 YLEPQRTAVVLSFRSDKEGEGED-SMAVVFDEKRVKAKAIVLKADNLIKQ 116
DB 61 YLDPVQRTAVVLLVNSDKDEGEKEVEENSQVAVFNEGVLTAEITLKAGDNLIKQ 120
QY 117 NTNENTNENTNDSSFTYSLKDLDTLTSVTEKLSFGANGKNVITSPTKGLNFAKETAG 176
DB 121 -----NGTNFTYSLKDLDTLTSVTEKLSFGANGKNVITSPTKGLNFAKETAG 170
QY 177 TNGDPTVHLNGISLTLLDILLNTGATTVNTNDVNTDEKKRAASVADVNAAGNIGVPR 236
DB 171 TNGDPTVHLNGISLTLLDILLNTGATTVNTNDVNTDEKKRAASVADVNAAGNIGVPR 230
QY 237 GTTASDNVDFVRYDVEEISADTKTTTVNVESKDNKTEVIGAKTSYIKKDKLYT 296
DB 231 GTTASDNVDFVRYDVEEISADTKTTTVNVESKDNKTEVIGAKTSYIKKDKLYT 290
QY 297 GKGDENGSSDDEGEIYAKVEYIDAVNKAQWMTTTFANGOGGADKFEVTSGRKYE 356
DB 291 GKGDENGSSDDEGEIYAKVEYIDAVNKAQWMTTTFANGOGGADKFEVTSGRKYE 350
QY 357 ASGNGTTATVSKDDQGNITVKKYDVNVGDA.LNVNOLNSGMNLSKAVAGSSGKVISGNS 416
DB 351 ASGNGTTATVSKDDQGNITVKKYDVNVGDA.LNVNOLNSGMNLSKAVAGSSGKVISGNS 410
QY 417 PSKGRNDEVNINAGNNIETTRNGKIDIDATSMTPPSSVSLGAGADAPLTVSDDEGAIN 476
DB 411 PSKGRNDEVNINAGNNIETTRNGKIDIDATSMTPPSSVSLGAGADAPLTVSDDEGAIN 469
QY 477 VGSKDNKPVRTITNVAAPGKESDVTNVAOLKGYAQNINRIDVDGNARAGIAQAIATAG 536
DB 470 VGSKKNNKPVRTITNVAAPGKESDVTNVAOLKGYAQNINRIDVDGNARAGIAQAIATAG 529
QY 537 LAQAVLPKSMMAIGGTYRGEAGVAIGYSSISDTGNMWYIKGTASGNSRHFASASVGY 596
DB 530 LVQAVLPKSMMAIGGTYRGEAGVAIGYSSISDGNMWIKGTASGNSRHFASASVGY 589
QY 597 QW 598
DB 590 QW 591

Search completed: July 3, 2002, 08:48:08
Job time: 699 sec

QY 598 W 598
Db 599 W 599

RESULT 13

Q9JPR7 ID Q9JPR7 PRELIMINARY: PRT: 598 AA.
AC Q9JPR7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SM2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42534.1;
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 89.9%; Score 2736; DB 2; Length 598;
Best Local Similarity 90.8%; Pred. No. 3.9e-107;
Matches 545; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

QY 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDDDDTLE 60
Db 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDDDDTLE 60
QY 61 PVORTAVVLSFSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLIKQNTNE 120
Db 61 PVORTAVVLSFSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLIKQNTNE 120
QY 121 NTNENTNDSSFTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSSFTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180
QY 181 PTVHNGISLTDTLTLMTGATNTNNDVDDDEKRAASVYDVANAMNITKGVAPGTA 240
Db 181 PTVHNGISLTDTLTLMTGATNTNNDVDDDEKRAASVYDVANAMNITKGVAPGTA 240
QY 241 --SDNVDEVRTYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVJKEKDGKLVYTK 298
Db 241 --SDNVDEVRTYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVJKEKDGKLVYTK 298
QY 299 GKDENGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEVTSIGTVTFAS 358
Db 299 GKDENGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEVTSIGTVTFAS 358
QY 359 GNGTATATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLSKAAVAGSSGKVISNVSPTS 418
Db 359 GNGTATATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLSKAAVAGSSGKVISNVSPTS 418
QY 419 KGMDETVINAGNIIETRNKNKIDATSMTPQSSVSLGAGADAPLTVSDEGALVNG 478
Db 419 KGMDETVINAGNIIETRNKNKIDATSMTPQSSVSLGAGADAPLTVSDEGALVNG 478
QY 479 SKDANKPVRIITVAPGVEGDTVNAOLKGAQONINNRIDVNGARAGIAQAIATAGLA 538
Db 479 SKDANKPVRIITVAPGVEGDTVNAOLKGAQONINNRIDVNGARAGIAQAIATAGLA 538

Db 479 SKDANKPVRIITVAPGVEGDTVNAOLKGAQONINNRIDVNGARAGIAQAIATAGLA 538
QY 539 QAYLPKSMMAIGGTYGEGAGYALGYSSISDTGMMVYIKGTASGNSRCHFGASASVGYQW 598
Db 539 QAYLPKSMMAIGGTYGEGAGYALGYSSISDTGMMVYIKGTASGNSRCHFGASASVGYQW 598

RESULT 14

Q9JPR7 ID Q9JPR7 PRELIMINARY: PRT: 591 AA.
AC Q9JPR7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42515.1;
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 89.5%; Score 2725.5; DB 2; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.1e-106;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDD--DDDL 57
Db 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDD--DDDL 57
QY 58 YLEPVORTAVVLSFSDKEGTEGEGED--SNMAYVFEDEKRVLKAGATLKAGDNLIKQ 116
Db 58 YLEPVORTAVVLSFSDKEGTEGEGED--SNMAYVFEDEKRVLKAGATLKAGDNLIKQ 116
QY 61 YLDPVORTAVVLSFSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLIKQ 120
Db 61 YLDPVORTAVVLSFSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLIKQ 120
QY 117 NTNENTNDSSFTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 176
Db 117 NTNENTNDSSFTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 176
QY 121 -----NNTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 170
Db 121 -----NNTYSLKDKLDTLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 170
QY 177 TNGDPTVHLNGISLTDTLTLMTGATNTNNDVDDDEKRAASVYDVANAMNITKGVAP 236
Db 177 TNGDPTVHLNGISLTDTLTLMTGATNTNNDVDDDEKRAASVYDVANAMNITKGVAP 236
QY 237 GGTASDNDVFAVTVTFEFLSADTKTTTVNESKDNKTEVKIGAKTSVJKEKDGKLVY 296
Db 237 GGTASDNDVFAVTVTFEFLSADTKTTTVNESKDNKTEVKIGAKTSVJKEKDGKLVY 296
QY 297 GKDENGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEVTSIGTVTF 356
Db 297 GKDENGSSSTDEGEGLVTAKEVIDAVNKAQWRKTTTANGQTGOADKFEVTSIGTVTF 356
QY 359 ASGKTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLSKAAVAGSSGKVISNVSPTS 410
Db 359 ASGKTATVSKDQGNITVYKDVNVGDALNVNOLNSGWNLSKAAVAGSSGKVISNVSPTS 410
QY 417 PSKGMDETVINAGNIIETRNKNKIDATSMTPQSSVSLGAGADAPLTVSDEGALVNG 476
Db 417 PSKGMDETVINAGNIIETRNKNKIDATSMTPQSSVSLGAGADAPLTVSDEGALVNG 476
QY 479 SKDANKPVRIITVAPGVEGDTVNAOLKGAQONINNRIDVNGARAGIAQAIATAGLA 538
Db 479 SKDANKPVRIITVAPGVEGDTVNAOLKGAQONINNRIDVNGARAGIAQAIATAGLA 538

AC Q9JPS3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.*;
RL Science 287:1816-1820(2000).
DR EMBL: AF226378; AAF42527.1; -;
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.1%; Score 2772; DB 2; Length 590;
Best Local Similarity 92.3%; Pred. No. 1.2e-108;
Matches 554; Conservative 10; Mismatches 24; Indels 12; Gaps 3;

QY 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAAATDDDDLY-L 59
DB 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAAATDEDEEDL 60
QY 60 EPVQRTAVVLSFRSDKGEKTEGTEDED-SNMAVYFDEKRVLKAGATTLKAGDNLIKONT 118
DB 61 DPVQRTAVVLSFRSDKGEKTEGTEKESNDMAVYFNEKGVLTAGTTLKAGDNLIKIQ-- 118
QY 119 NENTNENTNDSFTYSLKQDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 178
DB 119 -NCTNFTYSLKQDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 170
QY 179 GDPVHLNGIGSTLTDLTLMTGATNTNNDVDEKKRAASKVDYLNAGMNTKGVPQT 238
DB 171 GDTVHLNGIGSTLTDLTLMTGATNTNNDVDEKKRAASKVDYLNAGMNTKGVPQT 230
QY 239 TASDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 298
DB 231 TASDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 290
QY 299 GKEDNGSSSTDEEGGLVTAKEVIDAVNKAQRMTTTANGOTGQADKEFTVTSCTKVTFA 358
DB 291 GKEDNGSSSTDEEGGLVTAKEVIDAVNKAQRMTTTANGOTGQADKEFTVTSCTNVTFA 350
QY 359 GNGTATVASKDDOGNTTVKDVNVDGALNVNOLONGMNLDSKAVAGSSSKVTSIGNVSPS 418
DB 351 GNGTATVASKDDOGNTTVKDVNVDGALNVNOLONGMNLDSKAVAGSSSKVTSIGNVSPS 410
QY 419 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNVG 478
DB 411 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNVG 470
QY 479 SKDANKPVRTTNVAPGVKGGDTVNAQLKGVAONLNRRIDNDVGNARAAGIAAIAATAGLA 538
DB 471 SKDANKPVRTTNVAPGVKGGDTVNAQLKGVAONLNRRIDNDVGNARAAGIAAIAATAGLA 530
QY 539 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDPTGMVNTKGTASGNSRGHFGASASVGYQ 598
DB 531 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDPTGMVNTKGTASGNSRGHFGASASVGYQ 590

RESULT 12

Q9JPS8
ID Q9JPS8 PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.*;
RL Science 287:1816-1820(2000).
DR EMBL: AF226364; AAF42513.1; -;
SQ SEQUENCE 599 AA; 62693 MW; 46C2B974AF7F78E9 CRC64;

Query Match 90.5%; Score 2755.5; DB 2; Length 599;
Best Local Similarity 91.7%; Pred. No. 6e-108;
Matches 551; Conservative 15; Mismatches 30; Indels 5; Gaps 3;

QY 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAAATD-DDDLYL 59
DB 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFAVQAAATDEDEEYL 60
QY 60 EPVQRTAVVLSFRSDKGEKTEGTEGSHMGVYFDEKRVLKAGATTLKAGDNLIKONT 119
DB 61 EPVQRTAVVLSFRSDKGEKTEGTEGSHMGVYFDEKRVLKAGATTLKAGDNLIKONT 120
QY 120 ENTNENTNDSFTYSLKQDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 179
DB 121 ENTNENTNDSFTYSLKQDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 180
QY 180 DPTVHLNGIGSTLTDLTLMTGATNTNNDVDEKKRAASKVDYLNAGMNTKGVPQT 239
DB 181 DPTVHLNGIGSTLTDLTLMTGATNTNNDVDEKKRAASKVDYLNAGMNTKGVPQT 238
QY 240 A--SDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 297
DB 239 TGSSENVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 298
QY 298 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 357
DB 299 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 358
QY 359 SGKGTATVASKDDOGNTTVKDVNVDGALNVNOLONGMNLDSKAVAGSSSKVTSIGNVSP 418
DB 358 SGKGTATVASKDDOGNTTVKDVNVDGALNVNOLONGMNLDSKAVAGSSSKVTSIGNVSP 417
QY 419 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 478
DB 419 KGRMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLISVDEGALNV 478
QY 478 GSKDANKPVRTTNVAPGVKGGDTVNAQLKGVAONLNRRIDNDVGNARAAGIAAIAATAGLA 537
DB 479 GSKDANKPVRTTNVAPGVKGGDTVNAQLKGVAONLNRRIDNDVGNARAAGIAAIAATAGLA 538
QY 538 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDPTGMVNTKGTASGNSRGHFGASASVGYQ 597
DB 539 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDPTGMVNTKGTASGNSRGHFGASASVGYQ 598

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -
DR EMBL: AF157608; AAK68869.1; -
SQ SEQUENCE 599 AA; 62844 MW; BBA16BFB53C1970C CRC64;

Query Match 92.8%; Score 2824.5; DB 2; Length 599;
Best Local Similarity 92.7%; Pred. No. 7.9e-111;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

OY 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLYL 59
DB 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATDEDEEEL 60
OY 60 EPVQATAVVLSFRSDEKTEGEKTEDSDNMAVYFDEKRVLKAGATTLKAGDNLK 119
DB 61 EPVNSALVLPMDKDEGENESTGNIGWISLYDNHNTLHGATVTLKAGDNLK 120
OY 120 ENTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKEATAGNG 179
DB 121 KNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKEATAGNG 180
OY 180 DPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLGAMNIGVPGTT 239
DB 181 DTTVHLNGIGSTLDTLNTGATNTVNDNVTDDKKRAASVYKDVNLGAMNIGVPGTT 240
OY 240 ASDNDVFRYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGKLVYTGK 299
DB 241 ASDNDVFRYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGKLVYTGK 300
OY 300 KDENGSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVYTSCTKVTFA 359
DB 301 KGENSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVYTSCTKVTFA 360
OY 360 NGTATVSKDDOGNTVYKYDVNVGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPK 419
DB 361 KGTATVSKDDOGNTVYKYDVNVGDALNVNOLNSGMNLSKAVAGSSGKVISGNVSPK 420
OY 420 GKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLTSDVDKLANGS 479
DB 421 GKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLTSDVDKLANGS 480
OY 480 KDANKPVRITTVNAPGVKEDGYTNVQOLKGVQONLNRRIDNVGNRAGIAQIAIATAGLAQ 539
DB 481 KDANKPVRITTVNAPGVKEDGYTNVQOLKGVQONLNRRIDNVGNRAGIAQIAIATAGLAQ 540
OY 540 AYLPGKSMMAIGGTYRGAGAGTAIGSSISDPTGNVYIKGTASGNSRGHFGASASVGYOM 598
DB 541 AYLPGKSMMAIGGTYRGAGAGTAIGSSISDPTGNVYIKGTASGNSRGHFGASASVGYOM 599

RESULT 10
O9JPS6 PRELIMINARY; PRT; 600 AA.
AC O9JPS6;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.

OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.4%; Score 2781; DB 2; Length 600;
Best Local Similarity 91.7%; Pred. No. 5.2e-109;
Matches 555; Conservative 14; Mismatches 24; Indels 12; Gaps 3;

OY 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATD 53
DB 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOASADNVASADN 60
OY 54 DDDLYLEPVQATAVVLSFRSDEKTEGEKTEDSDNMAVYFDEKRVLKAGATTLKAGDNLK 113
DB 61 EEEVLEPVQATAVVLSFRSDEKTEGEKTEVENTNMGIYFDKNGVTKAGTTLKAGDNLK 120
OY 114 IKONTNENTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKE 173
DB 121 IKONTNENTN---SFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKE 176
OY 174 TAGTNGDPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLGAMNIGK 233
DB 177 TAGTNGDPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLGAMNIGK 236
OY 234 VKPGTTASDNVDFRTYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGK 293
DB 237 VKPGTTASDNVDFRTYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGK 296
OY 294 LVTGKRGKENGSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVYTSCTN 353
DB 297 LVTGKRGKENGSSSTDEGEGLYTAKEVIDAVNKAQRMKTTTANGOTGADKFEVYTSCTN 356
OY 354 VTFASGNGTTATVSKDDOGNTVYKYDVNVGDALNVNOLNSGMNLSKAVAGSSGKVISG 413
DB 357 VTFASGNGTTATVSKDDOGNTVYKYDVNVGDALNVNOLNSGMNLSKAVAGSSGKVISG 416
OY 414 NVSPSKGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLTSDVDK 473
DB 417 NVSPSKGKMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLTSDVDK 475
OY 474 ALNVSKRANKPVRITTVNAPGVKEDGYTNVQOLKGVQONLNRRIDNVGNRAGIAQIA 533
DB 476 ALNVSKRANKPVRITTVNAPGVKEDGYTNVQOLKGVQONLNRRIDNVGNRAGIAQIA 535
OY 534 TAGLQAVLTPGKSMMAIGGTYRGAGAGTAIGSSISDPTGNVYIKGTASGNSRGHFGAS 593
DB 536 TAGLQAVLTPGKSMMAIGGTYRGAGAGTAIGSSISDPTGNVYIKGTASGNSRGHFGAS 595

RESULT 11
O9JPS3 PRELIMINARY; PRT; 590 AA.
ID O9JPS3

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storti E., Zuo P.,
 RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.T., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 Meningococcus by Whole-Genome Sequencing.";
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226376; AAF42525.1; -
 DR EMBL: AF226369; AAF42518.1; -
 SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;

Query Match 94.8%; Score 2887; DB 2; Length 594;
 Best Local Similarity 95.5%; Pred. No.1.9e-113;
 Matches 571; Conservative 5; Mismatches 18; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANWVSELTFRNHTKRASATVATVATLTLFATVQANATDDDDLLYLE 60
 DB 1 MNKIRIIMNSALNANWVSELTFRNHTKRASATVATVATLTLFATVQASTDDDDLLYLE 60
 QY 61 PVORTAVVLSFRSDKEGTGEGTEGSDSNMAVYDEKRYLKAGAITTLKAGDNLKIKONTNE 120
 DB 61 PVORTAVVLSFRSDKEGTGEGTEGSDSNMGVYFDKKGVLTAAGITTLKAGDNLKIKONTDE 120
 QY 121 NTNENTNDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAAGTNGD 180
 DB 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAAGTNGD 176
 QY 181 PTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNIKGVKPGTTA 240
 DB 177 TTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNIKGVKPGTTA 236
 QY 241 SDNVDPRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDGKLVGTGDK 300
 DB 237 SDNVDPRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDGKLVGTGDK 296
 QY 301 DENSSSTDEBEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVVTSGTKVTFASGN 360
 DB 297 GENGSSSTDEBEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVVTSGTKVTFASGN 356
 QY 361 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGMNLDKRAVAGSSGKVISGNVSPSKG 420
 DB 357 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGMNLDKRAVAGSSGKVISGNVSPSKG 416
 QY 421 KMDETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480
 DB 417 KMDETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 476
 QY 481 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDGNAKRAIAIAIATAGLQA 540
 DB 477 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDGNAKRAIAIAIATAGLQA 536
 QY 541 YLPKSMMAIGGTYRGEAGTAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 598
 DB 537 YLPKSMMAIGGTYRGEAGTAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 594

RESULT 8
 Q930Y4
 ID Q930Y4 PRELIMINARY; PRT; 594 AA.
 AC Q930Y4
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE NHHA OUTER MEMBRANE PROTEIN.
 GN NHHA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN (1)
 RP SEQUENCE FROM N.A.

RC STRAIN-EG327;
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer
 membrane protein of Neisseria meningitidis";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF157605; AAK6886.1; -
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 93.8%; Score 2855; DB 2; Length 594;
 Best Local Similarity 94.6%; Pred. No.4.2e-112;
 Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANWVSELTFRNHTKRASATVATVATLTLFATVQANATDDDDLLYLE 60
 DB 1 MNKIRIIMNSALNANWVSELTFRNHTKRASATVATVATLTLFATVQASTDDDDLLYLE 60
 QY 61 PVORTAVVLSFRSDKEGTGEGTEGSDSNMAVYDEKRYLKAGAITTLKAGDNLKIKONTNE 120
 DB 61 PVORTAVVLSFRSDKEGTGEGTEGSDSNMGVYFDKKGVLTAAGITTLKAGDNLKIKONTNE 120
 QY 121 NTNENTNDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAAGTNGD 180
 DB 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKGLNFAKETAAGTNGD 176
 QY 181 PTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNIKGVKPGTTA 240
 DB 177 TTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGMNIKGVKPGTTA 236
 QY 241 SDNVDPRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDGKLVGTGDK 300
 DB 237 SDNVDPRITDYVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIREKDGKLVGTGDK 296
 QY 301 DENSSSTDEBEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVVTSGTKVTFASGN 360
 DB 297 GENGSSSTDEBEGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVVTSGTKVTFASGN 356
 QY 361 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGMNLDKRAVAGSSGKVISGNVSPSKG 420
 DB 357 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGMNLDKRAVAGSSGKVISGNVSPSKG 416
 QY 421 KMDETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480
 DB 417 KMDETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 476
 QY 481 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDGNAKRAIAIAIATAGLQA 540
 DB 477 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDGNAKRAIAIAIATAGLQA 536
 QY 541 YLPKSMMAIGGTYRGEAGTAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 598
 DB 537 YLPKSMMAIGGTYRGEAGTAIGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 594

RESULT 9
 Q9JPR8
 ID Q9JPR8 PRELIMINARY; PRT; 599 AA.
 AC Q9JPR8;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DE 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
 GN GNA992 OR NHHA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NGH38;
 RX MDDLINE=20175756; PubMed=10710308;
 RA Plaza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of *Neisseria meningitidis*."
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226368; AAF42517.1; -
DR EMBL: AF226368; AAF42507.1; -
DR EMBL: AF157604; AK68865.1; -
SQ SEQUENCE 594 AA; 62361 MW; 436BDEED68263C5C CRC64;

Query Match 97.6%; Score 2971; DB 2; Length 594;

Best Local Similarity 98.0%; Pred. No. 5.9e-117;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

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QY 1 MNKYYRIIMNSALNAAWVSELTNRHTRKASATATATLTLPAATVOANATDDDDLYLE 60
DB 1 MNKYYRIIMNSALNAAWVSELTNRHTRKASATATATLTLPAATVOANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFDEKRYLKAGATTLKAGDNLIKONTNE 120
DB 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFDEKRYLKAGATTLKAGDNLIKONTNE 116
QY 121 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 180
DB 121 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 176
QY 117 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 176
DB 117 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 176
QY 181 PTYHLNGIGSLTDTLNTGATNTVNDVDEKKRAASVDVLANAGMNKGVKPGTTA 240
DB 177 PTYHLNGIGSLTDTLNTGATNTVNDVDEKKRAASVDVLANAGMNKGVKPGTTA 236
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGKTEVKGAKTSVIEKDKGLVTGKG 300
DB 237 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGKTEVKGAKTSVIEKDKGLVTGKG 296
QY 301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGTGADKFEYVTSCTNYTFASGN 360
DB 297 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGTGADKFEYVTSCTNYTFASGN 356
QY 361 GTTATVSKDDGNTTVKVDVNWGDALNVNOLNSGMNDSKAVAGSSGKTVISGNVSPSKG 420
DB 357 GTTATVSKDDGNTTVKVDVNWGDALNVNOLNSGMNDSKAVAGSSGKTVISGNVSPSKG 416
QY 421 KMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
DB 417 KMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 476
QY 481 DANKPVRTTNAPGVKEGDDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
DB 477 DANKPVRTTNAPGVKEGDDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 536
QY 541 YLPKSMMAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRHHGASASVGYOM 598
DB 537 YLPKSMMAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRHHGASASVGYOM 594
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RESULT 6

09JPS2 PRELIMINARY; PRT; 594 AA.

AC 09JPS2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Malignani V., Giuliani M.M., Arico' B.,
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT *Meningococcus* by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 95.0%; Score 2891; DB 2; Length 594;

Best Local Similarity 95.7%; Pred. No. 1.3e-113;
Matches 572; Conservative 5; Mismatches 17; Indels 4; Gaps 1;

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QY 1 MNKYYRIIMNSALNAAWVSELTNRHTRKASATATATLTLPAATVOANATDDDDLYLE 60
DB 1 MNKYYRIIMNSALNAAWVSELTNRHTRKASATATATLTLPAATVOANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFDEKRYLKAGATTLKAGDNLIKONTNE 120
DB 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFDEKRYLKAGATTLKAGDNLIKONTNE 120
QY 121 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 180
DB 121 NTNNTNDSSFTYSLKDLDTLTSVETEKLSFGANGKRVNTTSPTKGLNFAKETAGTNGD 176
QY 181 PTYHLNGIGSLTDTLNTGATNTVNDVDEKKRAASVDVLANAGMNKGVKPGTTA 240
DB 177 PTYHLNGIGSLTDTLNTGATNTVNDVDEKKRAASVDVLANAGMNKGVKPGTTA 236
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGKTEVKGAKTSVIEKDKGLVTGKG 300
DB 237 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGKTEVKGAKTSVIEKDKGLVTGKG 296
QY 301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGTGADKFEYVTSCTNYTFASGN 360
DB 297 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGTGADKFEYVTSCTNYTFASGN 356
QY 361 GTTATVSKDDGNTTVKVDVNWGDALNVNOLNSGMNDSKAVAGSSGKTVISGNVSPSKG 420
DB 357 GTTATVSKDDGNTTVKVDVNWGDALNVNOLNSGMNDSKAVAGSSGKTVISGNVSPSKG 416
QY 421 KMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
DB 417 KMDETVINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 476
QY 481 DANKPVRTTNAPGVKEGDDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
DB 477 DANKPVRTTNAPGVKEGDDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 536
QY 541 YLPKSMMAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRHHGASASVGYOM 598
DB 537 YLPKSMMAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRHHGASASVGYOM 594
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RESULT 7

09JPI3 PRELIMINARY; PRT; 594 AA.

AC 09JPI3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/88, AND B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scariato V., Malignani V., Giuliani M.M., Arico' B.,

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OY 1 MNKIRIINMSALNANVAVVSELTNRHTKRASATVATVATLTLFATVOAATDDDDLYLE 60
DB 1 MNKIRIINMSALNANVAVVSELTNRHTKRASATVATVATLTLFATVOAATDDDDLYLE 60
OY 61 PVQRTAVVLSFRSDKEGTEKEGEDSNNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
DB 61 PVQRTAVVLSFRSDKEGTEKEGEDSNNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
OY 121 NTNENTNDSFFYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNPAKETAAGTNGD 180
DB 121 NTNENTNDSFFYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNPAKETAAGTNGD 180
OY 181 PTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKGTGA 240
DB 181 PTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKGTGA 240
OY 241 SDNVDFVRYDYVEFLSADTKTTTVAVESKDNKKEVKGAKTSYIKERDKLVTGKSK 300
DB 241 SDNVDFVRYDYVEFLSADTKTTTVAVESKDNKKEVKGAKTSYIKERDKLVTGKSK 300
OY 301 DENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEFTVSGTKVTFASGN 360
DB 301 DENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEFTVSGTKVTFASGN 360
OY 361 GTTATVSKDQOGNITVYKYVNVGDALNVNOLNSGWNLDKSKAVAGSSGKVISGNVSPSKG 420
DB 361 GTTATVSKDQOGNITVYKYVNVGDALNVNOLNSGWNLDKSKAVAGSSGKVISGNVSPSKG 420
OY 421 KNDDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDDEGALNVGSK 480
DB 421 KNDDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDDEGALNVGSK 480
OY 481 DANKPVRTINVAAPVKEGEGVTNVAQLKGYAQNINNRIDVNDGNARAGIAQAIATAGLAQA 540
DB 481 DANKPVRTINVAAPVKEGEGVTNVAQLKGYAQNINNRIDVNDGNARAGIAQAIATAGLAQA 540
OY 541 YLPGRSMMAIGGGTYRGEAGYALGYSSISDTGNNWIKGTASGNSRCHFGASASVGYOW 598
DB 541 YLPGRSMMAIGGGTYRGEAGYALGYSSISDTGNNWIKGTASGNSRCHFGASASVGYOW 598

RESULT 4
OQJPH9 PRELIMINARY; PRT; 598 AA.
AC 09JPH9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1;
SQ SEQUENCE 598 AA; 62718 MW; 9095FBE31AD7C76D CRC64;

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Query Match 98.7%; Score 3005; DB 2; Length 598;
Best Local Similarity 98.7%; Pred. No. 2.3e-118;

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Matches 590; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
OY 1 MNKIRIINMSALNANVAVVSELTNRHTKRASATVATVATLTLFATVOAATDDDDLYLE 60
DB 1 MNKIRIINMSALNANVAVVSELTNRHTKRASATVATVATLTLFATVOAATDDDDLYLE 60
OY 61 PVQRTAVVLSFRSDKEGTEKEGEDSNNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
DB 61 PVQRTAVVLSFRSDKEGTEKEGEDSNNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
OY 121 NTNENTNDSFFYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNPAKETAAGTNGD 180
DB 121 NTNENTNDSFFYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNPAKETAAGTNGD 180
OY 181 PTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKGTGA 240
DB 181 PTVHLNGISLTLDLTLNLTGATTNTNDVTDDEKRRASVYKDVNLNAGNNIKGVKGTGA 240
OY 241 SDNVDFVRYDYVEFLSADTKTTTVAVESKDNKKEVKGAKTSYIKERDKLVTGKSK 300
DB 241 SDNVDFVRYDYVEFLSADTKTTTVAVESKDNKKEVKGAKTSYIKERDKLVTGKSK 300
OY 301 DENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEFTVSGTKVTFASGN 360
DB 301 DENGSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEFTVSGTKVTFASGN 360
OY 361 GTTATVSKDQOGNITVYKYVNVGDALNVNOLNSGWNLDKSKAVAGSSGKVISGNVSPSKG 420
DB 361 GTTATVSKDQOGNITVYKYVNVGDALNVNOLNSGWNLDKSKAVAGSSGKVISGNVSPSKG 420
OY 421 KNDDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDDEGALNVGSK 480
DB 421 KNDDEVNINAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPLTVSDDEGALNVGSK 480
OY 481 DANKPVRTINVAAPVKEGEGVTNVAQLKGYAQNINNRIDVNDGNARAGIAQAIATAGLAQA 540
DB 481 DANKPVRTINVAAPVKEGEGVTNVAQLKGYAQNINNRIDVNDGNARAGIAQAIATAGLAQA 540
OY 541 YLPGRSMMAIGGGTYRGEAGYALGYSSISDTGNNWIKGTASGNSRCHFGASASVGYOW 598
DB 541 YLPGRSMMAIGGGTYRGEAGYALGYSSISDTGNNWIKGTASGNSRCHFGASASVGYOW 598

RESULT 5
OQJPH7 PRELIMINARY; PRT; 594 AA.
AC 09JPH7;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198;
RX MEDLINE=20175756; PubMed=10710308;
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

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Best Local Similarity 100.0%; Pred. No. 5.3e-120;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
DB 1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
OY 61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
DB 61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
OY 121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
DB 121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
OY 181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
DB 181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
OY 241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
DB 241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
OY 301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
DB 301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
OY 361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
DB 361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
OY 421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
DB 421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
OY 481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
DB 481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
OY 541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598
541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598
DB 541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598

RESULT 2
O9JPT0 PRELIMINARY; PRT: 598 AA.

AC O9JPT0; 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GMA992.
GN GMA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-2996;
RX MEDLINE-20175756; PubMed-10710308;
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Camanduci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hunt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL EMBL: AF226359; AAF42508.1;
DR EMBL: AF226359; AAF42508.1;
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 99.5%; Score 3030; DB 2; Length 598;
Best Local Similarity 99.5%; Pred. No. 2.1e-119;
Matches 595; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
DB 1 MNKIRIIMNSALNMAVVSSELTFRNHTKASATVATVATLTLFATVOANATDDDDLYLE 60
OY 61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
DB 61 PVORTAVVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120
OY 121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
DB 121 NTNENTNDSSEFTYSLKQDLTDLTSVETEKLSFGANGKNVNITSPTKGLNFAKETAGTNGD 180
OY 181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
DB 181 PTVHLNGISGLTDLTLMTGATNTNNDVTDDEKKRAASVYKDVNAGMNIKGVKPGTTA 240
OY 241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
DB 241 SDNVDFVFTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIEKDGKLVTKGK 300
OY 301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
DB 301 DENGSTDEGEGLYTAKEVDAVNAKAGRMKTTTANGOTGADKEFTVTSCTKVTFAAGN 360
OY 361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
DB 361 GTTAVVSKDDGDNITVKYDVNVDALNVOLONSGMNLSKRAVAGSSKVTISGNVSPSKG 420
OY 421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
DB 421 KMDETVINAGNIEITFRNGKNIDTATMTPOFSSVSLGAGADATLTVDEGALNVSK 480
OY 481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
DB 481 DANKVRITTNVAPGYKEDVTNVAOLKGAONLNRRINDVGNARAGIAQAATATAGLQA 540
OY 541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598
541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598
DB 541 YLPGKSMAIGGGTYRGEAGYAGISSISDGTGMNVIKGTASGNSRGRHFGASASVGYQW 598

RESULT 3
O93OY5 PRELIMINARY; PRT: 598 AA.

AC O93OY5; 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE NHIA OUTER MEMBRANE PROTEIN.
GN NHIA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B210;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF157603; AAK68864.1;
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 99.2%; Score 3021; DB 2; Length 598;
Best Local Similarity 99.3%; Pred. No. 4.9e-119;
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:29 ; Search time 100.13 Seconds
(without alignments)
1033.167 Million cell updates/sec

Title: US-09-771-382-7
Perfect score: 3044
Sequence: 1 MNKTYRITMNSALNAMYVS.....TASGNSRGHFGASASVGYOW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriaph:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3044	100.0	598	2	Q9JPS0	Q9JPS0 neisseria m
2	3030	99.5	598	2	Q9JPT0	Q9JPT0 neisseria m
3	3021	99.2	598	2	Q9JQY5	Q9JQY5 neisseria m
4	3005	98.7	598	2	Q9JPR9	Q9JPR9 neisseria m
5	2971	97.6	594	2	Q9JPH7	Q9JPH7 neisseria m
6	2891	95.0	594	2	Q9JPS2	Q9JPS2 neisseria m
7	2887	94.8	594	2	Q9JPT3	Q9JPT3 neisseria m
8	2855	93.8	594	2	Q9JQY4	Q9JQY4 neisseria m
9	2824.5	92.8	599	2	Q9JPR8	Q9JPR8 neisseria m
10	2781	91.1	600	2	Q9JPS6	Q9JPS6 neisseria m
11	2772	91.1	590	2	Q9JPS3	Q9JPS3 neisseria m
12	2755.5	90.5	599	2	Q9JPS8	Q9JPS8 neisseria m
13	2736	89.9	598	2	Q9JPR7	Q9JPR7 neisseria m
14	2725.5	89.5	591	16	Q9JPS7	Q9JPS7 neisseria m
15	2725.5	89.5	591	16	Q9JRI8	Q9JRI8 neisseria m
16	2718	89.3	592	2	Q9AQF0	Q9AQF0 neisseria m

17	2706.5	88.9	591	2	Q93QY3	Q93QY3 neisseria m
18	2705	88.9	600	2	Q9JPS5	Q9JPS5 neisseria m
19	2675	87.9	592	2	Q9JPS9	Q9JPS9 neisseria m
20	2667	87.6	592	2	Q93QY2	Q93QY2 neisseria m
21	2637.5	86.6	595	2	Q9JPH0	Q9JPH0 neisseria m
22	2621.5	86.1	589	2	Q9JPH0	Q9JPH0 neisseria m
23	2610.5	85.8	592	2	Q93QY1	Q93QY1 neisseria m
24	2524	82.9	592	16	Q9JQW4	Q9JQW4 neisseria m
25	2501.5	82.2	556	2	Q9JPS4	Q9JPS4 neisseria m
26	2493.5	81.9	530	2	Q9JPS1	Q9JPS1 neisseria m
27	2318.5	43.3	2353	2	P71401	P71401 haemophilus
28	1057	34.7	1098	2	Q48152	Q48152 haemophilus
29	450	14.8	1299	16	Q9F3X6	Q9F3X6 pasteurella
30	402	13.2	2059	16	Q9PD50	Q9PD50 xyella fas
31	395	13.0	1107	2	Q9F2D8	Q9F2D8 salmonella
32	382.5	12.6	1190	16	Q9PC04	Q9PC04 xyella fas
33	360	11.8	2712	16	Q9F3X5	Q9F3X5 pasteurella
34	269.5	8.9	1291	16	Q92KQ7	Q92KQ7 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98HJ2 rhizobium l
36	257.5	8.5	2276	2	Q93TY6	Q93TY6 staphylococ
37	254	8.3	1004	16	Q9PD63	Q9PD63 xyella fas
38	236	7.8	1039	2	Q9L6T7	Q9L6T7 escherichia
39	230.5	7.6	832	2	Q54356	Q54356 moraxella c
40	226	7.4	1040	2	Q9AL50	Q9AL50 shigella fl
41	225.5	7.4	1039	2	Q9L6T8	Q9L6T8 escherichia
42	222.5	7.3	1265	2	Q9PD80	Q9PD80 xanthomonas
43	221	7.3	989	2	Q9XD84	Q9XD84 escherichia
44	221	7.3	1018	16	Q9HW06	Q9HW06 pseudomonas
45	221	7.3	2747	2	Q9L800	Q9L800 aeromonas s

ALIGNMENTS

RESULT 1
ID Q9JPS0 PRELIMINARY; PRT; 598 AA.
AC Q9JPS0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH15;
RX MEDLINE=20175756; Pubmed=10710308;
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RT Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H15;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL, AF26381; AAF42530.1; -;
DR EMBL, AF157607; AAK68668.1; -;
SQ SEQUENCE 598 AA; 62763 MW; E6G7AEF0BB8A63CB CRC64;

Query Match 100.0%; Score 3044; DB 2; Length 598;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:22 ; Search time 104.77 Seconds
(without alignments)
533.980 Million cell updates/sec

Title: US-09-771-382-8
Perfect score: 3042
Sequence: 1 MNKTSRIWNSALNAWVVS.....TASGNSRGHFGTSASVGYQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802.*
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22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	3042	100.0	598 20 AAY23738	A surface protein
2	3042	100.0	598 22 AAU06178	N. meningitidis B2
3	3021	99.3	598 20 AAY23742	A surface protein
4	3021	99.3	598 22 AAU06177	N. meningitidis H1
5	2948	96.9	594 20 AAY23739	A surface protein
6	2948	96.9	594 22 AAU06179	N. meningitidis B2
7	2852	93.8	594 20 AAY23740	A surface protein
8	2852	93.8	594 21 AAY57044	BASB029 amino acid
9	2852	93.8	594 22 AAU06174	N. meningitidis EG
10	2821.5	92.8	599 20 AAY23743	A surface protein
11	2821.5	92.8	599 22 AAU06176	N. meningitidis H3

12	2732.5	89.8	591 21 AAY57045	BASB029 amino acid
13	2716.5	89.3	591 20 AAY27202	Amino acid sequenc
14	2716.5	89.3	591 20 AAY23746	A surface protein
15	2716.5	89.3	591 22 AAU06171	N. meningitidis PM
16	2709	89.1	592 20 AAY23737	A surface protein
17	2705.5	88.9	591 20 AAY23741	A surface protein
18	2705.5	88.9	591 22 AAU06175	N. meningitidis EG
19	2658	87.4	592 20 AAY23744	A surface protein
20	2658	87.4	592 22 AAU06172	N. meningitidis H4
21	2616.5	86.0	589 20 AAY23745	A surface protein
22	2616.5	86.0	589 22 AAU06173	N. meningitidis P2
23	2521	82.9	592 22 AAU06180	N. meningitidis Z2
24	2485	81.7	592 20 AAY27203	Amino acid sequenc
25	2451.5	80.6	513 22 AAU06183	N. meningitidis H4
26	2418	79.5	512 22 AAU06182	N. meningitidis PM
27	2335	76.8	502 22 AAU06186	N. meningitidis PM
28	2235	73.5	604 22 AAU06181	N. meningitidis su
29	2001.5	65.8	433 22 AAU06185	N. meningitidis PM
30	1855.5	61.0	407 22 AAU06184	N. meningitidis PM
31	1312.5	43.1	2353 17 AAR9393	Haemophilus adhesi
32	1286.5	42.3	2411 21 AAB23860	Haemophilus influe
33	1066	35.0	1094 21 AAB23858	Haemophilus influe
34	1054	34.6	1098 17 AAR9392	Haemophilus adhesi
35	1038	34.1	245 20 AAY27201	Amino acid sequenc
36	1004.5	33.0	679 17 AAR9394	Haemophilus adhesi
37	1004.5	33.0	679 21 AAB23855	Haemophilus influe
38	762	25.0	1002 21 AAB23854	Haemophilus influe
39	753	24.8	1004 21 AAB23857	Haemophilus influe
40	703	23.1	1104 21 AAB23856	Haemophilus influe
41	703	23.1	1104 21 AAB23859	Haemophilus influe
42	583	19.2	116 21 AAB37832	Neisseria conserv
43	412.5	13.6	2314 22 AAB69136	M. catarrhalis les
44	395.5	13.0	2123 22 AAE00701	Moraxella catarrha
45	392.5	12.9	1992 17 AAW04505	Moraxella 200 kDa

ALIGNMENTS

RESULT 1
AAY23738
ID AAY23738 standard; Protein; 598 AA.
XX
AC AAY23738;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI; 1999-418754/35.
DR N-PSDB; AAX85790.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections

Claim 1; Page 91-93; 132pp; English.

The present sequence represents a surface protein of *Neisseria meningitidis* which is approximately 62 kDa. The *N. meningitidis* surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of *N. meningitidis* infection in humans. The *N. meningitidis* surface glycoproteins can also be used to prevent or treat *N. meningitidis* infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

Sequence 598 AA:

```
Query Match      100.0%; Score 3042; DB 20; Length 598;
Best Local Similarity 100.0%; Pred. No. 5.6e-176;
Matches 598: Conservative 0; Mismatches 0; Indels 0;
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Qy	1	MNKISRIIWSALNAWVVSSELTRNHTKRSATVATAVIATLLFATVQANATDDDDLYLE	60
Db	1	mknisriiwsalnawvvsselftrnhtkrasatvataviatlilfatvqanattdddddyle	60
Qy	61	PVQRTAVVLSFRSKEGTEGTEGSNNNAVFDKRVVKAGAITLKAGDNLKIKQNTNE	120
Db	61	pvgrtavvlsfrskegtegtegsnnnavyfdkxrvikagaitlkagdnlikqntne	120
Qy	121	NTNENTNDSSFTYSILKKDILTDLTSVETEKLSFGANGKNVNTSDTKGLNPAKETAGTNGD	180
Db	121	ntnentndssftysilkkdiltlsveteklsfgangknvntsdtkglnfaketagntngd	180

QY 181 PTVHLNGIGSTLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240

Db 181 ptvhlngigstltdllntgattntvndnvtddekkraasvkdvl naqwnikvkvqpta 240

QY 241 SDNVDFVRTYDTVEFLSADTKTTVNVESKDNGKRTEVKIGAKTSVIKEKDGLVTGKGK 300

Db 241 sdnvdfvrtvdtveflsadtktttvpveskdqkrtevkiaqktsvikekdkllvtgkqk 300

OV 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGOADKFEETVTSGTKVTFASGN 360

Db 301 qengsstdegeglvtakeyidavnkagwrmktttangatgaadkfervttsatkvtfasn 360

361 GTTATVSKDDOGNITTVKYDVNVGDAI.NVNOI.ONSGWNI.DSKAVAGSSGKVTSGNVSPSKG A20

pb 367 attatvskddaanitvkvdyvnygdalnyng]ansawn]dskavagssckvi sanyvssckg 420

Qv 421 KMDETVNIACNNITEETPNCKVNTDIAETSMEDPDESSVCI CACADADDEI CVIDDECAI WCCV 190

[illegible]

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000 4bI6Acncc6rurfrcuufcncn6vutAuu6c00crccIfcrrfcnc6-fc6ccfcmwww.c6J=f nlc

RESULT 2

ID AAU06178 standard; Protein; 598 AA.

AA
AC AAU06178;

AA	DT	24-OCT-2001 (first entry)

XX
DE N. meningitidis BZ10 surface antigen NhbA polypeptide sequence

XX Surface antigen NhbA: meningococcal disease: meningitis vaccine

XX
50
Neisseria meningitidis strain B710

XX	Key	Location/Qualifiers
FT	Region	1..50
FT		/label= C1
FT		/note= "Conserved region 1"
FT	Region	51..104
FT		/label= V1
FT		/note= "Variable region 1"
FT	Region	105..116
FT		/label= C2
FT		/note= "Conserved region 2"
FT	Region	117..130
FT		/label= V2
FT		/note= "Variable region 2"
FT	Region	131..194
FT		/label= C3
FT		/note= "Conserved region 3"
FT	Region	195..216
FT		/label= V3
FT		/note= "Variable region 3"
FT	Region	217..235
FT		/label= C4
FT		/note= "Conserved region 4"
FT	Region	236..242
FT		/label= V4
FT		/note= "Variable region 4"
FT	Region	243..598
FT		/label= C5
FT		/note= "Conserved region 5"

WO200155182-A1.

02-AUG-2001.

25-JAN-2001: 2001WO-AU000069.

25-JAN-2000: 2000US-0177917

UNIVERSITY OF QUEENSLAND

Peak TRA: Jennings MP.

WPT: 2001-49977A/53

N-PSDB; AAS09168.

New NhhA surface antigen polypeptides and polynucleotides from *Neisseria meningitidis*, useful in producing vaccines for treating or preventing broad spectrum of *Neisseria meningitidis* -

Claim 9. Fig 1. 91pp. English.

The present invention relates to the isolation of novel *Neisseria meningitidis* mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly in the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of *N. meningitidis*, and in designing and/or screening of medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of *N. meningitidis* strains than would be expected from a corresponding wild-type surface antigen. The present sequence representing the wild type surface antigen Nhha from *N. meningitidis* strain B210 is 1 of 10 Nhha polypeptide sequences (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in the present invention.

XX
SO
Sequence 598 AA:

Query Match	100.0%;	Score 3042;	DB 22;	Length 598;
Best Local Similarity	100.0%;	Pred. No. 5.6e-176;		
Matches 598; Conservative	0;	Mismatches 0;	Indels 0;	

QY 1 MNKISRIIWNLSALNAWVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkisirliwnsalnawvvyvseltrnhtkrasatvatvatltilfatvqanatdddlyle 60
QY 61 PVQRTAVLSFRSDKEGTEGTEDESNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
DB 61 pvrqtavlsfrsdkegtegedsnwavyfdekrvlikagaitlkagdnlikikqntne 120
QY 121 NTNENTNDSSFTYSLKDLTDLTSLVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 121 ntntentndssffyslkkdltdltsveteklsfgangknvitsdtkglnfaketagtngd 180
QY 181 PRVHLNGIGSTLDTLLNTGATNTVNDVDEKRAASVKDVLNAGWNIKVGKPGTTA 240
DB 181 prvhlingigstltdlntgattntvndvdekkraasvkdvl nagwnikvgkpgtta 240
QY 241 SDNVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIREKDKGLVTGKKG 300
DB 241 sdnvdfvrttydveflsadtktttvnveskdngkrtvekigaktsvirekdkglvtgkkg 300
QY 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTMTTANGOTQADKPFETVTSKVTTFASGN 360
DB 301 gengstdegeglvtakevidavnkagwrmtmttangotqadkpfetvtskvttfasgn 360
QY 361 GTTATVSKDDQGNITVKYDYNVGDALNVQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420
DB 361 gttatvskddqgnitvkydyndvgdalnvqnsqwnldskavagssgkvisgnvpskg 420
QY 421 KMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
DB 421 kmdevtninagnnieitrngknidatsmtpqfssvslgagadaptlsdvdegalnvgsk 480
QY 481 DANKPVRTITNAPGVKEGDVTNVAQLKGVAQNLNNRINDVGNARAGIAQATATAGLAQA 540
DB 481 dankpvrtnnapgvkegdvtnvaqlkgvaqnl nndvgnaragiaqatataqlaqa 540
QY 541 YLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVIKGTASGNSRGHFGTSAVGQW 598
DB 541 ylpgksmmaigggtyrgeagyaigyssisdgtgnwvvikgtasgnsrghfgtsavgqw 598

RESULT 3

AA006177
ID AA006177 standard; Protein; 598 AA.

AC AA006177;

XX AA006177;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;

XX immunoreactive peptide.

OS Neisseria meningitidis.

XX W09031132-A1.

PN 24-JUN-1999.

PD 14-DEC-1998; 98WO-AU01031.

PF 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85794.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitis infections

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. CC The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

XX Sequence 598 AA;

Query Match 99.3%; Score 3021; DB 20; Length 598;

Best Local Similarity 99.3%; Pred. No. 1e-174;

Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKISRIIWNLSALNAWVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60

DB 1 mnkisirliwnsalnawvvyvseltrnhtkrasatvatvatltilfatvqanatdddlyle 60

QY 61 PVQRTAVLSFRSDKEGTEGTEDESNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120

DB 61 pvrqtavlsfrsdkegtegedsnwavyfdekrvlikagaitlkagdnlikikqntne 120

QY 121 NTNENTNDSSFTYSLKDLTDLTSLVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180

DB 121 ntntentndssffyslkkdltdltsveteklsfgangknvitsdtkglnfaketagtngd 180

QY 181 PRVHLNGIGSTLDTLLNTGATNTVNDVDEKRAASVKDVLNAGWNIKVGKPGTTA 240

DB 181 prvhlingigstltdlntgattntvndvdekkraasvkdvl nagwnikvgkpgtta 240

QY 241 SDNVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIREKDKGLVTGKKG 300

DB 241 sdnvdfvrttydveflsadtktttvnveskdngkrtvekigaktsvirekdkglvtgkkg 300

QY 301 GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTMTTANGOTQADKPFETVTSKVTTFASGN 360

DB 301 gengstdegeglvtakevidavnkagwrmtmttangotqadkpfetvtskvttfasgn 360

QY 361 GTTATVSKDDQGNITVKYDYNVGDALNVQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420

DB 361 gttatvskddqgnitvkydyndvgdalnvqnsqwnldskavagssgkvisgnvpskg 420

QY 421 KMDETVNIAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

DB 421 kmdevtninagnnieitrngknidatsmtpqfssvslgagadaptlsdvdegalnvgsk 480

QY 481 DANKPVRTITNAPGVKEGDVTNVAQLKGVAQNLNNRINDVGNARAGIAQATATAGLAQA 540

DB 481 dankpvrtnnapgvkegdvtnvaqlkgvaqnl nndvgnaragiaqatataqlaqa 540

QY 541 YLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVIKGTASGNSRGHFGTSAVGQW 598

DB 541 ylpgksmmaigggtyrgeagyaigyssisdgtgnwvvikgtasgnsrghfgtsavgqw 598

RESULT 4

AA006177
ID AA006177 standard; Protein; 598 AA.

AC AA006177;

XX AA006177;

DT 24-OCT-2001 (first entry)

DE N. meningitidis H15 surface antigen Nhma polypeptide sequence.

XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H15.
 XX FH Key Location/Qualifiers
 FT Region 1..50
 FT /label= C1
 FT /note= "Conserved region 1"
 FT Region 51..104
 FT /label= V1
 FT /note= "Variable region 1"
 FT Region 105..116
 FT /label= C2
 FT /note= "Conserved region 2"
 FT Region 117..130
 FT /label= V2
 FT /note= "Variable region 2"
 FT Region 131..194
 FT /label= C3
 FT /note= "Conserved region 3"
 FT Region 195..216
 FT /label= V3
 FT /note= "Variable region 3"
 FT Region 217..235
 FT /label= C4
 FT /note= "Conserved region 4"
 FT Region 236..242
 FT /label= V4
 FT /note= "Variable region 4"
 FT Region 243..598
 FT /label= C5
 FT /note= "Conserved region 5"
 XX WO200155182-A1.
 XX 02-AUG-2001.
 XX 25-JAN-2001; 2001WO-AU00069.
 XX 25-JAN-2000; 2000US-0177917.
 XX (UYQU) UNIV QUEENSLAND.
 XX Peak IRA, Jennings MP;
 XX WPI: 2001-488774/53.
 XX N-PSDB; AAS09167.
 XX New Nhha surface antigen polypeptides and polynucleotides from
 PT Neisseria meningitidis, useful in producing vaccines for treating or
 PT preventing broad spectrum of Neisseria meningitidis -
 XX Claim 9; Fig 1; 91pp; English.
 XX The present invention relates to the isolation of novel Neisseria
 CC meningitidis mutant polypeptides of the surface antigen Nhha
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
 CC characterised by deletions of non-conserved amino acids, particularly
 CC the deletion of variable regions. The deletion mutants are useful in
 CC diagnostics, therapeutic and prophylactic vaccines against a broader
 CC spectrum of N. meningitidis, and in designing and/or screening of
 CC medicaments. The mutant proteins when used as a vaccine can effectively
 CC immunise against a broader spectrum of N. meningitidis strains than
 CC would be expected from a corresponding wild-type surface antigen.
 CC The present sequence representing the wild type surface antigen Nhha
 CC from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequences
 CC (AAU0617-AAU06180) from 10 different N. meningitidis strains given in
 CC the present invention.
 XX Sequence 598 AA;

Query Match 99.3%; Score 3021; DB 22; Length 598;
 Best Local Similarity 99.3%; Pred. No. 1e-174;

Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLALLFATVQANATDDDDLYLE 60
 DB 1 mkiyriiwsalnawvvseltrnhtkrasatvatvatlatllfatvqanatdddlyle 60
 QY 61 PVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLRKAGAITLKGADNMLTKQNTNE 120
 DB 61 pvqrtavvlsfrsdegtgegtedsnwavyfdekrvlrkagaitlkagdnmlkikqntne 120
 QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
 DB 121 ntentndssftyslkkdltdltsveteklsfgangknvnitsdtkglnfaketagngd 180
 QY 181 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
 DB 181 ptvhlngigstltdtllntgattnvtndvtddekkraasvkdvlngwnikgvkpgtta 240
 QY 241 SDNVDFVRYTDTVEFLSADTKTTTNNVESKDNGKRTVEKIGAKTSVKEKDKLVTGKKG 300
 DB 241 sdnvdfvrytdtveflsadtktttnnveskdngkrtvekgikgktsvkekdglvtgkkg 300
 QY 301 GENGSSDTDEGEGLVTAKEVIDAVNKAGWRMKTITTTANGQTGOADKFETVTSCTKYTFASGN 360
 DB 301 dengsstdegeglvtakevidavnkagwrmttttangqtgoadkfetvtsctkytfasgn 360
 QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNOLNSGWNLDSKAVAGSSGKVIGSNVSPSKG 420
 DB 361 gttatvskddqgnitvkydvnvgdalnvnlqnswnldskavagssgkvigsnvpskg 420
 QY 421 KMDETVNINAGNNIEITRNGKNIDIIATSMTPQFSSVSLGAGADAPTLSVDEGALNVGSK 480
 DB 421 kmdetvninagnnieitrngknidiatsmtppqfssvslgagadaptilsvdegalnvgsk 480
 QY 481 DANKPVRIITNVAPGVKEGDTNVNAQLKGVAQNLRNNDVGNARAGIAQAIATAGLAQA 540
 DB 481 dankpvritnvapgvkegdvtnvaqlkgvaqnlrnnrdvgnaragialataglaqa 540
 QY 541 YLPKSMMAIGGGTYRGEAGYAIYSSISDTGNMVKGTASGNSRGHFGTSASVGYQW 598
 DB 541 ylpksmmaigggtyrgeagyaiyssi sdtgnmwkgtasgnsrghfgtasasvgyqw 598
 RESULT 5
 AAY23739
 ID AAY23739 standard; Protein; 594 AA.
 XX
 AC AAY23739;
 XX
 DT 08-SEP-1999 (first entry)
 XX
 DE A surface protein of Neisseria meningitidis.
 XX
 KW Surface protein; surface glycoprotein; infection; vaccine;
 KW immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9931132-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-AU01031.
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 PR 12-DEC-1997; 97GB-0026398.
 XX
 PA (ISIS-) ISIS INNOVATION LTD.
 PA (UYQU) UNIV QUEENSLAND.
 XX
 PI Jennings MP, Moxon ER, Peak IRA;
 XX
 DR WPI; 1999-418754/35.
 DR N-PSDB; AAX85791.


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XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1: Page 95-97; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;

Query Match          96.9%; Score 2948; DB 20; Length 594;
Best Local Similarity 97.3%; Pred. No. 2, 7e-170;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNAWVYSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkiyriiwnsalnawvvseiltnrhtrkasatvatavlatllfatvqanatdddddyle 60
QY 61 PVQRTAVVLSFRSDKRGCTGKTEGSDSNWAVYFDEKRVLKAGATYLLKAGDNLIKQNTNE 120
DB 61 pvqrtavvlsfrsdrgctgktdesnwavyfdekrvlikagaitlikagdnlikq---- 116
QY 121 NFNENINDSSFYSLKDLDTLSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 117 nfnenindssfyslkdldtltsveteklsfgangknvitsdtkglnfaketagctngd 176
QY 181 PTVHLNGIGSTLDTLLTNGATTNVTNDVDEKRAASVKDVLNAGWNIKVRPGTTA 240
DB 177 ptvhlingigstltdtlltngattntvndvndtdekkraasvkdvlnagwnikvpgttta 236
QY 241 SDNVDFVRYDVRFLSADTKTTTVNVEKDKGRTEVKIGAKTSVKEKDKGLVTGKSK 300
DB 237 sdnvdfvrydvrflsadtktttvnveskdngkktvkgigaktsvikekgdklvtgk 296
QY 301 GENGSTDEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKRETVTSGTKVTFASGN 360
DB 297 dengstdegeglvtakevidavnkgwrmtttangotgoadkretvtsgtkvtfasgk 356
QY 361 GTTATVSKDDQGNITVKYDVNVDALNVNQLNSGNWNLDSKAVAGSGKVIISGNVSPSKG 420
DB 357 gttatvskddqgnitvkdydvngdnlvnlqnsqwnldskavagsgkviisgnvpskg 416
QY 421 KNDFTVWINAGNIEITRNKKNIDTATSMTPQSFVSLGAGADAPPTLSVDDGALNVGSK 480
DB 417 kndftvinagnieitrngknidiatstmapqfssvslgagadapptlsvddgalnvsgk 476
QY 481 DANKPVRITNAPGVKGEVDVTNVAOLKGAQNLNDRIDNVNAGIQAQIATAGLAQA 540
DB 477 dnakpvrilcnvpgvkgegdvtnvaqlkgvaqlnlnrindvngnragieqatagilvga 536
QY 541 YLPKGSMAIGGTYRGEAGYAIQYSSISDGTGNWVIKGTASGNSRGHFTSAGVQW 598
DB 537 ylpkgsmaiggdtyrgeagyaigysissdgggnwiikgtasgnsrghfgasavgygw 594

RESULT 6
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX
AC AAU06179;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis Bz198 surface antigen Nhha polypeptide sequence.
```

Query Match 96.9%; Score 2948; DB 22; Length 594;
Best Local Similarity 97.3%; Pred. No. 2.7e-170;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNAAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnklyriiwsalnawvseltrnhkrasatvatvatlatllfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKAGDNLIKQNTNE 120
DB 61 pvqrtavvlsfrsdektegtegsdsnwavfyfdekrvllrkagaitlkagdnlikqntne 116

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 117 ntentndssftyslkkdltdltsveteklsfsgangknvitsdtkglnfaketagngd 176

QY 181 PTVHLNGIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNILKGVKPGTTA 240
DB 177 ptvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnilkgvkgpghta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSVKEKDGKLVTKGK 300
DB 237 sdnvdfvrtvdtveflsadtktttnnveskdngkrtvkegktsvkekdglvtgk 296

QY 301 GENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTNTTANGOTGQADKFEVTSCTKVTFASGN 360
DB 297 dengsstdegeglvtakevidavnkagwrmtnttangotgqadkfetvsgtnvtfasgk 356

QY 361 GTTATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVLISGNVSPSKG 420
DB 357 gttatvskddqgnitvdydvnvgdalnvnqlqnsqwnldskavagssgkvlsngvpskg 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOQSSVSLGAGADAPTLSVDDEGALNVGSK 480
DB 417 kmdetvinagnnieitrnkniidiatsmtppqssvslgagadaptsvdddegalnvg 476

QY 481 DANKPVRITNVAPGVKGGDVTNVAQLKGVQNLNNDVNDGNARAGIAOAIATAGLAQA 540
DB 477 dtnkpvrntnvapgvkggdvtnvvaqlkgvqnlndvndgnaraglaiaiataglvqa 536

QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDTGNMVIKGTASGNSRGRHFGTSASVGYQW 598
DB 537 ylpcksmmaigggtyrgeagayagysisdtgnmviikgtasgnsrgrhfgtsasvgyqw 594

RESULT 7

AAV23740
ID AAY23740 standard; Protein; 594 AA.

AC AAY23740;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;
immunoreactive peptide.

OS Neisseria meningitidis.

PN W09931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX

DR WPI; 1999-418754/35.
DR N-PSDB; AAX85792.

XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections

XX Claim 1; Page 100-101; 132pp; English.

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 594 AA;

Query Match 93.8%; Score 2852; DB 20; Length 594;
Best Local Similarity 94.6%; Pred. No. 1.7e-164;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNAAVWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnklyriiwsalnawvseltrnhkrasatvatvatlatllfatvqastdddlyle 60

QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKAGDNLIKQNTNE 120
DB 61 pvqrtavvlsfrsdektegtegsdsnwavfyfdekrvllrkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
DB 121 ntentndssftyslkkdltdltsveteklsfsgangknvitsdtkglnfaketagngd 176

QY 181 PTVHLNGIGSTLTDLTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNILKGVKPGTTA 240
DB 177 ptvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnilkgvkgpghta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSVKEKDGKLVTKGK 300
DB 237 sdnvdfvrtvdtveflsadtktttnnveskdngkrtvkegktsvkekdglvtgk 296

QY 301 GENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTNTTANGOTGQADKFEVTSCTKVTFASGN 360
DB 297 gendsstdegeglvtakevidavnkagwrmtnttangotgqadkfetvsgtnvtfasgk 356

QY 361 GTTATVSKDDQGNITVYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVLISGNVSPSKG 420
DB 357 gttatvskddqgnitvdydvnvgdalnvnqlqnsqwnldskavagssgkvlsngvpskg 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOQSSVSLGAGADAPTLSVDDEGALNVGSK 480
DB 417 kmdetvinagnnieitrnkniidiatsmtppqssvslgagadaptsvdddegalnvg 476

QY 481 DANKPVRITNVAPGVKGGDVTNVAQLKGVQNLNNDVNDGNARAGIAOAIATAGLAQA 540
DB 477 dtnkpvrntnvapgvkggdvtnvvaqlkgvqnlndvndgnaraglaiaiataglvqa 536

QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDTGNMVIKGTASGNSRGRHFGTSASVGYQW 598
DB 537 ylpcksmmaigggtyrgeagayagysisdtgnmviikgtasgnsrgrhfgtsasvgyqw 594

RESULT 8

AAV57044
ID AAY57044 standard; Protein; 594 AA.

XX AAY57044;

XX 21-FEB-2000 (first entry)

PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
PR (UYQU) UNIV QUEENSLAND.
XX
PA Peak IRA, Jennings MP;
XX
PI WPI: 2001-488774/53.
XX N-PSDB; AAS09164.
DR
DR New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PT
XX Claim 9; Fig 1; 91pp; English.
PS
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
XX Sequence 594 AA;
SQ

Query Match 93.8%; Score 2852; DB 22; Length 594;
Best Local Similarity 94.6%; Pred. No. 1.7e-164;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;
QY 1 MNKISRIWNSALNAWVVSLETRNHKRSATVATVATLTLFATVOANATDDDDLYLE 60
Db 1 mnkiyriwnsalnawvavseltrnhkkrasatvatavlatilfatvgastdddddlyle 60
QY 61 PVQRTAVVLSFRSKDEGTGEGEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
Db 61 pvqrtavvlsfrskdegtgekevledsnwgyfdkkgvtagtltlkagdnkikqntne 120
QY 121 NTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
Db 121 ntne----ssftyslkkdltltsvgtelksfsgangknvntsdtkglnfakktagntgd 176
QY 181 PTVHLNGIGSTLTDTLLTGATTTNNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTA 240
Db 177 ttvhlngigstltdlntgattnndvntdtddekkraasvkdvlngwnikgvkpgtta 236
QY 241 SDNYDVRTYDTVEFLSADTKTTTVNYESKDNKRTVEKIGAKTSVKEKDKGLVTGKGK 300
Db 237 sdnydvrtvdytveflsadtktttvnveskdngkrtvekvigaktsvkekgkltvgkdk 296
QY 301 GENGSSSTDEGEGLYTAKEVIDAVNKAQWRMKTMTTANGQTGQADRFETVTSCTKYTFASGN 360
Db 297 gendsstdekgeglvtakevidavnkagwrmtttangqtgqadrfetvtsctkynvtfasgk 356
QY 361 GTTATVSKDDOGNTVYKVDVNVGALNVQNLQNSGWNLDKAVAGSSGKVIISGNVSPSKG 420
Db 357 gttatvskddognitvnykvdvngvalnvqnlqnsqwnldskavagssgkvisgnvpspgk 416
QY 421 KMDETVINAGNNIEITRNKGNIDIAIATSMTPQPSVSIAGACADAPTLSVDDGALNVGSK 480
Db 417 kmdetvinagnnieitrnknidiaiaismtpqpsvsiagacadaptilsvddgalnvgsk 476

-QY 481 DANKPVRITNVAPGVKEGDVTNVQAQLKGVQNLNNRINDVNGNARAGTAAIATAGLAQA 540
Db 477 dankpvrtnvapgvkegdvtnvaqlkgvqnlnnhidnvdgnaragiagataglvqa 536
QY 541 YLPKSNMAIGGGTYRGEAGYAIGYSSISDFTGNVVKIKTAGSNGRHFCTASVYQW 598
Db 537 ylpkssmaigggtyrgeagyaigysisdsdgnwllktagsgnrgfhigasvgyqw 594
RESULT 10.
AAZ23743
ID AAZ23743 standard; Protein; 599 AA.
XX
AC AAZ23743;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-AI.
XX
PD 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI: 1999-418754/35.
DR N-PSDB; AAX85795.
DR
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 114-115; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 599 AA;
SQ

Query Match 92.8%; Score 2821.5; DB 20; Length 599;
Best Local Similarity 92.7%; Pred. No. 1.2e-162;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 1 MNKISRIWNSALNAWVVSLETRNHKRSATVATVATLTLFATVOANATD-DDDLYL 59
Db 1 mnkiyriwnsalnawvavseltrnhkkrasatvatavlatilfatvqanatdedeeel 60
QY 60 EPVORTAVVLSFRSKDEGTGEGEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119
Db 61 epvortavvlsfrskdegtgekestnawvfyfdekrvklagaitlkagdnkikqntn 120
QY 120 ENTNENTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
Db 121 kntnenndssftyslkkdltltsveteklsfgangknvntsdtkglnfaketagntng 180

Db 421 gkmdetvnnagnnietrnngknidiatmtptqfssvslgagadaptslsvddkgalnvg 480
QY 480 KDANKPVRITNVAPGVKEGSDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAATAGLAQ 539
|||||
Db 481 kdankpvrictnvagpkvegdtvnaqlkgvaqlnnrldnvdgnaragiataglvq 540
QY 540 AYLPKSKMMAIGGTYRGEAGYAGYSSISDGTGNWVKGVTASGNSRCHFGTSASVGYQW 598
|||||
Db 541 ayipgksmmaigggtyrgeagyaigyssisdgggnwliikgtasgnsrghfgasasvgyq 599

RESULT 12

AAV57045

ID AAY57045 standard; Protein: 591 AA.

XX AC AAY57045;

XX DT 21-FEB-2000 (first entry)

XX DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

XX KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;

XX KW infection; treatment; prevent; antibacterial drug.

XX OS Neisseria meningitidis.

XX FH Key Location/Qualifiers

FT Misc-difference 90 /note= "Encoded by AAT"

FT Misc-difference 92 /note= "Encoded by GAT"

FT Misc-difference 98 /note= "Encoded by AAC"

FT Misc-difference 108 /note= "Encoded by AATC"

FT Misc-difference 123 /note= "Encoded by ACA"

FT Misc-difference 269 /note= "Encoded by AAA"

FT Misc-difference 389 /note= "Encoded by CGT"

XX W09958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI; 2000-053103/04.

XX N-PSDB; AA239865.

XX New polypeptide from neisseria meningitidis useful for diagnosis,

XX treatment or prevention of bacterial infections in mammal

XX Claim 4; Fig 2; 74pp; English.

XX This is the Neisseria meningitidis BASB029 amino acid sequence from

XX serogroup B strain H44/76. The BASB029 protein is homologous to the

XX Haemophilus influenzae surface fibril (HSF) protein. The invention

XX relates to BASB029 polynucleotide sequences (AA239864-239865) and

XX polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.

XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria

XX meningitidis infection in a mammal. Compositions containing BASB029

XX polynucleotides and polypeptides are useful for generating an immune

XX response in an animal. A therapeutic composition comprising an antibody

XX directed against BASB029 is useful in treating humans with Neisseria

XX meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX Sequence 591 AA;

Query Match 89.8%; Score 2732.5; DB 21; Length 591;
Best Local Similarity 91.4%; Pred. No. 2.8e-157;
Matches 550; Conservative 8; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNKISRIIWNALNAWVYSELTRNHTKRASATVATVATLTLFATVOANATD--DDDL 57
|||||
Db 1 mnkiyriiwnsalnawvavseltrnhtkrasatvktavlatllfatvqasannee 60
QY 58 YLEPVORTAVVLSFRSDKEGTGEKGT-EDSNNAVYFDEKRVLKAGAITLKAGDNLIKIK 116
|||
Db 61 yldpvqrtvavlivnsdkegtgekeveedsnwavyfdekgvitareitlkagdnlikik 120
QY 117 NTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAG 176
|||
Db 121 -----ngsnftyyslkkdltdltsvteklslfsangknvniitdtkglnfaketag 170
QY 177 TNGDPTVHLNGIGSTLTDLTLNTGATNTVNDVNDVDEKRAASVKDVLNAGNIIKGVKP 236
|||||
Db 171 tngdptvhlngigstltdlntgattntvndvndvdekkraasvkdvlalnagniikgvkp 230
QY 237 GTTASDNVDFVRYDYTVFELSDTKTTTVNVESKDNGKRTVEVIGAKTSVIKEDGKLVT 296
|||||
Db 231 gttdsnvdfvrydytveflsadtktttvnevskdngkrttevkigaktsvikekdgklvt 290
QY 297 GKKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFTFTVSGTKVTF 356
|||||
Db 291 gkdkgengsstdegeglvtakevidavnkagwrmktttangtqgqdkfetvsgtntvf 350
QY 357 ASGNITATVSKDDQGNITVYKDYVNVGDALNVQLNSGWNLDKAVAGSGKVISGNVS 416
|||||
Db 351 asgnttatvskddqgnitvmydvnvgdalnvnlqngswnldskavagsgkvvisgnvs 410
QY 417 PSKGKMDETVINAGNNIETRNKKNIDIATSMTPQFSSVSLGAGADAPTLSVDEGALN 476
|||||
Db 411 pskgkmdetvinagnnietrnknidiatmtptqfssvslgagadaptslsvdgd-aln 469
QY 477 VGSKDANKPVRITNVAPGVKEGDTNVNVAQLKGVAQNLNNRIDNVGNARAGIAQAATAG 536
|||||
Db 470 vgskkdnkpvrictnvapgvkegdvtnvaqlkgvaqlnnrldnvdgnaragiatag 529
QY 537 LAQAYLPKSKMMAIGGTYRGEAGYAGYSSISDGTGNWVKGVTASGNSRCHFGTSASVGY 596
|||||
Db 530 lvdaylpgksmmaigggtyrgeagyaigyssisdgggnwliikgtasgnsrghfgasasvgy 589
QY 597 QW 598
Db 590 qw 591

RESULT 13

AAV27202

ID AAY27202 standard; Protein: 591 AA.

XX AC AAY27202;

XX DT 24-SEP-1999 (first entry)

XX DE Amino acid sequence of N. meningitidis protein ORF40-1.

XX KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;

KW bacterial infection; treatment.

OS Neisseria meningitidis.

PN WO9936544-A2.

XX 22-JUL-1999.

XX 14-JAN-1999; 99WO-IB00103.

XX 09-OCT-1998; 98GB-0022143.

PR 14-JAN-1998; 98GB-0000760.

PR 01-SEP-1998; 98GB-0019015.

XX (CHIR-) CHIRON SPA.

PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;

XX WPI; 1999-444400/37.

DR N-PSDB; AAX99124.

XX New protein and its nucleotide sequence, useful in vaccines or

PT diagnostic compositions for treating and/or preventing Neisseria

PT meningitidis infections

XX Claim 1; Page 62; 123pp; English.

PS The invention provides proteins (AAY27201-245) from Neisseria

CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)

CC encoding the proteins. Compositions comprising the protein, nucleic acid

CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a

CC vaccine composition or a diagnostic composition. The composition is also

CC useful for treating or preventing an infection due to Neisseria

CC bacteria, especially Neisseria meningitidis.

XX Sequence 591 AA;

SQ

Query Match 89.3%; Score 2716.5; DB 20; Length 591;
Best Local Similarity 90.7%; Pred. No. 2.6e-156;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57

DB 1 mnkiyriiwnsalnawvyseltrnhtkrasatvktavltilfatvqasanneeedl 60

QY 58 YLEPQVORTAVLSFRSDKEGTGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIQ 116

DB 61 yldpvqrvavliivnsdkegtgekekeveensdwavyfnekglvtareitlkagdnlikq 120

QY 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAG 176

DB 121 -----ngnfyslkkdltltsvgteklsfsgangknvntsdtkglnfaketag 170

QY 177 TGGDPTVHLNGIGSTLTLTLLNGATNTVNDVDEKRAASVDRVLDVNLGNWIKGVKP 236

DB 171 tngdptvhlngigstltiltngatntvndvdekkraasvdkvlnagwnikgvkp 230

QY 237 GTTASNDVFRTYDVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVIEKDGKLVY 296

DB 231 gttasndvfvrtvdtvelfsadtktttvnveskdngkktvekgaktsviekdgklvt 290

QY 297 GKKGNGSGSTDEGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFTVTSGTKVTF 356

DB 291 gkdkgngsgstdegeglvtakevdaivnkgwrmtttangqgqadkfetvtsgtnvtf 350

QY 357 ASGNGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGWNLDLSKAVAGSSGKVISGNYS 416

DB 351 asgngtatvskddqgnitvymvngdnlvnlqnsqwnldskavagssgkvisgnys 410

QY 417 PSKGMDEVTNINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDDREALN 476

DB 411 pskgmdetvniagnnieitrngknidiatmtpqfssvslgagadaptlsvdgd-ain 469

QY 477 VGSKDANKPVRITNVAPGVKEGDTNVQAQLKGVAQNLRNDRIDNVGNARAGIAQAIATAG 536
DB 470 vgskdankpvrntnvpagvkegdvtnvaqlkgvaqnlrdrdnvgnaragiatatag 529
QY 537 LAQAYLPGKSMMAIGGTYRGEGAGYAIGYSSISDTCNNWIKGTASGNSRGHFTSASVGY 596
DB 530 lvqaylpgkmmaiggytyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgy 589
QY 597 QW 598
DB 590 qw 591

RESULT 14

AAY23746

ID AAY23746 standard; Protein; 591 AA.

XX AAY23746;

XX AC AAY23746;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

OS Neisseria meningitidis.

XX WO9931132-A1.

PN 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85798.

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 127-128; 132pp; English.

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX Sequence 591 AA;

SQ

Query Match 89.3%; Score 2716.5; DB 20; Length 591;
Best Local Similarity 90.7%; Pred. No. 2.6e-156;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57

DB 1 mnkiyriiwnsalnawvyseltrnhtkrasatvktavltilfatvqasanneeedl 60

QY 58 YLEPQVORTAVLSFRSDKEGTGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIQ 116

DB 61 yldpvqrvavliivnsdkegtgekekeveensdwavyfnekglvtareitlkagdnlikq 120

FT		/label= C3	
FT	Region	/note= "Conserved region 3"	
FT		189..210	
FT		/label= V3	
FT		/note= "Variable region 3"	
FT	Region	211..229	
FT		/label= C4	
FT	Region	230..236	
FT		/label= V4	
FT		/note= "Variable region 4"	
FT	Region	237..591	
FT		/label= C5	
FT		/note= "Conserved region 5"	
XX	WO200155182-A1.		
PX	02-AUG-2001.		
XX	25-JAN-2001; 2001WO-AU000069.		
PF	25-JAN-2000; 2000US-O177917.		
XX	(UYQU) UNIV QUEENSLAND.		
PA	Peak IRA, Jennings MP;		
XX	WPI: 2001-488774/53.		
PI	N-PSDB; AAS09161.		
XX	New Nhha surface antigen polypeptides and polynucleotides from		
PT	Neisseria meningitidis, useful in producing vaccines for treating or		
PT	preventing broad spectrum of Neisseria meningitidis -		
XX	Claim 9; Fig 1; 91pp; English.		
CC	The present invention relates to the isolation of novel Neisseria		
CC	meningitidis mutant polypeptides of the surface antigen Nhha		
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are		
CC	characterised by deletions of non-conserved amino acids, particularly		
CC	the deletion of variable regions. The deletion mutants are useful in		
CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
CC	spectrum of N. meningitidis, and in designing and/or screening of		
CC	medicaments. The mutant proteins when used as a vaccine can effectively		
CC	immunise against a broader spectrum of N. meningitidis strains than		
CC	would be expected from a corresponding wild-type surface antigen.		
CC	The present sequence representing the wild type surface antigen Nhha		
CC	from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences		
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in		
XX	the present invention.		
SQ	Sequence 591 AA;		
Query Watch 89.3%; Score 2716.5; DB 22; Length 591;			
Best Local Similarity 90.7%; Pred. No. 2.6e-156;			
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;			
QY	1	MNKISRIIWNLSALNAVVVVSELFRNHTRKRASATVAVTATLTLFATVQANATD---DDDL 57	
Db	1	mnlklyrlwnslanawvvvselrlnrkrtkrasatvtktavtatlflfatvqasanneeqeel 60	
QY	58	YLEPQVORTAVVLFSRDSKEGTGEKGETED--SNNAVVFDEKRVLRKAGAITILKAGDNLIKIQ 116	
Db	61	yldpqvrtvaavlinsdkegtgekkeveensdwavyfnekgvitareitlkagdnlikiq 120	
QY	117	NTNENTNNTNDSSFYSLKKKLDLTDTLSVTEKLSPGANGKNVNITSDTKGLNFAKETAG 176	
Db	121	-----ngcnfyfsllkkdditdtstvgteklsfsangnkvnitsdtktglnfaketag 170	
QY	177	TNGDPVTVHLNGIGSTLTDTLLNTGATTNVNTDNVTDDEKKRAASVKDVLNAGNNIKGVKP 236	
Db	171	tngdptvhlngigstltdtlilnlgattnv cndnvtdekkraasvkdvlnagwnikgvkp 230	

QY 237 GTTASDNVDFVRTYDTVEPLSADFTTTVNVESKONGKRTVEKIGAKTSVKEKDGKLV 296
 Db |||||
 QY 231 gttasdnvdfvrtvdtveplsadtktttnveskngkktvkgaktvikekgklvt 290
 Db |||||
 QY 297 GKGKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTTTTANGOTGOADKFETVTSKTKVTF 356
 Db |||||
 QY 291 gkdkgengsstdegeglvtakevidavnkagwrmttttanggtgqadkfetvtsgtntvf 350
 Db |||||
 QY 357 ASGNCTTATVSKDDGNITVKYDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVS 416
 Db |||||
 QY 351 asgkgttatvskddgnitvmydvnvgdalnvnglqnsqwnldskavagssgkvvisgnvs 410
 Db |||||
 QY 417 PSKGMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDDEGALN 476
 Db |||||
 QY 411 pskgmdetvniagnnieitrngknidiatsmtptqfssvslgagadaptilsvdgd-aln 469
 Db |||||
 QY 477 VGSKDANKPVRITNVAPGVKEGDVTNVAOLKGVAQNLRNDRIDNVGNARAGIAQAIATAG 536
 Db |||||
 QY 470 vgskkdnkpvr itnvapgvkegdvtnvaqlkgvaqnlrdrdnvgnaragialatag 529
 Db |||||
 QY 537 LAQAYLPCKSMMAIGGTYRGEAGYAGYSSISDGTGNWVIKGTASGNSRGHFGTSASVGY 596
 Db |||||
 QY 530 lvqaylpcksmmaigggtyrgeagyalgyssisdggnwlikgtasgnsrghfgasasvgy 589
 Db |||||
 QY 597 QW 598
 Db |||||
 QY 590 qw 591

Search completed: July 3, 2002, 08:36:23
 Job time: 319 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:08 ; Search time 39.66 Seconds
(without alignments)
368.293 Million cell updates/sec

Title: US-09-771-382-8
Perfect score: 3042
Sequence: 1 MNKISRIIWNLSALNAWVVS.....TASGNSRGHGTASVGYQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pap.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pap.*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	3042	100.0	598	US-09-377-155-5	Sequence 5, Appli
2	3042	100.0	598	US-09-669-974-5	Sequence 5, Appli
3	3021	99.3	598	US-09-377-155-13	Sequence 13, Appl
4	3021	99.3	598	US-09-669-974-13	Sequence 13, Appl
5	2948	96.9	594	US-09-377-155-7	Sequence 7, Appli
6	2948	96.9	594	US-09-669-974-7	Sequence 7, Appli
7	2852	93.8	594	US-09-377-155-9	Sequence 9, Appli
8	2852	93.8	594	US-09-669-974-9	Sequence 9, Appli
9	2821.5	92.8	599	US-09-377-155-15	Sequence 15, Appl
10	2821.5	92.8	599	US-09-669-974-15	Sequence 15, Appl
11	2716.5	89.3	591	US-09-377-155-21	Sequence 21, Appl
12	2716.5	89.3	591	US-09-669-974-21	Sequence 21, Appl
13	2709	89.1	592	US-09-377-155-2	Sequence 2, Appli
14	2709	89.1	592	US-09-669-974-2	Sequence 2, Appli
15	2705.5	88.9	591	US-09-377-155-11	Sequence 11, Appl
16	2705.5	88.9	591	US-09-669-974-11	Sequence 11, Appl
17	2658	87.4	592	US-09-377-155-17	Sequence 17, Appl
18	2658	87.4	592	US-09-669-974-17	Sequence 17, Appl
19	2616.5	86.0	589	US-09-377-155-19	Sequence 19, Appl
20	2616.5	86.0	589	US-09-669-974-19	Sequence 19, Appl
21	1312.5	43.1	2353	US-09-377-155-33	Sequence 33, Appl
22	1312.5	43.1	2353	US-08-913-942-4	Sequence 4, Appli
23	1312.5	43.1	2353	US-09-669-974-33	Sequence 33, Appl
24	1311.5	43.1	2354	US-09-268-347-47	Sequence 47, Appl
25	1286.5	42.3	2411	US-09-268-347-36	Sequence 36, Appl
26	1245	40.9	607	US-08-409-995-6	Sequence 6, Appli
27	1245	40.9	607	US-08-685-467-6	Sequence 6, Appli

28	1245	40.9	607	4	US-08-913-942-6	Sequence 6, Appli
29	1245	40.9	1912	1	US-08-409-995-4	Sequence 4, Appli
30	1245	40.9	1912	3	US-08-685-467-4	Sequence 4, Appli
31	1066	35.0	1094	4	US-09-268-347-32	Sequence 32, Appl
32	1054	34.6	1098	1	US-08-409-995-2	Sequence 2, Appli
33	1054	34.6	1098	3	US-08-685-467-2	Sequence 2, Appli
34	1054	34.6	1098	4	US-09-377-155-32	Sequence 32, Appli
35	1054	34.6	1098	4	US-08-913-942-2	Sequence 2, Appli
36	1054	34.6	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1054	34.6	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1040	34.2	658	1	US-08-409-995-5	Sequence 5, Appli
39	1040	34.2	658	3	US-08-685-467-5	Sequence 5, Appli
40	1040	34.2	658	4	US-08-913-942-5	Sequence 5, Appli
41	1004.5	33.0	679	4	US-08-913-942-15	Sequence 15, Appl
42	1004.5	33.0	679	4	US-09-268-347-26	Sequence 26, Appl
43	762	25.0	1002	4	US-09-268-347-24	Sequence 24, Appl
44	753	24.8	1004	4	US-09-268-347-30	Sequence 30, Appl
45	703	23.1	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match	100.0%	Score 3042;	DB 4;	Length 598;
Best Local Similarity	100.0%;	Pred. No. 4.5e-239;		
Matches 598;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNKISRIIWNLSALNAWVVS	ELTRNHTKRASATVAVLATLLFATVQANATDDDLYLE	60
Db	1	MNKISRIIWNLSALNAWVVS	ELTRNHTKRASATVAVLATLLFATVQANATDDDLYLE	60
QY	61	PVORTAVLSFRSDKEGTEGSDSNNAVYFEDRRVLKAGAITLKAGNLKIKONTNE	120	
Db	61	PVORTAVLSFRSDKEGTEGSDSNNAVYFEDRRVLKAGAITLKAGNLKIKONTNE	120	
QY	121	NTNENTNDSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD	180	
Db	121	NTNENTNDSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD	180	
QY	181	PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA	240	
Db	181	PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA	240	
QY	241	SDNVDFRVYDVEFVSADTKTTTVNVESKDNKRTVEKIGAKTSVIKEKDKGLVTGKKG	300	
Db	241	SDNVDFRVYDVEFVSADTKTTTVNVESKDNKRTVEKIGAKTSVIKEKDKGLVTGKKG	300	
QY	301	GENGSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGQTQADKFFETVTSKTVTFASGN	360	

Db 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420
Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420
QY 421 KMDETVINAGNNEITRNKGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
Db 421 KMDETVINAGNNEITRNKGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
QY 481 DANKPVRITNVAPGVKSGDVTNVQALKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
Db 481 DANKPVRITNVAPGVKSGDVTNVQALKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
QY 541 YLPCKSMMAIGGGTYRGEGAGYAGYSSISDTGNVWIKGTASGNSRGHFGTSASVGYOW 598
Db 541 YLPCKSMMAIGGGTYRGEGAGYAGYSSISDTGNVWIKGTASGNSRGHFGTSASVGYOW 598

RESULT 2

US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match 100.0%; Score 3042; DB 4; Length 598;
Best Local Similarity 100.0%; Pred. No. 4.5e-239;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLIKQNTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
QY 181 PTVHLNIGISTLTDLTLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
Db 181 PTVHLNIGISTLTDLTLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
QY 241 SDNVDFVRTYDVEFLSADTKTTTVNYESKDNKRGKTEVKIGAKTSVKEKDKGLVTGKGK 300
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNYESKDNKRGKTEVKIGAKTSVKEKDKGLVTGKGK 300
QY 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360
Db 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360

Db 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420
Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420
QY 421 KMDETVINAGNNEITRNKGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
Db 421 KMDETVINAGNNEITRNKGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
QY 481 DANKPVRITNVAPGVKSGDVTNVQALKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
Db 481 DANKPVRITNVAPGVKSGDVTNVQALKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
QY 541 YLPCKSMMAIGGGTYRGEGAGYAGYSSISDTGNVWIKGTASGNSRGHFGTSASVGYOW 598
Db 541 YLPCKSMMAIGGGTYRGEGAGYAGYSSISDTGNVWIKGTASGNSRGHFGTSASVGYOW 598

RESULT 3

US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 99.3%; Score 3021; DB 4; Length 598;
Best Local Similarity 99.3%; Pred. No. 2.3e-237;
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLIKQNTNE 120
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
QY 181 PTVHLNIGISTLTDLTLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
Db 181 PTVHLNIGISTLTDLTLNTGATTNVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240
QY 241 SDNVDFVRTYDVEFLSADTKTTTVNYESKDNKRGKTEVKIGAKTSVKEKDKGLVTGKGK 300
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNYESKDNKRGKTEVKIGAKTSVKEKDKGLVTGKGK 300
QY 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360
Db 301 GENGSSDEGEGLTAKEVIDAVNKAGRMKMTTANGOTGOADKFETVTSCTKVTFFASGN 360
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420

Query Match	99.3%; Score 3021; DB 4; Length 598;
Best Local Similarity	99.3%; Pred. No. 2.3e-237;
Matches 594; Conservative	1; Mismatches 3; Indels 0; Gaps 0;

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Db	1	MNKYRIIWSALNANVVVSELTRNHHKRSATVATVATLTLFPATVQANATDDDDLYLE	60
Qy	61	PVQRTAVVLFSRDKEGTGEKGEDSNWVYFDEKRVKLKAGATLKGADNLKIKQNTNE	120
Db	61	PVQRTAVVLFSRDKEGTGEKGEDSNWVYFDEKRVKLKAGATLKGADNLKIKQNTNE	120
Qy	121	NTNENTNDSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	180
Db	121	NTNENTNDSFTYSLKKDLTDLTSTVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	180
Qy	181	PTVHLNGIGSTLTDTLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNTKGVKPGTTA	240
Db	181	PTVHLNGIGSTLTDTLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNTKGVKPGTTA	240
Qy	241	SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGKRTVEVIGAKTSVTEKDGKLVTCGK	300
Db	241	SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGKRTVEVIGAKTSVTEKDGKLVTCGK	300
Qy	301	GENGSSTDEBGLVTAKEVIDAVNKAQRMKTTTTANGOTGQADKFETVTSCTKVTFAASN	360
Db	301	DENGSSSTDEBGLVTAKEVIDAVNKAQRMKTTTTANGOTGQADKFETVTSCTKVTFAASN	360
Qy	361	GTTATFVSKDDGNTTVTKYDVNVGDALVNLQNSGWNLDKSAVAGSGSKVTSIGNVPSKG	420

Query Match	96.9%	Score 2948;	DB 4;	Length 594;	
Best Local Similarity	97.3%;	Pred. No. 2e-231;			
Matches 582;	Conservative	2;	Mismatches 10;	Indels 4;	Gaps 1;
Qy	1	MNKISRIWNSALNAWVVVSELTRNHTKRASATVATAVLATLTLFATVOANATDDDDLYLE	60		
Db	1	MNKIYRIWNSALNAWVVVSELTFENHTKRASATVATAVLATLTLFATVOANATDDDDLYLE	60		
Qy	61	PVQRTAVVLFSRDSKEGTGKEGTEDSNWAVYFDEKRVLRKAGATITLKAGONLKITQWNE	120		
Db	61	PVQRTAVVLFSRDSKEGTGKEGTEDSNWAVYFDEKRVLRKAGATITLKAGONLKITQ----	116		
Qy	121	NTNENTNDSFYSLLKKDLTDLTSVETEKLSFGANGKNKVNITSDTKGLNFAKETAGTNGD	180		
Db	117	NTNENTNDSFYSLLKKDLTDLTSVETEKLSFGANGKNKVNITSDTKGLNFAKETAGTNGD	176		
Qy	181	PTVHLNGIGSTLDTPLTNTGATTNVTDNDVTDDEKKRAASVKDVLNAGWNIKGVPQTGA	240		
Db	177	PTVHLNGIGSTLDTPLTNTGATTNVTDNDVTDDEKKRAASVKDVLNAGWNIKGVPQTGA	236		
Qy	241	SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKRTVEKIGAKTSVIREKDGKLVTCGK	300		
Db	237	SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKRTVEKIGAKTSVIREKDGKLVTCGK	296		
Qy	301	GENGSSTDECEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSGTKVFASGN	360		
Db	297	DENGSSSTDECEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFASGK	356		
Qy	361	GTTATVSKDDOGNTIVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSK	420		
Db	357	GTTATVSKDDOGNTIVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSK	416		
Qy	421	KMDETVINAGNNIEITIRNGKNIDIASMTPOQFSVSILGACADAPTLLSVDDGALNVGSK	480		

Db 417 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476
QY 481 DANKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
Db 477 DTNKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNDVNDGNARAGTAQAIAIATAGLVQA 536
QY 541 YLPCKSMAAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 598
Db 537 YLPCKSMAAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 594

RESULT 6
US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 96.98; Score 2948; DB 4; Length 594;
Best Local Similarity 97.38; Pred. No. 2e-231;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;
QY 1 MNKISRIIWSALNANVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNANVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 116
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180
Db 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 176
QY 181 PTVHLNGIGSLTDLTLNLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240
Db 177 PTVHLNGIGSLTDLTLNLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236
QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVKEKDKLVTKGK 300
Db 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVKEKDKLVTKGK 296
QY 301 GENSSSTDEGGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSCTKVTFASGN 360
Db 297 DEKSSSTDEGGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSCTKVTFASGN 356
QY 361 GTTATVSKDDOGNTTVKYDYNVGDALNVQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDOGNTTVKYDYNVGDALNVQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 421 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
Db 417 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476

Db 417 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476
QY 481 DANKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540
Db 477 DTNKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNDVNDGNARAGTAQAIAIATAGLVQA 536
QY 541 YLPCKSMAAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 598
Db 537 YLPCKSMAAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 594

RESULT 7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

Query Match 93.8%; Score 2852; DB 4; Length 594;
Best Local Similarity 94.6%; Pred. No. 1.2e-223;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;
QY 1 MNKISRIIWSALNANVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNANVWVSELTRNHTKRASATVATAVLATLFLFATVQASTDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
Db 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 180
Db 121 NTNA----SSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD 176
QY 181 PTVHLNGIGSLTDLTLNLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240
Db 177 PTVHLNGIGSLTDLTLNLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236
QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVKEKDKLVTKGK 300
Db 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKNGRTEVKIGAKTSVKEKDKLVTKGK 296
QY 301 GENSSSTDEGGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSCTKVTFASGN 360
Db 297 GENSSSTDEGGLVTAKEVIDAVNKAGWRMKTNTTANGOTGOADKFEVTSCTKVTFASGN 356
QY 361 GTTATVSKDDOGNTTVKYDYNVGDALNVQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDOGNTTVKYDYNVGDALNVQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 421 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
Db 417 KMDFTVINAGNNEITRNNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476
QY 481 DANKPVRITNVAPGVKEGDTNVAQLKGVAQNLRNDVNDGNARAGTAQAIAIATAGLAQA 540

Db 477 DANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 536
QY 541 YLPGKSMAIGGTYRGEAGYAIGYSSISDTGNWVTKGTASGNSRGHFGTSAVGYQW 598
Db 537 YLPGKSMAIGGTYRGEAGYAIGYSSISDTGGNWIITKGTASGNSRGHFGASASVGYQW 594

RESULT 8

US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 93.8%; Score 2852; DB 4; Length 594;
Best Local Similarity 94.6%; Pred. No. 1.2e-223;
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MKKISRIIWNLSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60
Db 1 MKKIYRIIWNLSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60

QY 61 PVORTAVLSFRSDGEGTGEKEDTSNWAYVFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVORTAVLSFRSDGEGTGEKEDTSNWAYVFDEKRVLKAGAITLKAGDNLKIKONTNE 120

QY 121 NTNENTNDSSTYSLLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNGD 180
Db 121 NTNA----SSFTYSLKKDLTDLTSVETEKLSFGANSKNVNIITSDTKGLNFAKTAETNGD 176

QY 181 PTVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
Db 177 TTVVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNIKGVKPGTTA 236

QY 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVKEKDKGLVTGKG 300
Db 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVKEKDKGLVTGKDK 296

QY 301 GENGSTDEGELVTAKEVIDAVNKGWRMKTITANGOTGQADKFTVTSGTKVTFASGN 360
Db 297 GENDSTDKGELVTAKEVIDAVNKGWRMKTITANGOTGQADKFTVTSGTNVTFASGK 356

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKG 420
Db 357 GTTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSKG 416

QY 421 KMDETVNIAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 480
Db 417 KMDETVNIAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 476

QY 481 DANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 540
Db 481 DANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 540

Db 477 DANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 536
QY 541 YLPGKSMAIGGTYRGEAGYAIGYSSISDTGNWVTKGTASGNSRGHFGTSAVGYQW 598
Db 537 YLPGKSMAIGGTYRGEAGYAIGYSSISDTGGNWIITKGTASGNSRGHFGASASVGYQW 594

RESULT 9

US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 92.8%; Score 2821.5; DB 4; Length 599;
Best Local Similarity 92.7%; Pred. No. 3.8e-221;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 1 MKKISRIIWNLSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL 59
Db 1 MKKIYRIIWNLSALNAWVYSELTRNHTKRASATVATAVLATLLFATVQANATDEDEEEL 60

QY 60 EPQORTAVVLSFRSDGEGTGEKEDTSNWAYVFDEKRVLKAGAITLKAGDNLKIKONTN 119
Db 61 EPVRSALVQLFMIDKEGNESTGICWSIYVDNHNHTLHGATVTLKAGDNLKIKONTN 120

QY 120 EYTNENTNDSSTYSLLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 179
Db 121 KNTNENTNDSSTYSLLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180

QY 180 DPTVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNIKGVKPGTT 239
Db 181 DPTVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNIKGVKPGTT 240

QY 240 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVKEKDKGLVTGKG 299
Db 241 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDKNGKRTVEKIGAKTSVKEKDKGLVTGKG 300

QY 300 KGENGSTDEGELVTAKEVIDAVNKGWRMKTITANGOTGQADKFTVTSGTKVTFASG 359
Db 301 KGENGSTDEGELVTAKEVIDAVNKGWRMKTITANGOTGQADKFTVTSGTNVTFASG 360

QY 360 NGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 419
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVSPSK 420

QY 420 KMDETVNIAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 479
Db 421 KMDETVNIAGNNIETTRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 480

QY 480 KDKANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 539
Db 481 KDKANKPVRITNAPGVKEGDTVNTVAQLKGVAQNLNHNIDNVNVDGNARAGIAQAATATAGLVA 540

QY 540 AYLPKGSMAIGGTYRGEAGYAIGYSSISDTGNWVTKGTASGNSRGHFGTSAVGYQW 598

Db 530 GLVQAVLPGRSMNAIGGTYRGEAGYAIGYSSISDGGNMIKGTASGNSRGHFGASAYG 589
QY 596 YQW 598
Db 590 YQW 592

Query Match	89.1%	Score	2709;	DB	4;	Length	592;
Best Local Similarity	90.4%	Pred.	No. 5.4e-212;				
Matches	545;	Conservative	12;	Mismatches	30;	Indels	16;
Gaps							
4;							
Qy	1	MNKISRIIWSALNAWVVVSELTRNHTKRASATVATATLALLFATVOANATDD---DD	56				
Db	1	MNKYRIIWSALNAWVVVSELTRNHTKRASATVKTAVLATLLFATVOASANNERPRKKD	60				
Qy	57	LYLEPVORTAVVLSFRDSKCEGTGSKEGTED--SNWAVFDERRVLKAGAITLUKAGDNLKIK	115				
Db	61	LYLDPVORTAVVLVNSDKCEGTGGEKEKVEENSDWAVFNEKGVLTARITLUKAGDNLKIK	120				
Qy	116	QNTNENTNENTNSSFYSLSLKKDLTDLTTSVTEKLSFGANGKNVITSDTKGLNFAKETA	175				
Db	121	Q-----NGTNFYLSLKKDLTDLTTSVTEKLSFGANGKNVITSDTKGLNFAKETA	170				
Qy	176	GTNGDPTVHLNGIGSTLDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNKIGVK	235				
Db	171	GTNGDPTVHLNGIGSTLDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNKIGVK	230				
Qy	236	PGTTASDNVDFVRYDVFELFADTKTTTVNVESKDNGKRTVEVIGAKTSVIEKDKGKLV	295				
Db	231	PGTTASDNVDFVRYDVFELFADTKTTTVNVESKDNGKRTVEVIGAKTSVIEKDKGKLV	290				
Qy	296	TGKGKGENGSSTDEGEGVLTAKEVIDAVNKGWRMKTITANGQTQOADKFETVTSGETVT	355				
Db	291	TGRDKGENGSSTDEGEGVLTAKEVIDAVNKGWRMKTITANGQTQOADKFETVTSGETVT	350				
Qy	356	FASNGGTATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV	415				
Db	351	FASGKGTTATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV	410				
Qy	416	SPSKGKDEFTVINAGNNIETTRNGKNDIATSMTPQFSSVSLGAGADAPTLTSDVDEGAL	475				
Db	411	SPSKGKDEFTVINAGNNIETTRNGKNDIATSMTPQFSSVSLGAGADAPTLTSDVGD--AL	469				
Qy	476	NVSGSKDANKPVRIITNVPAGVKEGDTVINVAQLKGVQAQLNNRINDVGNARAGIAQATATA	535				

Db	470	NVCSKKDKPVRITNVAPGVKGDVTNVAQLKCGVAQNLNRRINDNVQGNARAGTAQAIA	529
Qy	536	GLAQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDTCNNVIKCTASGNSRGHFGTSA	595
Db	530	GLYQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDTCNNVIKCTASGNSRGHFGAS	589
Qy	596	YQW	598
Db	590	YQW	592

Query Match	88.9%	Score	2705.5	DB	4	Length	591
Best Local Similarity	90.4%	Pred. No.	9.9e-212				
Matches	544	Conservative	14	Mismatches	29	Indels	15
Gaps	4						
QY	1	MNKSIRLIWNSALNAWVVVSELTRNHTKRASATVATVATLTLLEATVOANATD--	DDDL	57			
DB	1	MNEILRIWNSALNAWVVVSELTRNHTKRASATVKVATVATLTLLEATVOASANNDEEDL	60				
QY	58	YLPBPVQRTAVVLSPRSDEKGTGEKGTED-SNMAVYDFDEKRVLKAGAITLKAGDNLKIKQ	116				
DB	61	YLPVLRVAVLIWNSDEKGTGEKEVYENSDMWAVYNEKGVLTAREITLKAGDNLKIKQ	120				
QY	117	NTNENTNENTNDSFTVSLKKDLTDLTSLVFETEKLSFGANGKNVITSDTKGLNFAKETAG	176				
DB	121	-----NGTNFTVSLKKDLTDLTSLVGTEKLSFSAANGKNVITSDTKGLNFAKETAG	170				
QY	177	TNGDPTVHLNGIGSTLTDTLLNTGATTNVTVNDNVTDDDEKRAASVKDVLNAGWNIKGVPK	236				
DB	171	TNGDPTVHLNGIGSTLTDTLLNTGATTNVTVNDNVTDDDEKRAASVKDVLNAGWNIKGVPK	230				
QY	237	GTTASDNVDFRVYDVTVEFLSADPTKTTTVNVESKDCKRTVEVKGAKTSVKEKDGKLVLT	296				
DB	231	GTTASDNVDFRVYDVTVEFLSADPTKTTTVNVESKDCKRTVEVKGAKTSVKEKDGKLVLT	290				
QY	297	GKKGKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGQTQADKFETVTSGTKVTF	356				
DB	291	GKDKGENSGSTDEGEGLVTAKEVIDAYNKAGWRMKTTTANGQTQADKFETVTSGTNVT	350				
QY	357	ASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVS	416				
DB	351	ASGKGTTATVSKDDQGNITVMYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVS	410				
QY	417	PSGKMDETVINAGNNIEITRNCKNIDTATSMTPQFSSVSLGAGADAPTLISVDDDEGALN	476				
DB	411	PSGKMDETVINAGNNIEITRNCKNIDTATSMTPQFSSVSLGAGADAPTLISVDDG-ALN	469				
QY	477	VGSKDANKPVRITNVAPGVKEGDDVTNTVAQLKGVAQNLLNRRIDNDVGNARAGIAQAIATAG	536				

Db 470 VGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGAQNLRIDNVDGNARAGIAQAATAG 529
QY 537 LAQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDTCNWWIKGTASGNSRGHFGTSASVGY 596
Db 530 LVOAYLPKSMMAIGGGTYRGEAGYAIGYSSISDTCNWWIKGTASGNSRGHFGTSASVGY 589
QY 597 QW 598
Db 590 QW 591

Search completed: July 3, 2002, 08:37:10
Job time: 336 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:17 ; Search time 58.79 seconds
(without alignments)
977.401 Million cell updates/sec

Title: US-09-771-382-8

Perfect score: 3042

Sequence: 1 MNKISRIIWNLSALNAWVVS.....TASGSRGHFGTSASVGYOW 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_71.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2716.5	89.3	591	2	G81133	adhesin NMB0992 [i
2	2521	82.9	592	2	A81888	probable surface f
3	622	20.4	298	2	I64138	adhesin homolog HI
4	403	13.2	2059	2	D82671	surface protein XF
5	390	12.8	1107	2	AC0976	probable autotrans
6	383.5	12.6	1190	2	A82615	surface protein XF
7	365	12.0	1588	2	A86036	probable adhesin Z
8	365	12.0	1588	2	H31188	probable adhesin E
9	342	11.2	658	2	AH0110	probable surface p
10	241	7.9	1004	2	C82672	surface-exposed ou
11	223	7.3	1091	2	G4964	hypothetical prote
12	220	7.2	1910	2	AF0394	probable adhesin h
13	217	7.1	1536	2	A43855	high-molecular-wei
14	216	7.1	3705	2	A80123	probable autotrans
15	214	7.0	4919	2	T31105	hypothetical prote
16	213	7.0	949	2	D98083	Aida-I adhesin-lik
17	213	7.0	1005	2	H85611	probable adhesin Z
18	213	7.0	1018	2	H83135	probable adhesin P
19	211	6.9	1608	2	A28182	hemolysin A - Serr
20	210	6.9	1361	2	T03415	S-layer protein -
21	209	6.9	1286	2	S28634	adhesin AIDA-I pre
22	208.5	6.9	1109	2	A56143	surface-array prot
23	206.5	6.8	961	2	A50548	putative autotransp
24	203.5	6.7	1325	2	A64905	ydek protein - Esc
25	203	6.7	2551	2	B98047	hypothetical prote
26	202	6.6	5188	2	B85547	probable RTX famil
27	202	6.6	5291	2	F90696	hypothetical prote
28	201	6.6	585	2	F85809	hypothetical prote
29	200	6.6	1635	2	A10452	hemolysin [importe

30	199	6.5	585	2	F90961	flagellin [importe
31	199	6.5	2249	2	A41477	190K surface anti
32	199	6.5	4936	2	AH2515	hypothetical prote
33	198.5	6.5	1417	2	A83080	hypothetical prote
34	198	6.5	3013	2	A80480	probable invasin Y
35	197	6.5	1275	2	T33369	hypothetical prote
36	195	6.4	1577	2	A35140	hemolysin A precu
37	195	6.4	3029	2	S76109	hypothetical prote
38	192.5	6.3	1430	2	AF0351	probable autotrans
39	192.5	6.3	1487	2	AG2560	hypothetical prote
40	192	6.3	2468	2	A83412	hypothetical prote
41	191.5	6.3	936	2	I40711	sapB protein - Cam
42	191.5	6.3	1651	2	JC1340	outer membrane pro
43	191	6.3	1477	2	B43855	high-molecular-wei
44	190.5	6.3	1327	2	B90674	Aida-I adhesin-lik
45	190.5	6.3	1349	2	E85524	probable beta-barr

ALIGNMENTS

RESULT 1

G81133

adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000.#sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133

R:Rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.B.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755

A:Accession: G81133

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-591 <TEF>

A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF1395.1; PID:g722 A:Experimental source: serogroup B, strain MC58

C:Genetics:

A:Gene: NMB0992

Query Match 89.3%; Score 2716.5; DB 2; Length 591;
Best Local Similarity 90.7%; Pred. No. 3.8e-131;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWNLSALNAWVVSSELTRNHTKRASATVATATLTLFATVQANATD---DDDL 57

DB 1 MNKIYRIIWNLSALNAWVVSSELTRNHTKRASATVATATLTLFATVQASANNEQEDL 60

QY 58 YLEPQVQTAVVLVSFRSDKEGTEGEGED- SNNAVYFDEKRVLKAGAITLKAGDNLIKIQ 116

DB 61 YLDPQVQTAVVLIVNSDKEGTGEKEKEVEENSDNAVYFNEKGVLTAREITLKAGDNLIKIQ 120

QY 117 NTNENTNTNDSSSTYSLLKDLTLDTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 176

DB 121 -----NGTNFTYSLKKDLTLDTSVGTEKLSFGANGKNVNTSDTKGLNFAKETAG 170

QY 177 TNGDPTVHLNGISLTDLTLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKP 236

DB 171 TNGDPTVHLNGISLTDLTLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKP 230

QY 237 GTTASDNVDVFRYDTVEFLSADTKTTTNNVESKONGKRETKVIGAKTSVIEKDGKLVTF 296

DB 231 GTTASDNVDVFRYDTVEFLSADTKTTTNNVESKONGKRETKVIGAKTSVIEKDGKLVTF 290

QY 297 GKGKGENSGSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFETVTSGTKVTF 356

DB 291 GKGKGENSGSTDEGELVTAKEVIDAVNKGWRMKTITTTANGOTGQADKFETVTSGTKVTF 350

QY 357 ASSNGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVS 416

Db 351 ASKGGTATVSKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSGKVISGNVS 410
QY 417 PSKGMDETNIINAGNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDEGALN 476
Db 411 PSKGMDETNIINAGNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLSDVGD-ALN 469
QY 477 VGSKDANKPVRITNVAPGVKEGDTNVNVAQLKGVAQNLRNIDNDVGNARAGIAQAATAG 536
Db 470 VGSKKNKPVRITNVAPGVKEGDTNVNVAQLKGVAQNLRNIDNDVGNARAGIAQAATAG 529
QY 537 LAQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRGRHFGTSASVGY 596
Db 530 LVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRGRHFGTSASVGY 589
QY 597 QW 598
Db 590 QW 591

RESULT 2
A:181888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249)
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 82.9%; Score 2521; DB 2; Length 592;
Best Local Similarity 85.5%; Pred. No. 3.4e-121;
Matches 520; Conservative 16; Mismatches 46; Indels 26; Gaps 8;
QY 1 MNKISRIIWNALNNAVWVSELFRNHTKRSATVATAVLATLTLFATVQANATD-DDDLYL 59
Db 1 MNKIRIWNALNNAVWVSELFRNHTKRSATVATAVLATLTLFATVQANATDEDEEEL 60
QY 60 EPVORTAVLSFRSDKECTGKEG-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL 112
Db 61 ESQVR-SVSGIOASMEGSELETISLWNTDSKEFVDPYI-----VVLKAGDNL 110
QY 113 KIKONTNENTNDSFTYSLKDLTLTSVETEKLSFGANGKNVITSDTKGLNFAK 172
Db 111 KIKONTNENTNA-----SSFTYSLKDLTLGLINVETEKLSFGANGKNVITSDTKGLNFAK 166
QY 173 ETAGTNGDPTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 232
Db 167 ETAGTNGDPTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 224
QY 233 GVKPGTFA--SDNVDFVRYTDFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEK 290
Db 225 GVKTGTGSGESENWDFVRYTDFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEK 284
QY 291 DGKLVTKGKGNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 350
Db 285 DGKLVTKGKGNGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 344
QY 351 GTRKVTFASGNGTTATVSKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSGSKV 410
Db 345 GTNVTFASGKGTATVSKDDQGNITVMDVNVGDALNVQLNSGWNLDKAVAGSGSKV 404

QY 411 ISGNVSPSKGMDETNIINAGNIEITRNKKNIDIAITSMTPQFSSVSLGAGADAPTLSDV 470
Db 405 ISGNVSPSKGMDETNIINAGNIEITRNKKNIDIAITSMAPQFSSVSLGAGADAPTLSDV 464
QY 471 DEGALNVGSKDANKPVRITNVAPGVKEGDTNVNVAQLKGVAQNLRNIDNDVGNARAGIAQ 530
Db 465 DEGALNVGSKDANKPVRITNVAPGVKEGDTNVNVAQLKGVAQNLRNIDNDVGNARAGIAQ 524
QY 531 AIATAGLAQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRGRHFGT 590
Db 525 AIATAGLVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRGRHFGA 584
QY 591 SASVGYQW 598
Db 585 SASVGYQW 592

RESULT 3
I64138
adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequence sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.4%; Score 622; DB 2; Length 298;
Best Local Similarity 46.2%; Pred. No. 6.6e-25;
Matches 150; Conservative 39; Mismatches 90; Indels 46; Gaps 9;
QY 1 MNKISRIIWNALNNAVWVSELFRNHTKRSATVATAVLATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIFKIVNVTQTWVWVSELTRAHTKRTSATVATAVLATVLSATVQA----- 49
QY 61 PVORTAVLSFRSDKECTGKEGTEDSNNAVYFDEKRVLKAG-AITLKAGDNLKIKONTN 119
Db 50 -INDAGTFVVKVQSTEDDIEDSAATKDDN-----KNOALKAGDTLTLKAGNKLAKL--- 99
QY 120 ENTNENTNDSFTYSLKDLTLTSVETEKLSFGAN-----GNKVNITSDTKGLNFAK 172
Db 100 -----DOGGKSVTFALAKDLVKAKVSDTLTIGGNTPAAGGATPKVSIITADGLKAK 154
QY 173 ETAGTNGDPTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 232
Db 155 ---GTNGDTAVHNLGLASTLPDVTNTGASTSVT-FPSDIEKTRAATIKDVLNAGNNIK 210
QY 233 GVKPGTASDNVDFVRYTDFEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVKEKDG 292
Db 211 GAKVAGGNTENVLDVAGYDNVEFTIGDKNTLDVVLTAKEGKTEVKTPTKTSVKNNG 270
QY 293 KLVTKG-----GKGNGS-STDE 309
Db 271 KLVTKGKLDKANTGATNATEDTDE 295

RESULT 4
D82671
surface protein xF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <SIM>

A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R.Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briiones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H

as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1529

Query Match 13.2%; Score 403; DB 2; Length 2059;

Best Local Similarity 24.7%; Pred. No. 1.le-12;

Matches 172; Conservative 100; Mismatches 219; Indels 204; Gaps 33;

QY 78 TGEKEGTDSNNAVYFDE-----KRVLKAGAITLKAGD-NLKTK 115

DB 1395 SGTAGTEID-AVNFSQLKSTSTAVDQGWTLTASGANGSKVASGGTVDLKNTDGLNLTIS 1453

QY 116 Q-NTNE---NTNENTNDSSFTY---SLKKOLDTLTS-----VETELKSFANGKNVNTSD 164

DB 1454 KSGSDNVVFNLSDELKESITVGTQDLDKGVKSSVLLDSNELVITSHSSTSSVKTL 1513

QY 165 TKGLNFAKETA---GTNGDPTVHLNGI-----GSTLTDLTLLTNGA---TTNVT-----N 207

DB 1514 ANGESVNNVTVVGDNVIDVVDNLGLSTVGGASLTLSGINAGSHKITNVTAGTEPT 1573

QY 208 DNVTDDKRAASVVDVNLNAGWNI-----KGVPKGTASDNVD-----EVRTYDT 252

DB 1574 DAVNFSOLK---SVSEAVDQKHTLTASGANGSKVSGGTVDLKDNTDGLNLAISKSGSDNDV 1630

QY 253 VEFLSADTK-----TTTVNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGKGEN-- 303

DB 1631 VFNLSKDFKVDVETAGTVVNTDGVKVG--SDVSLGAMGLFIANGPSVTASGFNAGDKVI 1688

QY 304 -----GSSTDEGEGLVTAKEVIDAVNKAQWRTTANGQTG-----QADKFTVTS 350

DB 1689 SHVAVGMADTDAVNVSQLQAQVSVTVKATRYSTVNDGCTGGNVDGCGATGSKAIAAGV 1748

QY 351 GKVT-----FASNGGTT-----ATVSKD-----DOG-----NITVKYD- 379

DB 1749 GTQASGEAAVSGAASGKSTAGRNAIASADGSVALGDGKDGGRGAESYTGKYS 1808

QY 380 -----VNVG-----DALNVNL-----QNSGNWLDs----- 400

DB 1809 VQNTVGTVSVGDAAKGETRSISNVADAKEAMDVNLRLQDVAQKSNLQTDMDRHEINN 1868

QY 401 -----KAVAGSGKVISGNVSPSKEMDETIVINA---GNNTEITRN-----GKNIDIA 447

DB 1869 IEDVPKITKDSASSYK-----MGVNMAIGTNAAVSGSTESVALGKNTNVSA 1916

QY 448 SMTPOFSSVSLGADAPTLSDDEGALNVGSKDKANKPVRIITNVAPYKVGQDVTVNAQLK 507

DB 1917 D-----NAVAINGSV-----DRANSVSVGGGGER---QVTNVAAGTADTDAVNVSQLN 1964

QY 508 GVAQNLNNRIDNVGNAR-----AGIAQAATATAGLAQAYLPKGSMAIGGTVRGEAGYAI 563

DB 1965 QGLITAKQYTDGMVGNLRRRETSGGVAATAATANLPQAYVQGRGMTSGVGVSSYQGQSAIAV 2024

QY 564 GYSSISDGTGNWIKGTASGNSRGHFTSASVGYQW 598

DB 2025 GVSAVSESHWVFKFSGSANTRSHVCGVAGVGYQW 2059

RESULT 5

AC0976

probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001

C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0976

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

C:Genetics:

A:Gene: sapB

Query Match 12.8%; Score 390; DB 2; Length 1107;

Best Local Similarity 21.8%; Pred. No. 2.3e-12;

Matches 182; Conservative 114; Mismatches 262; Indels 278; Gaps 30;

QY 27 TKRASATVAT---AVLATLLFAT---VOANATDDDLYLEPQVQRTAVVLSPRSKEGTG 79

DB 286 TNLAACTLAADSDAVNGSQLYETNQKVDQNTSAIADINTSITNLSNDLSMNETTNSFS 345

QY 80 EKEGTDSNNAVYFDEKRVLKAGAITLKAGD-----NLKIKQNTNE---NTNENT 126

DB 346 ASHGSTTN-----KITNVAAGELSEESTDAVNGSQLFETNEKVDQNTDTIAANTNIT 399

QY 127 NDSSFTYSLKKOLDTL-TSV-----ETEKLSFGAN--GNKNVITSDTKGLNFAKE 173

DB 400 QNSTATENLTVSDINTSITGLTDNALLWDEDTGAFSANHGSGTSKIITNVAAGALSEDS 459

QY 174 TAGTNGDPTVHLNGIGSTLTDTL--LNTGATNTVNDVTDDEKRAASVKVDVNLNAGWNI 231

DB 460 TDAVNGSQLYETNQKVDQNTSAIADINT-SITNLGTDALSWDDEGAFSASHGTSGTNKI 518

QY 232 KGVPKGTASDNVDV---RTYDT-----VEFLSADTKTTVN-----VESK 270

DB 519 TNVAAGEIASDSDAINGSQLYETNMLISQYNESISQLAGDTSYITENGTCVKYIRTN 578

QY 271 DNGKRTVEKIGAKTSVKEKDKLVTKGK---KGENSGSTDEG----- 310

DB 579 DNGLEGQDAYATCGNATAVGYDAVAGSAGCLALGQNSSSSIEGSIAGSGSTSNRAITTG 638

QY 311 -----EGLV-----TAKEVIDAVNKA-----GWRMKTNTANGQTG----- 341

DB 639 IRETSATSDGVVGYNTTDRLLGALSGLTGDGESYRQITNVADGSEAQDAVTVRQLQNAI 698

QY 342 -----ADKFEVTSCTKVTFFASNGTATTATVSKDDOGNITVKVDVNVGALNVNLQN-- 393

DB 699 GAVTTPTPTKYIHANSTEEDSLAVGTDLSLAKGAK-----TIVNADAGIGTGLNTFLVMADAI 753

QY 394 SGWNLDKSAVAGSSGKVISGNVSP-----SKGKMD---ETV 426

DB 754 NGIATGSNARAHANSIANGNGSQITRGAQTDYTAIYMDTPQNSVGEFSVSGEDGQRIIT 813

QY 427 NINAGN-----NIEITRNKNI-----DIATSM 450

DB 427 NINAGN-----NIEITRNKNI-----DIATSM 450

Db 814 NVAAGSADTDVAVNGQKLVTAQVSRNTQSIITNLNTQVSNLDRVTNIENIGDITVTS 873
QY 451 PQF-----SSVSLGAGADAP-----TSLVDE-CALNVGSKDANKPV 486
Db 874 TKYFKNTDGDADANAQADSVAGSGIAAENSVALGTNSVADEANTVSGSSTQOR-- 931
QY 487 RITNVPVKGEGDVTNVAQLK-----507
Db 932 RITNVAAGVNTDAVNVAQLKASEAGSVRYETNADGSVNYVLNLGDSGGTTRIGNVSA 991
QY 508 -----GVAQ-----NLNRRIDVNDGNARAGIAQAATAGLAQAAYL 542
Db 992 AVNDTDAVNTAQLKRSVEEANTYTDQKMGEMNSKIKIENKSGGSIASAMAGLPOAYA 1051
QY 543 PGKSMIAIGGTVRGEAGYAGYSSISDTGNWVTKGTASNSRGHFTCSASVGYOW 598
Db 1052 PGANMTSIAGGTNGESAIVAIGVSMVSESGWYKLGQTSQGDYSAATGAGFOW 1107
RESULT 6
A82615
surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: A82615
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: A82615
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1190 <SIM>
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF4783.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canaro, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigh
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Status: annotation
C:Genetics:
A:Gene: XF1981

Query Match 12.6%; Score 383.5; DB 2; Length 1190;
Best Local Similarity 24.6%; Pred. No. 5.5e-12;
Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;
QY 47 VOANATDDLLYLPVORTAVVLSFRSDKPGTGKEKTESNNNAVYPDEKRVLKAGAITL 106
Db 572 VAAGTADTDAVNFSQLQ-----AVSSTASKGNLLASGANSN-----VVPGESVDL 618
QY 107 KAGD-NLKIKONTNENTNENTNDSSTFY--SLKKD--LTDLTSVETEKLSFGAN----- 155
Db 619 KNSDGNLLTKTT-----DSNOVTFMLATALKVDSLTGNTAMTDDGVTVGSNVLGST 672
QY 156 -----GNK--VNI-----TSDTKGLNFA-----171
Db 673 GLVITDGPSTSSGISAGNQKIITNVAAGTADTDAVNFSQLQAVSSSTASKGNLLASGANS 732
QY 172 -----KETAGT-----NGDPTVHLNGIGS-----TLTDTLLNTGATF---NV 205
Db 733 SNVAPGESVDLKNTDGNINIVISKESGSDNVLNLSLSLKDLKLTGDTVMTNGTVGSGV 792

QY 206 TNDN-----VTDEKKRAASVKDYLNAG--WNKIGVKPQTTASD-----N 243
Db 793 TLGSMGLVITDGPVSISGGI-----NAGSQKITNVAAGTADTDAVNLSQLTAMAGSGAKS 848
QY 244 VDPVRYDVTEFLSADTKTTTNNVESKDNKGRTEVIGAKTSVIKEKDKLVTKGKGEN 303
Db 849 VHYSTYD-----GGTGGNYNGDGTGTRSTIAGVGTGLASA-----EGATAVSGSAAS 898
QY 304 G-SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGQTQADKEETVTSGTKVTFASNGT 362
Db 899 GKSTAIGRNAVASADGSVALGD--GAKDARGAEESTYTGKYGQNNNTVGTVSGVDASKGE 957
QY 363 TATVSKDDQGNITVKYDVNVGDALNVNQL-----QNSGWNLDKSAVAGSGSVISGNVSPS 418
Db 958 TRVVS-----NVADAKEAT--DAVNLRQLDRVAQDANRYVDNKIESLSESGTFF----- 1003
QY 419 GKMDETVINAGNNTIEITRNKNIDIATSWTPOFSSVSLGAGADA-----PTL 467
Db 1004 -----VKVNSLNN-----SATPIAAGVDATAIGVGTASGADSIAMGNKASA 1045
QY 468 SVDEGAL-----NVGSKDANKPVRTITNVAPVKEGDTVNTVAQLKGAQNLLN 515
Db 1046 SADNAVAIGNHVSADRANTVSVGSAGSER--QVTNVAAGTADTDAVNVSQNLGLITAKQ 1103
QY 516 RIDNVGNAR-----AGTAAQAIATAGLAQAAYLPCKSMIAIGGTVRGEAGYAGYSSISDT 571
Db 1104 YTCGVVGSRLARDTDGGVAAAIATIANLPQAVIPGRGTSVGVSSYRGOSATAVGVSSVSES 1163
QY 572 GNWVIKGTASGNSRGHFTCSASVGYOW 598
Db 1164 GRWVFKFGSANTRSQVIGAGVGYOW 1190
RESULT 7
A86036
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1598 <STO>
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5029
Query Match 12.0%; Score 365; DB 2; Length 1588;
Best Local Similarity 25.0%; Pred. No. 6.9e-11;
Matches 144; Conservative 81; Mismatches 252; Indels 98; Gaps 19;
QY 111 NLKIKONTNENTNENTNDSSTFYSLKKDLTDLTSVET--EKLSE-----GANGNKVNIT 162
Db 1025 NMIEQNT-QIINQAGTADATY-IQENGAGINVTNRNDGLAFNDASAQGVGATAIGN 1082
QY 163 SDTKGLNFAKETAGTCDPTVHLNGIGSTLTDLLNTGA--TTNVTNDV-----TDEK 215
Db 1083 SVARGDSSVAIGGQSDVDVTGIALGSSSVSRVIARSGRDTISITENGVIWIGVDTTDEL 1142
QY 216 KRAASVKD-----VLNAGWNKIGVKPQTTASQNDVDPVRYDTVEFLSADTKTTTVNES 269
Db 1143 LGALSTGDDCKYRQIIN-----VADGSEAHDAVT--VROLNAGAVATPTPKYFHANS 1194
QY 270 KDNKG-----RTEVKIGAKTSVIKEK-----DGKLVTKGKGE----- 302

Db 1195 TEEDSLAVGTDSLAMGAKTIVNGDKIGIGYAYVDANALNGIAIGSNAQVHVNSIAIG 1254
QY 303 NGSSDTEGEGELVTAKEVIDAVNKAHRMKTITTTANGO-----TGQADKFEVTSCTKYT 355
Db 1255 NGSTTRGAQNTAYNMDAPONSVEFSVGSADGQRTINVAAGSADTDVNVGOLKVT 1314
QY 356 FASGNGTTATVSKDDQ-----GNITVKYDVNVGDAL-----NVNQLQNSGWNLDS 400
Db 1315 DAQVQSQNTQITNLDNRVTNLDNRVTNIENGIGDIVTTGTSKYFKTNDGVDASAQKDS 1374
QY 401 KAVAGSGKVISGNVSPSKGM---DETNNINAGNIEITRN---CKNDIATSWTPQPS 454
Db 1375 VAIGSGSIAAANDNSVALGTGCVATEENTISVGSSTNORRITNVAAGKNATDAVNVAQLKS 1434
QY 455 SVSLGAGADAPTLSDVDEGALNVGSDANKPVRITNVAPGVKGDVTNVAQLKGVAQ--- 511
Db 1435 SEAGGVRYDTKDGSDIDYDNITLGGNGG--TTRISNVSAVNNNDVVNVAQLKQSVQETK 1493
QY 512 -----NLNNRIDNVGDNARAGIAQAATAGLAQAYLPKGSMMAIGGGTYRGEAGYAI 563
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPOAYTPGASMASIGGGTYNGESAVAL 1553
QY 564 GYSSISDGTGNWYIKGTASGNSRGHFGTSASVGYQW 598
Db 1554 GVSWSANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 8
H91188 probable adhesin Ecs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H91188
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-References: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: Ecs4480

Query Match 12.0%; Score 365; DB 2; Length 1588;
Best Local Similarity 25.0%; Pred. No. 6.9e-11;
Matches 144; Conservative .81; Mismatches 252; Indels 98; Gaps 19;
QY 111 NLKIKONTNENTNDSSTFYSLLKDLTDLTSVET--EKLSF-----GANGNKVNIT 162
Db 1025 NMIEQNT-QIINQLAGNTDATY-IOENGAGINVRVTDNDGLAFNDASAQGVGATAGYN 1082
QY 163 SDTKGLNFAKETAGTNGDPTVHLNGISLTDLTLNFGA--TTNVTNDNV-----TDDEK 215
Db 1083 SVAKGSSVAIGOGYSVDVDTGTALGSSSVSSRVIAKGRSDTSITENGVIYDITDDEL 1142
QY 216 KRAASVKD-----VLNAGNKGKVPKPGTASDNVDFVRYDTVEFLSADTKTTNNVES 269
Db 1143 LGALSTGDDGKYQIIN-----VADGSEAHDAVT-VRLQNAIGAVATTPKYFHANS 1194
QY 270 KNGK-----RTEVKIGAKTSVIEK-----DGKLVTKGKGKE----- 302
Db 1195 TEEDSLAVGTDLSAMGAKTIVNGDKIGIGYAYVDANALNGIAIGSNAQVHVNSIAIG 1254
QY 303 NGSSDTEGEGELVTAKEVIDAVNKAHRMKTITTTANGO-----TGQADKFEVTSCTKYT 355
Db 1255 NGSTTRGAQNTAYNMDAPONSVEFSVGSADGQRTINVAAGSADTDVNVGOLKVT 1314
QY 356 FASGNGTTATVSKDDQ-----GNITVKYDVNVGDAL-----NVNQLQNSGWNLDS 400

Db 1315 DAQVQSQNTQITNLDNRVTNLDNRVTNIENGIGDIVTTGTSKYFKTNDGVDASAQKDS 1374
QY 401 KAVAGSGKVISGNVSPSKGM---DETNNINAGNIEITRN---CKNDIATSWTPQPS 454
Db 1375 VAIGSGSIAAANDNSVALGTGCVATEENTISVGSSTNORRITNVAAGKNATDAVNVAQLKS 1434
QY 455 SVSLGAGADAPTLSDVDEGALNVGSDANKPVRITNVAPGVKGDVTNVAQLKGVAQ--- 511
Db 1435 SEAGGVRYDTKDGSDIDYDNITLGGNGG--TTRISNVSAVNNNDVVNVAQLKQSVQETK 1493
QY 512 -----NLNNRIDNVGDNARAGIAQAATAGLAQAYLPKGSMMAIGGGTYRGEAGYAI 563
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPOAYTPGASMASIGGGTYNGESAVAL 1553
QY 564 GYSSISDGTGNWYIKGTASGNSRGHFGTSASVGYQW 598
Db 1554 GVSWSANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 9
AH0110 probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0110
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-References: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 11.2%; Score 342; DB 2; Length 658;
Best Local Similarity 22.5%; Pred. No. 3.3e-10;
Matches 144; Conservative 87; Mismatches 254; Indels 156; Gaps 19;
QY 27 TKRASATVAT-----AVLATLLFPATVQ-----ANATDDDDLLLEPVQRTAVVLSFRSDK 75
Db 105 TNLAPATISTSTDAVVGSQLYLVQDGTTRYFHANSVNPPTDSLASGLETIAV----- 156
QY 76 EGTGEKEGTSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNENTNDSSTFYSYL 135
Db 157 -----GPATVVSQDNGVIGINTALVGAATGGAIGTAV 190
QY 136 KDLDTLTSVET-----EKLSFGANGKNVITSDTKGLNFAKETAGTNG----- 179
Db 191 QVTAACATAIGSAQAQAQAGSLAGAGA---VTSQANSIALGAASINTVGAOSSYSAYA 246
QY 180 -----DPTVHLNGISLTDLTLNFGATVNTNDNV-----DDEKRAASVKDVLNA 227
Db 247 LTAPOASVGBELGCTALGNRKITGVAAGSASSDAVNVAQLTAVGDOVQOQTANITSLGGR 306
QY 228 GWNKGVKPCPTTASDNVDFVRYDT--VEFLSADTKTTTNNVESKDNCKRT-----EVKI 280
Db 307 VTTIEGSMASIANGGVKYFHANSTQPDSPDSVAGTSNVSAIGPASLAGSNAALASAGAVAI 366
QY 281 GAKTSVIEKDKGLVTGKKGKENGSSSTDEGELVTAKEVIDAVNKAHRMKTITTTANGQT 340
Db 367 G--DGAASADGSAIGQSGDNGRGE-----NYIG 396
QY 341 QADKFEVTSCTKYTASGNGTATVSKDQGNITVKYDVNVGDALNVNQLQNSGWNLDS 400
Db 397 KYSNASNTSSGTVSVGNTATGETRTVSNVADG-----LQATDAVNLRQLDQ----- 442

Qy	181	PTVHLNGISGL-----DTLLNTG-----ATTNTVNDNVTDDEKKRAASVKDVLNA	227
		: : : :	
Db	183	DTVISAGGOSLGRAVNTTLLAGGEQWMHEGAIATGTVINDK-----	224
Qy	228	GNWIKGVKPTTASDNVDVPT-----YDVEFLSADTKTTTVNVESKONGKRT	277
		: : : : : : : : : : : : :	
Db	225	GWQV--VKPCTVATDIV--VNTCAEGGPDANGDFGQFVRGDAVPTTIN-----KNGHQIV	276
Qy	278	VKIG-AKTSVIKEKDKLVTKGKGKGENSGSTDEGELGVTAKEVIDAVNKAWRMKTTTAN	336
		: : : : : : : : : : : : :	
Db	277	RAEGTANTTVVY-----AGGDQTVHGHAL-----DTLLNGYQY---VHN	313
Qy	337	GOTGQADKETVTSGTKVTFASNGTTATVSKDDOGNITVKYDYNVGDALVNOLONGSW	396
		: : : : : : : : : : : : :	
Db	314	GGTAS---DTVVNSGQOIVNKGVGAGNTTVNQKRLQV--DAG-GTATNVTLKQ--GG	364
Qy	397	NLDSKAVAGSSGKVISGNYSPSKGMDETVINAGNNIEITRNGKNIDIATSMTPQPSV	456
		: : : : : : : : : : : : :	
Db	365	ALVTSTAATVTGINRLGAFSVVEGRADNV-----LENGRLDVLTGHTATNTRV	414
Qy	457	SLGA-----GADAPTLSDDEGALNVGSKDANKPVRITNVAPGVKEGDTVNAQLKGVA	510
		: : : : : : : : : : : : :	
Db	415	DDGGTLDVRNGGTATVSMNGSGVLLADSGAIVSGTRSDGKAFSIGGGQADALLMERGSS	474
Qy	511	QNLNRRIDNVGDNARAGIAQATATAGLAQAYLPUGKSMMAIGGTVTGBA-----GYAIGY	565
		: : : : : : : : : : : : :	
Db	475	FTLNAGDTATDTVNGGLFTARGGTLAGTTTLNNGAILTSGKTVNNDTLTIREGDAL-L	533
Qy	566	SSISDTGNWVIKTASG	582
Db	534	QGGSLTGNGSVKESGSG	550

RESULT 12
AF0394
probable adhesin hmwA [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0394
E:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <R>
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:gl5981183; GSPDB:GN00175
C:Genetics:
A:Gene: hmwA

Query Match	7.2%	Score 220;	DB 2;	Length 1910;
Best Local Similarity	22.0%	Pred. No. 0.0021		
Matches 145; Conservative		72; Mismatches 226;	Indels 216;	Gaps 31;

Qy	79	GEKEGTED-----SNWVYDFDKRVLKAGA-ITLKAGDNLUKIKO-----	116
		: : : :	
Db	1154	GSSAGTGDVYFTTWELNATAGNVYAETKTALSTSLNAVLSLGGNNSIKAQNGWLICKA	1213
Qy	117	-NTNMENTNDSSFTYSILKDLTDLTSVETEKLS-----FGAN-----GNKVNI	161
		: : : : :	
Db	1214	FNTTQAGAGIFRANS---SLUSDGNIILKETEGVGATRKGIDFGANTLIUKGSQSL	1270
Qy	162	TSDTKGLNFAKETAGTNG-----DPTVHLNGI---GSTLTDTLLTGTATTTWTDNV	210
		: : : : :	
Db	1271	LGENKG---AQDTAGNGISYTSLAKLTVNNNGSLKMEGRSTSGTGINFPSNNTLVFG	1327
Qy	211	TDEKKRAASVKDVLNAGWNIKGVKPGTTASDNVDVRYTDT-VEFLSADTKTTTVNVES	269
Db	1328	DGDTPLIKGSS---VAGTGAAGISGVNNSGPMPTIGISTDGAGVHLFSAEHRIDRNV--	1382

Qy	270	KDNGKRTE---	VKIGAKTSV	IKEKDGLKV	TGKGKENG	SSTD----	EGBGLVT	AKEVIDA	322	
		: :	: :	:	:	:	:	:		
Db	1383	--TGSSTHAE	GLRISGNAI	IVD-----	TTLTGKS	INGSVK	IDSLPGC	SVVT--RS	VD-1432	
		: :	: :	:	:	:	:	:		
Qy	323	VNKAGWRMKT	TTTANGOTG	QADEFVT	SGTKVTF	PASGNGT	TATYSK	DDOGNI	TVKYDVNV 382	
		: :	: :	:	:	:	:	:		
Db	1433	-----NATL	GSSSGKGV	ETSDING	IHHSSIN	GTTTGCTG	-----	YGIDI	1473	
		: :	: :	:	:	:	:	:		
Qy	383	GDALNV----	NOLQNSGN	LDSKAVG-	-----				405	
		: :	: :	:	:	:	:	:		
Db	1474	GENSNVTGT	SEADLLILO	GVAITGTG	TIKLGNN	DLSNT--	SLNSSA	VDGIALD	ITGPL 1531	
		: :	: :	:	:	:	:	:		
Qy	406	-SSGKYISG	NVSFSK-	-----	KMETVN	INAGNN	IEITRN	-----	439	
		: :	: :	:	:	:	:	:		
Db	1532	ANQGNVILN	TASGGIGA	QVNGS	SDSVYNT	STNGIG	VQVING	SLKNR	INGISANGSG 1591	
		: :	: :	:	:	:	:	:		
Qy	440	-----GK	NIDTATSM	TPOFSSV	SLGAGAP	TLTSLV	DEGALN	VGS	479	
		: :	: :	:	:	:	:	:		
Db	1592	VKIDGESTL	DNALNCN	STEGKGV	DLAANL	SGNSHV	SGDTVHG	TGIDVGK	DVTLSGGG 1651	
		: :	: :	:	:	:	:	:		
Qy	480	KDANKPVR	TNVAPGV	KEGYTN	VNAQLK	GVAQN	LNRNDN-	VDCNAR	AGTAGQAIA	TAGL 537
		: :	: :	:	:	:	:	:	:	
Db	1652	TD--EPLT	VSGNASG	KBGTGV	---QLG-	-----	NNTLDNT	LTSGNAT	PDHGVET	---- 1695
		: :	: :	:	:	:	:	:	:	
Qy	538	AQAYLPCK	MMAITGC	GTYRGE	AGYAICY	SSIISD	TGNWV-I	KGTASGN	S-RGHFGT	SASV 594
		: :	: :	:	:	:	:	:	:	
Db	1696	-----NS	RLLNNGNT	TINKGT	-----	SDDCHGV	HINGAI	SGGEING	SDNSHCV	1739
		: :	: :	:	:	:	:	:	:	
RESULT	13									
A43855										
C:	high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae									
C:	Species: Haemophilus influenzae									
C:	Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999									
C:	Accession: A43855									
R:	Barenkamp, S.J.; Leininger, E.									
I:	Infect. Immun. 60, 1302-1313, 1992									
A:	Title: Cloning, expression, and DNA sequence analysis of genes encoding n									
A:	della pertussis.									
A:	Reference number: A43855; MUID: 92192797									
A:	Accession: A43855									
A:	Status: preliminary									
A:	Molecule type: DNA									
A:	Residues: 1-1536 <BAR>									
A:	Cross-references: GB:U08876; GB:M4616; NID:g475770; PIDN:AAA20527.1; PID									
A:	Note: sequence inconsistent with the nucleotide translation									
A:	Note: sequence extracted from NCBI backbone (NCBN:89235, NCBIp:89239)									

Query Match	7.1%	Score 217;	DB 2;	Length 1536;
Best Local Similarity	22.8%;	Pred. No.	0.0023;	
Matches 133;	Conservative	88;	Mismatches 200;	Indels 162; Gaps 32;

QY	152	FCANG	-----NKVNITSDTGLNEAKETACT--	-	NGDPTVALNG--	IGSTL----	192
Db	814	-GTDGMIGKIVAKKNITFECCNITFCRSKAVTEIEGNVTINNANVTILGSDFDNHQKP	872				

[illegible]

QY 415 -----VSPSKGKMDETVN---INAGNIEITRNGK--NIDIATSMTPQFSSVSLGAGAD 463
Db 876 SNSLLDISVAEGK--KTFNNGTIESGKNLNTTGAFLNVDNATIR-----SFGVLNI 926
QY 464 APTLSVDDDEGALNVGSK-DANKPVRITNVAPG-----VKEGDVTN-----V 503
Db 927 TSTGNVSNNGTLISNERLNTSAAFTNESNCTVMSNGLLNIIAKQGNITNKNLIASROQ 986
QY 504 AOLKGAQNLNRRIDNVDCNARAGIAQAIAATAGLA-----QAYLPG----- 544
Db 987 LNLTAADNITN-----DSNTSNKIAVLHSLGNISLNSKDQVYNLGEIYAGNNISVKAHQ 1041
QY 545 -----KSMMAIGGTYRGEAGYAIGYSSISDGTGNWVINGTASGNSRGHFGTSASVGY 596
Db 1042 LKNDVKLMGDITTKKEGOASYKLYQAS-----NGGHFGNDGSSGY 1082

Search completed: July 3, 2002, 08:38:24
Job time: 295 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:50 ; Search time 29.79 Seconds
(without alignments)
777.250 Million cell updates/sec

Title: US-09-771-382-8
Perfect score: 3042
Sequence: 1 MNKISRIIWSALNAWVVS.....TASGNSRGHFGTSASVGYQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	223	7.3	1039	1 AG43_ECOLI	P39180 escherichia
2	211	6.9	1608	1 HLYA_SERMA	P15320 serratia ma
3	209	6.9	1286	1 AIDA_ECOLI	Q03155 escherichia
4	203.5	6.7	1325	1 YDBK_ECOLI	P32051 escherichia
5	199	6.5	2249	1 OMPA_RICRI	P15921 rickettsia
6	195	6.4	1577	1 HLYA_PROMI	P16466 proteus mir
7	190.5	6.3	2003	1 YDBA_ECOLI	P33666 escherichia
8	189	6.2	2021	1 OMPA_RICCN	Q52657 rickettsia
9	185.5	6.1	1654	1 OMPB_RICRI	Q53047 r outer mem
10	185	6.1	1300	1 L20K_RICRI	P14914 rickettsia
11	185	6.1	1953	1 BIGA_SALTY	P25927 salmonella
12	184.5	6.1	1655	1 OMPB_RICCN	Q9kka3 r outer mem
13	182	6.0	1567	1 ICEN_XANCT	P18127 xanthomonas
14	181	6.0	918	1 YMJB_CAEEL	P34487 caenorhabdi
15	181	6.0	1645	1 OMPB_RICTY	P66989 r outer mem
16	180.5	5.9	2334	1 WAPA_BACSU	Q07833 bacillus su
17	180	5.9	1569	1 YPJA_ECOLI	P52143 escherichia
18	178.5	5.9	1656	1 OMPB_RICJA	O06653 r outer mem
19	177.5	5.8	933	1 SLAP_CAMFE	P35827 campylobact
20	171	5.6	671	1 ALYS_ENTFA	P37710 enterococcu
21	169	5.6	1228	1 SLAP_BACST	P35825 bacillus st
22	168	5.5	825	1 GUN3_BACSA	P19570 bacillus sp
23	168	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
24	167.5	5.5	2329	1 YS89_CAEEL	Q09624 caenorhabdi
25	166	5.5	1007	1 Y741_CHLMU	Q9pj16 chlamydia m
26	165	5.4	1694	1 IGA0_HAEIN	P44969 haemophilus
27	165	5.4	1702	1 IGA2_HAEIN	P45384 haemophilus
28	164.5	5.4	1861	1 APU_THETU	P38536 t amylopull
29	164	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
30	164	5.4	1025	1 SLAP_SHIFL	P35828 caulobacter
31	163.5	5.4	928	1 HXA2_HAEIN	P45354 haemophilus
32	161	5.3	504	1 FLIC_SALNA	O52959 salmonella
33	161	5.3	504	1 FLIC_SALRO	Q06982 salmonella

34	160.5	5.3	788	1 SPL_RAT	Q01714 rattus norv
35	160.5	5.3	917	1 HXA3_HAEIN	P45355 haemophilus
36	160.5	5.3	928	1 PM10_CHLPN	Q9rb65 chlamydia p
37	160	5.3	497	1 FLIC_ECOLI	P04949 escherichia
38	160	5.3	504	1 FLIC_SALSE	Q06983 salmonella
39	159.5	5.2	1322	1 ICEA_PANAN	P20469 pantoea ana
40	159	5.2	504	1 FLIC_SALBU	Q06969 salmonella
41	159	5.2	504	1 FLIC_SALDU	Q06971 salmonella
42	158.5	5.2	1200	1 ICEN_PSESY	P06620 pseudomonas
43	158	5.2	948	1 HP11_DEIRA	P58867 deinococcus
44	158	5.2	1310	1 VAC3_HELPY	Q48253 helicobacte
45	158	5.2	1637	1 MRSP_STAAU	P80544 staphylococ

ALIGNMENTS

RESULT 1
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT: 1039 AA.
AC P39180: P76360; P75614; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nishimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horluchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RX Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded

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CC or send an email to license@isb-sib.ch).

CC	EMBL; M22618; AAA50323.1; -;
DR	PIR; A28182; A28182.
DR	Hemolysis; Toxin; Outer membrane; Signal.
KW	
FT	SIGNAL
FT	1 30
FT	CHAIN
FT	31 1608
FT	SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;
CC	HEMOLYSIN.

```
Db 466 SAAKPEDAEVYSGKQTVYLRGIWYNSFLTAVMSFPGTASGANVNLGRLNAFAGNVV 525
QY 351 GT-----KVTFAAGNGTTATVSKDDGNITVKYDVNVGDALNVNOLQ--NSGNLDSKA 402
Db 526 GTILNQEGROYVYSGATATVGNNEGREVLSGGITDGVVLSGGLOAVSSGGKASATV 585
QY 403 VAGSSGKVI--SGNVSPSKGMDVTNINAGN---NIEITRNKNIDIAATSMT-POFSSV 456
Db 586 INEGGAQFVYDGGQVGTCTNIKNKGTIRVDSSASALNALS-SGNLFTSGATLPETITM 644
QY 457 -----SLGAGAD-----APTLSDVDEGALN----- 476
Db 645 AALSVSQNHASNIVLENGLLRVTSGGTATDTTNSAGRLRIDDDGFTINGTTINADGIV 704
QY 477 VGSKDANKPVRIINVA-----PGVKEGDTVNVAAQLKGV---AQLNNRIDNVDG 522
Db 705 AGNIQNDGNFNLNLAENYDFETELSGSLVVKDNTGIMTYAGTLTQAQGVNKK----- 758
QY 523 NARAGTAQAIAATAGLA---QAYLPKSKSMAIGGTYRGEAGYAGYSSISDYG-----NW 574
Db 759 NGGIIFDSAVVNADMAVNQAINISDOATING-----SVNNGSIVINNS 804
QY 575 VIRGTASGNSRGHFGTS 591
Db 805 IINGNITNDADLSFGTA 821

RESULT 4
YDEK_ECOLI STANDARD; PRT; 1325 AA.
ID YDEK_ECOLI
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1993 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasaundaram S., Tagami H., Takeda J.,
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
```

```
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
CC EMBL; A5000248; AAC74583.1; -
CC EMBL; D90793; BAA15190.1; ALT_INIT.
CC EMBL; D90794; BAA15197.1; ALT_INIT.
CC EMBL; X73295; CAA51730.1; ALT_FRAME.
CC PIR; S34315; S34315.
CC EcoGene; EG11780; ydek.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal;
FT Complete proteome.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
FT CONFLICT 884 884 N -> K (IN REF. 3).
FT CONFLICT 1317 1317 M -> S (IN REF. 3).
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 6.7%; Score 203.5; DB 1; Length 1325;
Best Local Similarity 22.6%; Pred. No. 0.0057;
Matches 149; Conservative 72; Mismatches 274; Indels 163; Gaps 29;

QY 1 MKRISRIINNALNAVWVSELTRNHRKASATVATATLTLFATVVOANATDDDDLYLE 60
Db 1 MNRIYRVINWCTLQVFOACSELTTRRACKSTVNLKSSGLTTRKFSRL----- 47
QY 61 PVORTAVVLSFRSDKEGTG---EKEGTEDSNWAVYFDEKRV--LKAGAITLKAGDNLKIK 115
Db 48 ---TLGVLLALSGSASGASLEVDNDQITNIDTDVAYDAYLVGWYGTGLVNLAGNASLT 104
QY 116 QNT-----NENTNENTNDSSFTYSLKKDLTDLTSLVETKLSFGANGKNVNI-TSDFKGL 168
Db 105 TIITSVIGANEDSEGVNVVLCGTWRL-----YDSGNARPLNVGSGTGL 150
QY 169 N-----FAKETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNTVNDNDDEKKRA 218
Db 151 NIKQKHVDGGLRLGSGTGGTVNVVEGDSVLTTFEIG-SYGTGSLNITD----- 203
QY 219 ASVKDVLNAGWNKIGVKPGTITASDNVDVFTYDTVEFLSADTKTTTVNVESKNGRTEV 278
Db 204 -----KG-----YVTSSIVA-----ILGYQAGSNGQVVE 228
QY 279 KIGAKTSVIEKDGKLVTKGKCGKSGSSTDEGELVTAKEVIDAVNKGWRMKTTFANGQ 338
Db 229 KGG--EWLKNNDSSEFEIGNOGTGEATIREGLVTAENTIGGNATG-----IGTLNVQ 282
QY 339 TGQADFETVTSKTKVTFASGNGTTATVSKDDQGNITVK-YD-VNVGDALN--VNLQNS 394
Db 283 ----DQDSVITVRLRYNGVFGNG---TVNISNGLNINKEYSLVGQDGHGVVNVTDKG 335
QY 395 GWNL-----DSKAVAGSSKGVISGNVSPSKGMDVTNINAGN----- 432
Db 336 HWFLGTGEAFRIYITGADAGDGLNVSSEKGVDSGIITAG---MKET---GTGNITVKDK 389
QY 433 NIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALN-----GSKDANKPVR 487
Db 390 NSVITNLGTLNGDGHGEMNISNOGLVSVNGSSLSLGGTGVGNVSIITGGMVEVKNVY 449
QY 488 ITNVAPGVKEGDTVNVAAQLKGVAAQNLNINRIDVNGNARAGIAQIA---TAGLAQAYLPG 544
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Db 450 TTIGVAGVGNLISDGG--KFVSONITELGDKASGIGTLNLMMDATSSDETVCINVGNE-G 506
Qy 545 KSMMAIGGTYRGEAGYAI-----GYSSISDGNVGNVIKGTASGNSR-----GHFGT 590
Db 507 SGIVNVNGATLNGTYGFIGNASKGIVNISTDSLMLK-TSSTNAQLQGVGLGT 563

RESULT 5
OMPA_RICRI
ID OMPA_RICRI STANDARD: PRT: 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
  antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
  repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
  S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31227; AAA26380.1; -
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.5%; Score 199; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. NO. 0.018;
Matches 143; Conservative 71; Mismatches 261; Indels 166; Gaps 29;
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Qy 34 VATAVLATILLFATVQANATDDDDLYLEPVQRTAVVLSFRSDEKGTCEKGTEDSNWAVF 93
Db 39 VATGVIAINNNAAFNNGNN--WNEITAAGV-----ANGTPAGGQNNWAFY 86
Qy 94 D-----EKRVUKA-----GAI-----TLKAGDNLKIKQ 116
Db 87 GGDYTVTADAADRIIKAINVAGTTPVGLNITQNTVGSIIKGNLLPVTNAGKSLTLNG 146
Qy 117 NTNENTNENTNDSSTYSILKDLTDLTSVETEKLSFGANG-----NKYNITS--DT 165
Db 147 NNAANHGFDAPADNY-----TGLNIALG-----GANAALIISOAPSRIAGNIDG 196
Qy 166 KGLNEFAKETAGTNGDPTVHLNGIGSTLTLLTNTGATTNTVNDV---TDDEKKRAASYK 222
Db 197 GGIITVTDAAINGT-----IGNNALATVNVGAGTATLGGAVIKATTTKLTNAASVL 249
Qy 223 DVLNAGNIIKGVKPGTASDNVDVFTVYDVEFLSADTKTT---TVNVESKD---NG-- 273
Db 250 TLTNANAVLTGAIDNTTGGDNVGLNGLASQVTDIGNTNSLATISVGAGTATLGGAV 309
Qy 274 -KRTEVKIGAKTSVIKEDGKLVG---KGKGENCSSTDEGGLVTAK---EVIDAVN 324
Db 310 IKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANGIVFTTGNSTVGNVGNATLATVN 369
Qy 325 KAGWRMKTTTANGQTQADKFETVSGTKVTFASNGITATVSKDDQGNIT---VKYDYN 381
Db 370 VCAGLLQ---VOGGVVKANTINLTNDSAVTFT--NPVVVTGAIDNTGNANGIVTFTGN 424
Qy 382 ---VGDALNVNLQNSGWNLDKAVAGSGKVIISGNSPSKMKMETVINA--GNNIEI 436
Db 425 SVTVDIGNTALATVNVGAGTATLGGAVIKATTTKLTNAASVLTLT--NANAVLTGAIDN 483
Qy 437 TENGKNIDIAT-----SMTPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 484
Db 484 TTGGDNVGLNGLASQVTDIGNTNSLATISVGAG--TATLGGAVIKATTTKLTDAAS 541
Qy 485 PVRTINAPVKGEDVNTVNAQLKGVAQNLNNRINDVNGNARA---GIAQAIATAGLAQA 540
Db 542 AVKFTN--PVVVTGAIDNTG-----NANGIVFTTGNSTVTDIGNTNSLAT----- 586
Qy 541 YLPKGSMMAIGGTYRGEAGYAGYSSISDGTGNWVKGTPAS 581
Db 587 -----ISVGAGT-----ATLGGAVIKATTT 606

RESULT 6
HLIA_PROMI
ID HLIA_PROMI STANDARD: PRT: 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
  hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
  Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
  CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
  DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
  ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
  REQUIRES HPMB FUNCTION.
CC
```

CC -1- SUBCELLULAR LOCATION: Outer membrane.
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -1- SIMILARITY: TO S. MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M30186; AAA25657.1; .
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.4%; Score 195; DB 1; Length 1577;
Best Local Similarity 20.5%; Pred. No. 0.018;
Matches 152; Conservative 110; Mismatches 233; Indels 246; Gaps 39;

QY 23 TRNTRKRATVATA-----VLATLFLFATVQANATDDDDLLYLEPQRTAVVLSF 71
DB 619 TNKQTSSELISDAQLTVYSGNDVNVIGSLIKSADKLGIHSLGLDINVKSAQQVTKIDDE 678
QY 72 RSKQEGTGEKGTEDSNWAVYFEKRVLKAGATLTKAGDNLTKONTNENTNTNDSSF 131
DB 679 KTSIAITGHAKEDVQKYSAGF-----HITHTKNTSTETEQAQS 719
QY 132 TYS-----LKKDLT-----DL-----TSVETKLSFGANGKVNITSDTKGLNFAKET 174
DB 720 TISGANVDLQANKDVTAGSGLTKTAGNASITGDVNAFVSTENK-----KQT 766
QY 175 AGTNGDPTVH-----LNGIGS-----TLTDTLLNTGATTVTND-NVTDDEK 215
DB 767 -DNTDPTTSGFSYTGVDKVGSKADFOYDKQHTQTEVTKNRGSQTEVAGDLTIPTAN-- 822
QY 216 KRAASVKDLNAGNKGKPGTTASDNDV--FVRTYDVTVEFL-----SADTKTTTVNV-- 267
DB 823 -----KDLLHEG-----ASHHVEGRYQESGENTQHLAVNDSETSKTDSLNVGI 865
QY 268 -----ESKDNKRTVEKIGAKTSVKE---KD-----G 292
DB 866 DVGVDLYSGVTPVKKAIEDGVNT--TKPGNNTDLTKKVTARDIAIANLNSLETNPVG 924
QY 293 KLVTGKKGKSGSSTDPE---GEGLVTAKEVIDAVNK---AGWRMKTTP-----TANGQTG 340
DB 925 VEVGKGGGSGSQSDTSQAVSTSNAGKIDIDSNNKLHDQGTQYQSGIGSLTANTHTS 984
QY 341 QA--DKPETVTSGTK-----VTFASNGGTTATVSKDDGNTITVKYDVNVGDLNVLNQLNS 394
DB 985 EATLDKHQTTFHETKGGQICGVSTKGTSDITVAIKGSGQTT-----DNALMETRAKGS 1037
QY 395 GW--NLDSKAVAGSGKVISGNSPSKGMDETWINAGNNIETR-----NG 440
DB 1038 QFTSNGDISINVENAHEYGAQDAQKGG---TV-INAGGDLTLAQATDTHSESQSNNVG 1093
QY 441 K-NIDITATSTPQFSSVSLAGADAPTL--SVDDDEGALNVGSKDANKPVRTITNVPAGYKEG 498
DB 1094 SANLKVGT--TPE--SKDYGGGFGNAGTTHHSKEQTAKVCTIGTSQGIENLGNHNTLQG 1149
QY 499 DVTNVAOLKGVANLNRIID-----NVDGNARAGIAQ-----AIATAGLAQA 540
DB 1150 --THLSSEQDIALNATNKVDLQSSASEHTEKGNLNSGGVQAGFGCKKMTDDASSVNGL--- 1204
QY 541 YLPCKSKMWAIG-----GGTYRGEAGYAGYSSI-----SDTCGNV 575
DB 1205 ---GSAQFAIGKODEKSVSREGGTINNSGNLTINGNSVHLQGAQVNSKDTQLTQSQGDIE 1261

QY 576 IKGTASGNSRGHFGTASVGY 596
DB 1262 ITSAQSTDYKNNWGT--DIGF 1280

RESULT 7
YDBA_ECOLI STANDARD; PRT; 2003 AA.
ID YDBA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-PEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydBA.
GN YDBA OR B1401/B1405.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sasaki S., Seki Y., Sivasubraman S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RX STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
RT Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -1- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYS8 (AC P25928).
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
CC BETWEEN AMINO ACIDS 839 AND 840.
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CC -----
DR EMBL; A5000237; AAC74483.1; ALT_SEQ.
DR EMBL; A5000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR EcoGene; EG11307; ydBA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

[illegible]

```
FT CONFLICT 92 126 137 157 368 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 126 137 157 368 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 137 157 368 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 157 368 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 368 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 374 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 640 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 669 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 793 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 803 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 804 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 823 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 898 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 908 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 985 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1009 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1013 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1182 1314 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
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FT CONFLICT 1451 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1624 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1628 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1872 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1875 1878 1936 1965 1970 1997 2021
FT CONFLICT 1878 1936 1965 1970 1997 2021
FT CONFLICT 1936 1965 1970 1997 2021
FT CONFLICT 1965 1970 1997 2021
FT CONFLICT 1970 1997 2021
FT CONFLICT 1997 2021
FT SEQUENCE 2021 AA; 203328 MW; 327FC42D/CB24668 CRC64;

Query Match 6.2%; Score 189; DB 1: Length 2021;
Best Local Similarity 21.6%; Pred. No. 0.048;
Matches 176; Conservative 86; Mismatches 287; Indels 264; Gaps 40;

QY 10 NSALNAAVVVSELTNR-HTKRASATVAT-AVLATLLFATVQANATDDDD-----LYLEPV 62
DB 415 NNGIVTFGTGDTGNTGNATLISVGAGKATLGGAIKATTKLTNDASAVTFNPV 474
QY 63 QRTAV-----VLSFRSDEKGEKGTEDSNWAVFDEKRVLKAGAI-----TLKA 108
DB 475 VVTGAIDNTGNANNGIVTFGTGDTGNTGNATLISVGAGKATLGGAIKATTKL 533
QY 109 GDNLIKQNTN-----ENT-NEN-----TNDSEFTYSL-KKDLTDLTSVETEKLSF 152
DB 534 TDNASAVTFNPVVVGAIDNTGNANNGIVTFGTGDTGNTGNATLISVGAGKATL 593
QY 153 GA-----NGKNVITSDTKGLNPAKETAGTN-----GDPTVHLNGIGSTLT 193
DB 594 GGAIKATTKLTNDASAVTFNPVVVGTGAIDNTGNANNGIVTFGTGNTGN-IGNTNA 652
QY 194 DTLNLTGA-----TTNVNDNVTDDEKRAASVKDLVNLGNWIKGVKPGTTA 240
DB 653 LATNVVAGIATLEGAVIKATTKLTN-----AASVLTNTNVNAVLTGAIDNTTG 702
QY 241 SDNVDFVRYTYTFEFLSADTKTT-----TVNV-----ESKDNQ-----KRTVEKIGAKTSVKEK 290
DB 703 VDNVGVNLNGALSQVGTGNTGNATLISVGAGKATLGGAVIKATTKLTNDASAVTF 762
QY 291 DGLVLTG-----KKGKNGSSSTDEGEGLVTAK-----EVIDAVNKA-----GWRMKTTTA 335
DB 763 NPVVVGTGAIDNTGNANNGIATFGDSTVTGNTGNATLISVGAGKATLGGAVIKATTKLTNDASAVTF 822
QY 336 N-----GOTQADK-FEVTSGTKVTFASGN-GTTATVS-----367
DB 823 NLTDNASAVTFNPVVVGTGAIDNTGNANNGIVTFGTGDTGNTGNATLISVGAGKAT 882
QY 368 -----KDDQGNITVKYDVNVGDALNVNOLQNSGNWLDKSAVAGSGKVI 413
DB 883 TLGGAIKATTKLTNDASAVTFNPVVVGTGAID-----NIG-NANNGIVTFGTGDTG 936
QY 414 NVSPSKGMDVTVNINAGNNIEI--TRNGKNIDIATSMTPQFSSVSLGADAP-----T 466
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DB 937 NIGNTNAL--ATNVVGAGVTLQAGGSLDANNIDFGARSTLEFNGPLDGGGNAIPYFKGA 994
QY 467 LSVDDGEGALNVGSK-----DANK-PVRIYN-----DANK-PVRIYN-----490
DB 995 IANGNNAILNVNTKLLTAYHLTTGTVAEINIGAGNLFADASAGDVTLLNAQDHFALD 1054
QY 491 -----VAPGVKEGDV-----TNYAOLKGVQAQNLNNR 516
DB 1055 SALVLSNLTCGVYNNILLAADLVAPGVDEGTVDGVDGVLNIGSNVA---GAARN---1107
QY 517 IDNVGNA-----RAGTAQAIATAGLAQAYLPK-----SMAIGGGTYR-GEAGYAI 563
DB 1108 IGDVGKNTLLIYNAVTTTDDVNLGIONVLINNADFTSSTAFNAGTIQINDATYTI 1167
QY 564 -----GYSSISDTGNWIKGTASGNSR 585
DB 1168 DANNGNLINPAGNIKFAHAQAQILQNLSSGNDR 1200

RESULT 9
OMP_RICRI STANDARD; PRT; 1654 AA.
ID OMP_RICRI AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";
RT Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii.";
RT Mol. Microbiol. 3:1579-1586(1989).
CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
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CC EMBL: X16353; CAA34403.1;
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
```


Db 381 NTLTGSSVDTGATGMVIGSGDGTNTTISGHSVDNATGALISGNGTTTTFAGDIAVSGG 440
 QY 181 PTVHLNGIGSTLTDPR----LLNTGATTNTNDVTDDEKKRAASKVDVLNAGNKGKVP 236
 Db 441 PTAIIIDGNATIKNTGSDISAGSGTVIDGNARVNNDGDMTITD-----GGRG 491
 QY 237 GTTASDNDFVRYTDFEFLSADTTRTTTNNVESKNGKREYKIGAKTSVIREKDGKLYT 296
 Db 492 GHITGDNVVI-----DNAGSTTVSGADATALIYEGDNALVI 527
 QY 297 GKG-----KGNGSSDDEGEGLVT--A 316
 Db 528 NEGNOTISGAVGTRIDGDDAHTNTGDIADVAGSAAVINDNGSLTQAGDLLVTDGA 587
 QY 317 KEVI--DAVNKAGWRMKTTTANGQCOADKFETVTSKTKVF-----ASNGGTTATVS 367
 Db 588 MGIIHYGTGNEA-----KNTGNATVRDADSVGFVAGEKNTFNKGGIDIVSLNGTGALVS 642
 QY 368 KDDOGNITKYDVNVGDALNVNQLNSGNWLDKSKAVAGSGKRV--ISGNVSPS-----418
 Db 643 -GDMSQVTLDDGINV--VSVDSEGVFSATGVSVSGSDNAVDITGNVNISADYQDDDL 698
 QY 419 -GKKWDETIVNAGNIEITRNGK-NI-----DIATSMTPQFSSVSLGAGADATLSVDDRG 473
 Db 699 AAGAPPLTGCVVVGNGTNTVTLNGLNIDNDLSATGGQYLDVVGLSVTGGDNDVEID--G 756
 QY 474 ALNVGSKDANKPRTITNAPVKGEGDVNTVAQLKGAQNLNRIIDNVGNARAGIAQATA 533
 Db 757 GINI--THSEDPDGTG-----ADITGISVSGNSTVTLNGH-STIDTNTVVGGHVILA 806
 QY 534 -----TAGLAQAYLP-----GKSMMAIGGTYRGEAG-----YAI----563
 Db 807 RVNNGSLLIGDSDVVVDNVNVIPTCYTYNNALLMADGEGSTENKNGDITSHGVYSVIRA 866
 QY 564 -GYSSISDTGNVIVKGTASGNSRGHGTSAVSG 595
 Db 867 DNGSEVNSGDIIVATYNSNSEDRAAIPRASG 899

RESULT 12
 ID OMPB_RICCN STANDARD; ID OMPB_RICCN PRT; 1655 AA.
 AC Q9KKA3; Q9KKA3; Q9KKA3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)
 DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
 DE (rOmpB) [Contains: 120 kDa surface-exposed protein (Surface protein
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
 GN OMPB OR RC1085
 OS Rickettsia conorii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID=781;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Malish 7;
 RX MEDLINE=21442074; PubMed=11557893;
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
 RA Raoult D.;
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";
 RL Science 293:2093-2098(2001).
 RN [2]
 RP SEQUENCE OF 33-1649 FROM N.A.
 RC STRAIN-Indian tick typhus, and Malish 7;
 RX MEDLINE=20393643; PubMed=10939649;
 RA Roux V., Raoult D.;
 RT "Phylogenetic analysis of members of the genus Rickettsia using the
 RT gene coding the outer-membrane protein ompB (ompB).";
 RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
 RN [3]

RP SEQUENCE OF 353-1655 FROM N.A.
 RC STRAIN-Malish 7;
 RA Stenos J., Walker D.;
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia
 RT australis, the most divergent rickettsia of the spotted fever group.";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
 CC SIMILARITY).
 CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
 CC (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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 CC
 CC EMBL; AE008659; AAL03623.1; -
 CC EMBL; AF123721; AAF34124.1; -
 CC EMBL; AF123726; AAF34129.1; -
 CC EMBL; AF149110; AAD39533.1; -
 CC InterPro; IPR003858; rOmpA_rOmpB.
 CC Pfam; PF02708; rOmpA_rOmpB; 1.
 KW Antigen; S-layer; Cell wall; Complete proteome.
 FT CHAIN 1 1334
 FT CHAIN 1335 1655
 FT VARIANT 61 61
 FT VARIANT 75 75
 FT VARIANT 78 78
 FT VARIANT 251 251
 FT VARIANT 413 413
 FT VARIANT 959 959
 FT VARIANT 988 988
 FT VARIANT 1139 1139
 FT CONFLICT 353 354
 FT CONFLICT 776 776
 FT CONFLICT 1159 1159
 FT CONFLICT 1177 1177
 FT CONFLICT 1492 1492
 FT SEQUENCE 1655 AA; 168342 MW; E49E19377D9FCE37 CRC64;
 SQ
 Query Match 6.1%; Score 184.5; DB 1; Length 1655;
 Best Local Similarity 22.1%; Pred No. 0.063;
 Matches 147; Conservative 76; Mismatches 292; Indels 149; Gaps 30;
 QY 10 NSALNAAVVVSELTNRHTRASATVATVATLTLFATVQANATDDDDLLYLEPVQRTAVVL 69
 Db 211 NGTLN-----VTNGFIKVSSEFATVNVINIGDGGIMFADNVNLTNLQANGATI 263
 QY 70 SFRSDKEGTEGEGTESNVAVFDEKRVLKAGAILKAGDNLK-----IKQ 116
 Db 264 TF-----NGTDGTGLRLVLLSKNAATDFNVVTSGLGSLNGKIEFTNVAVNGOLKA 313
 QY 117 NTNEN-----TNTENTDSS-FTYSLKKDLTDLTSVETKLSFGANGKNVNITSDTKGLNF 170
 Db 314 NAGANAATVGTNNGAGRAAGVVSVD-----NKGATIDQGVYAKDM 355
 QY 171 AKETAGTNGDPT-----VHLNGIGSTLTDLTLLNTGATTNTVNDVTDDEKRAASVKD--- 223
 Db 356 VIQSANAVGVNFRHIVDVGTDGTTAFKTAASKVAIKVATQNSNFGCTDFGNLAAQIIVPNTM 415
 QY 224 VLNAGNINIKVPGTTSASNDVDFRYD---TVEFLSADTKTTTVN-----VESKNG--- 273
 Db 416 TLNGNFTGDSNPGNTAG-----VITFDANGTLASASADANAVAVTNNTAIEASGAGVVQ 470

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QY 274 ----KRTEVIGAKTSVKEKDGKLVTK-----GKGENSGSTDEGLVTAKEVID 321
Db 471 LSGTHAAELRGNAGSVFKLADGVINGKYNQTFALVGLAAGTITLDGSAITG-----D 526
QY 322 AVNKAGWRMTTNTANGTGQADKPEYVT-----SGTKVTFASNGTTFATVSKDDQG 372
Db 527 IGNAGG----AAALQGITLANDATKTLTGLGANIGANGGTINFQANGGTIKLTS---TQN 580
QY 373 NITVKYDV-----NYGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKGM-DE 424
Db 581 NIVVDFDLAIATDGTGVVDASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDG 640
QY 425 TVNIN--AGNN--IEITRGNKNDIATSMTPQ-----FSSV-----SILGACADAPTLSDV 470
Db 641 DVAINELVIGNGAVQFAHNTYLTIRTNAGQGKIIFNPVNNNTTLAGTGNLGS-ATN 699
QY 471 DEGALNVGSKDANKPVRITNVAPGVKEGDTNVAOLKGVQNLNNDVNDG-NARAGIA 529
Db 700 PLABINFGSKGAANVDVNLNVGKGNL-YATNITTTDA---NVGSFIFNAGGTNIVSG-- 753
QY 530 QAIATAGLAO-----AYLPKGSMAIGGTYRGEAGYALGYSSISDGTGNWIKGTASG 582
Db 754 ----TVGGQGNKFNVALONGTIVKFLGNATFNNGNTTIAAN-STLQIGGNYTADFVASA 808
QY 583 NSRG 586
Db 809 DGTG 812
```

RESULT 13

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ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=22593339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
RL Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
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EMBL: X52970; CAA37140.1; -
DR PIR: S11672; S11672.
DR HSSP: P06620; IINA.
DR InterPro: IPR000258; Ice_nucleatn.
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DR Pfam; PF00818; Ice_nucleation; 81.
DR PRINTS; PR00327; ICENUCLEATN.
DR PROSITE; PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; CBB451D959ECAD63 CRC64;
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Query Match 6.0%; Score 182; DB 1; Length 1567;

Best Local Similarity 20.2%; Pred. No. 0.079;
Matches 115; Conservative 83; Mismatches 274; Indels 98; Gaps 19;

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QY 77 GTGKEGTEGDSNVAAYFDEKRVLRKAGAITLKAGDNLKIKONTN-----ENTNENTNDSSE 131
Db 735 GSTQSGSDSLTAGYGSTQTARKGSDVTAGYGSTGTAGADSTLIAGYGSTQTSKSSDSSL 794
QY 132 TYSUKKDLT-----DLTSVETEKLSFGA-----NGKNVNTSKTKLNTAKE 173
Db 795 TAGYGSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSKSSDSSLTAGYGSTQTSARE 854
QY 174 -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATTNVTNDVTDKKAASV 221
Db 855 GSDVTAGYGSTGTAGADSTLIAGYGSTQTSKSSDSSLTAGYGSTQTSKSSD----- 905
QY 222 KDVLNAGWNINKGVKPGTASDNVDVFRVTDVFEFLSADTKTTTNNVESKDKGRTEVKIG 281
Db 906 ---VTAGYGSTG-----TAGADSTLIAGYGSTQTSKSSDSSLTAGYGSTQTSKSSDWTAG 957
QY 282 AKTSVIRKEKDGKLVTKGKGENSGSTDEGELVTAKEVIDAVNKAGWRMTTNTANGTQ 341
Db 958 YGSGTAGADSTLIAGYGSTQTSKSSD-----DSSLTAGYGSTQTSKSSDVT 1003
QY 342 ADKFETVTSKTVTFASNGTTFATVSKDDQGNITVKYDVNVNVDALNVNQLNSGNWLDK 401
Db 1004 AGYSGTAGADSTLIAGYGSTQTSKSSD---SSLTAGY-----GSTQTSKSSDVTAGYGST 1057
QY 402 AVAGSSGKVISGNVSPSKGMDETNINAGNNIETIRNGKNIDIATSMTPFSSVSLGAG 461
Db 1058 GTAGADSTLIAGYGSTQTSKSSDSSLTAGYGST-QTARQGSDI-----TAGYSGTGT-AG 1109
QY 462 ADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDTNVAOLKGVQNLNNDVND 521
Db 1110 ADSSLIA--GYGSTQTAGYDSNLTAGYGSTQTSKSSDSSLTAGYGSTTAGHDSLIAGY 1167
QY 522 GNARAGIAQAIAATA-GLAQAYLPCKSMMAIGGTYRGEAGY-----AIGYSSISDTG--NW 574
Db 1168 STQTAGYNSILTYGYGSTQTSKSSDSSLTAGYGST--STAGYDSTLTAGYGSTQTSKSS 1225
QY 575 VIKGTASGNSRGH-----FGTSSASVGYQ 597
Db 1226 LTAGYGSNSTAGHSSSLIAGYGSTQIAGYE 1255
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RESULT 14

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YMBJ_CAEEL STANDARD; PRT; 918 AA.
ID YMBJ_CAEEL
AC P34487;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.
DE F59B2.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
```

RA	Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA	Latrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA	Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA	Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA	Wohlman P.,
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL	elegans.";
RL	Nature 368:32-38(1994).
CC	-----
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CC	or send an email to license@lsb-sib.ch).
CC	-----
DR	EMBL: Z11505; CAA77581.1; -
DR	PIR: S31132; S31132.
DR	WormPep: F5982.12; CE01024.
DR	Hypothetical protein.
DR	KW
DR	SEQUENCE 918 AA; 965660 MW; E64F8DB6B14945DE CRC64;
DR	-----

Query Match 6.0%; Score 181; DB 1; Length 918;
Best Local Similarity 21.8%; Pred. No. 0.047;
Matches 129; Conservative 89; Mismatches 216; Indels 158; Gaps 29;

Qy	65	TAVVLSRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLTKAGDNLIKQ-----NT	118
Db	91	TVVGADGKNITENSEKKDG-----YNKESKY-----DEANENTKIKSADGSVIET	135
Qy	119	NEINTNEINTDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTISDFKGLNFAKETAG-T	177
Db	136	GKSHNKSSDDAAS--SYGLEK--SSKYADKNGTMLUSSNTKINNOSRSAAALDEGNEFVNQ	192
Qy	178	NGDPTVHLINGTSLTD-----TLNLTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIK	232
Db	193	NADGTFLRNNTGHNKTDEHLSSHNVLDENAQMSIGADGTSNITNKRKSGVGDShNA-----	247
Qy	233	GVRPGTTASDNVDVRYDVFELADTKTTTVNVESKDNGKRTVEVIGAKTSV-----	286
Db	248	-----ASD-----AHSNFESLDAOG-----NKKSQNTSKKAASASGNADPESNLES	289
Qy	287	IKKDGKLVTKGKGENGSSSTDEGEGLVTAKEVITDAVNKAGWRMKTITANGOTQADKFE	346
Db	290	LKNADGTFMNGSTGNFNNTSYDK-----ATAEVMSS-----KKNYNADG--TSSMEASH	336
Qy	347	TVTSGTKVTFTASG-----NG--TTATVYSKDDQ-----GNITVKYDVNVNGD	384
Db	337	AGNSSKINSASGQSDLSVMVGPNGIKSHSTSNKTDNYALDEANQASGISEQIGKNGQR	396
Qy	385	ALNVNQIQLONGWNLDSK--AVAGSSGV--TSGNVSPSGKGMDETVTNINAGNN-----	433
Db	397	SLNESSIE--SQRKAESRNTAADPLDSVDANGTVSSSHSKSASGTSIDENHNKTHALQAS	455
Qy	434	IEITRNCKNIDIATS----WTPQFSSVSLGA-----GADAPTLSDVDEGALNVGSKDANKPV	486
Db	456	VDEHGNKKNISIDGYNRKKTGEFGENSEMSASIKNADGTMSQVKNKDTNRTNTYEAEKSA	515
Qy	487	RITNVAPGVREGDVTNVQALKGVAQNLNRRIDNVDGNRAGIAQAIATAGLAQAYLPCKS	546
Db	516	LEKN---HEKNSDGT---FKDESKGNSRVNRTDGG-----S	546
Qy	547	MMATGGGTYRGEAGYATGYSSISDTGNWVIGKTASGNSRGHGTGTSVGYQW	598
Db	547	NLAYI-----SYSYCKGQVSSN-----ETIASNA---FNTSDAESNF	582

RESULT 15
OMPB_RICTY

OMP8-RICTY STANDARD; PRT; 1645 AA.

P36989;

15-JUL-1998 (Rel. 36, Created)

15-JUL-1998 (Rel. 36, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (Scs5) (römp8) (römp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].

OMP8 OR SLP.

Rickettsia typhi.

Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

Rickettsiaceae; Rickettsiae; Rickettsia.

NCBI_TaxID=785;

[1]

SEQUENCE FROM N.A.

STRAIN=WILMINGTON;

MEDLINE=94040787; PubMed=8224886;

Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;

"Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";

Gene 133:129-133(1993).

[2]

PARTIAL SEQUENCE.

STRAIN=WILMINGTON;

MEDLINE=92114896; PubMed=1370573;

Ching W.M., Carl M., Dasch G.A.;

"Mapping of monoclonal antibody binding sites on CNBR fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";

Mol. Immunol. 29:95-105(1992).

[3]

IDENTIFICATION OF CLEAVAGE SITE.

MEDLINE=92104688; PubMed=1729180;

Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

"Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.";

Rt Infect. Immun. 60:159-165(1992).

-1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

-1- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP8 FAMILY.

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Query Match	6.0%;	Score 181;	DB 1;	Length 1645;
Best Local Similarity	20.6%;	Pred. No. 0.093;		
Matches 156; Conservative	91;	Mismatches 271;	Indels 238;	Gaps 38;

Gaps 38;

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QY 28 KRASATVATAVLATLLEA-----TVQANATDDDDLYLE-----PVQRT 65
Db 10 KIISAGLVTAATVAGSGVAMGAVMQNRTTNAATTVDGAGFDQTGAGVNLPAVN 69
QY 66 AVVLSFRSDKEGCEKEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN-----119
Db 70 SVI-----TANSNAITFTPNP--NLNSLFDTANTLAVTINENTTLGFV 113
QY 120 ENTNENTNDSFTYSLKKDLT---DLTSVETEKLSFGAN--GNKVNI-----TSDTKGLN 169
Db 114 TNVTKQGNFFNTIGACKSLITIGHGITAQAAATTKSAQNVVSKVNAGAAINDNLSGVG 173
QY 170 FAKETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNVNTD-----NVTDEKKRAASYKDV 224
Db 174 SIDFTAAPS---VLEFNLIPTTQEAPLTGLGDNAKIVNGANGILNITNGFVK-----VSDK 226
QY 225 LNAWNKIKGVKPGTASDNVDVFTYTFVEELSADTKTTTVNVESKD-----NGK 274
Db 227 TFAG--IKTINIGD--NOGLMFTTPDAANALNLQGGGNTINFNGRDGTGKLVLSKNGN 282
QY 275 RTEVKI----GAKTSVIKED----GKLVTKGKG-----ENGSS-----STDEG- 310
Db 283 ATEFNVTGSLGGLNKGVIEFDTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSDVNGN 342
QY 311 ----EGLVTAKEVIDAVNKAQRKTTTANGQT-----GQADKFETVTSGTKVTF 356
Db 343 AATISGOVYAKDIV-----IQSANAGQVTFEHLVDVGLGKTNFKTADSKVIITE 393
QY 357 ASGNGTATVSKDQGNITVKYDVN-----VGDAINVNQLONGWNLDSKAVAGSS 407
Db 394 NASFGST-----DFGNLAVQIVVPNNKILTGNF IGDA-----KNNG-NTAGVITFNAN 440
QY 408 GKVISGNVSPS-----GKMDETVNI-----NAGNNIEITRNGKNIDIAT 447
Db 441 GTLVSGWTDPNIVVTNKAIEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPV 499
QY 448 SMTPOFSVSLGAGA---DAPTLSDVD--EGALNVGSKD---ANKPVRTITNVP-----GV 495
Db 500 NONPLVNNALAGSIQLDGSIIITGDIGNGAVNAALQDITLANDASKILTSGANIIGA 559
QY 496 KEG-----DVTNVAQLKGVAON-----LNNRIDNV 520
Db 560 NAGGAIHFQANGGTIQLTSTONNILDVDFDLDTDTQGVVDASSLTNNQTLTNGSIGTI 619
QY 521 DGNAR-----AGIAQAIATAG---LAQAYLPKGSMAIGGTY-----RGEAGYAIG 564
Db 620 GANTKTLGRFNVGSSKTLNAGDVAINELVWENDGSVHLTHNTYLYLTKTINAANQGGKIIV 679
QY 565 YSSISDTGNWVIKGTASGNSRG-----HFQTSASVG 595
Db 680 AADPINTDTALADGTNLGSAESPLSNTHFATKAANG 715
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Search completed: July 3, 2002, 08:48:58
Job time: 704 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:08 ; Search time 100.13 seconds
(without alignments)
1033.167 Million cell updates/sec

Title: US-09-771-382-8
Perfect score: 3042
Sequence: 1 MNKISRIIWNLSALNAWVVS.....TASGSRGHTSASVGYQW 598

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3042	100.0	598	2 Q93QY5	Q93qy5 neisseria m
2	3036	99.8	598	2 Q9JPT0	Q9jpt0 neisseria m
3	3021	99.3	598	2 Q9JPS0	Q9jps0 neisseria m
4	2982	98.0	598	2 Q9JPR9	Q9jpr9 neisseria m
5	2948	96.9	594	2 Q9JPH7	Q9jph7 neisseria m
6	2882	94.7	594	2 Q9JPS2	Q9jps2 neisseria m
7	2878	94.6	594	2 Q9JPI3	Q9jpi3 neisseria m
8	2852	93.8	594	2 Q9JQY4	Q9jqy4 neisseria m
9	2821.5	92.8	599	2 Q9JPR8	Q9jpr8 neisseria m
10	2772	91.1	600	2 Q9JPS6	Q9jps6 neisseria m
11	2769	91.0	590	2 Q9JPS3	Q9jps3 neisseria m
12	2752.5	90.5	599	2 Q9JPS8	Q9jps8 neisseria m
13	2733	89.8	598	2 Q9JPR7	Q9jpr7 neisseria m
14	2716.5	89.3	591	2 Q9JPS7	Q9jps7 neisseria m
15	2716.5	89.3	591	16 Q9JRI8	Q9jri8 neisseria m
16	2709	89.1	592	2 Q9AQF0	Q9aqf0 neisseria m

17	2705.5	88.9	591	2 Q93QY3	Q93qy3 neisseria m
18	2702	88.8	600	2 Q9JPS5	Q9jps5 neisseria m
19	2666	87.6	592	2 Q9JPS9	Q9jps9 neisseria m
20	2658	87.4	592	2 Q93QY2	Q93qy2 neisseria m
21	2634.5	86.6	595	2 Q9JPH0	Q9jph0 neisseria m
22	2627.5	86.4	589	2 Q9JPI0	Q9jpi0 neisseria m
23	2616.5	86.0	589	2 Q93QY1	Q93qy1 neisseria m
24	2521	82.9	592	16 Q9JQW4	Q9jqw4 neisseria m
25	2507.5	82.4	526	2 Q9JPS4	Q9jps4 neisseria m
26	2499.5	82.2	530	2 Q9JPS1	Q9jps1 neisseria m
27	1312.5	43.1	2353	2 P71401	P71401 haemophilus
28	1054	34.6	1098	2 Q48152	Q48152 haemophilus
29	450	14.8	1299	16 Q9F3X6	Q9f3x6 pasteurella
30	403	13.2	2059	16 Q9PD50	Q9pd50 xylella fas
31	390	12.8	1107	2 Q9F2D8	Q9f2d8 salmonella
32	383.5	12.6	1190	16 Q9PC04	Q9pc04 xylella fas
33	365	12.0	2712	16 Q9F3X5	Q9f3x5 pasteurella
34	263.5	8.7	1291	16 Q92K07	Q92kq7 rhizobium m
35	255.5	8.4	1953	16 Q98HJ2	Q98hj2 rhizobium l
36	253.5	8.3	2276	2 Q93TY6	Q93ty6 staphylococ
37	241	7.9	1004	16 Q9PD63	Q9pd63 xylella fas
38	228	7.5	2747	2 Q9L800	Q9l800 aeromonas s
39	225.5	7.4	1557	2 Q9RN12	Q9rni2 haemophilus
40	223	7.3	1039	2 Q9L6T7	Q9l6t7 escherichia
41	219	7.2	3705	2 Q9F285	Q9f285 versinia pe
42	217.5	7.1	832	2 Q54356	Q54356 moraxella c
43	217.5	7.1	1039	2 Q9L6T8	Q9l6t8 escherichia
44	217	7.1	1536	2 Q48031	Q48031 haemophilus
45	216	7.1	1040	2 Q9AL50	Q9al50 shigella fl

ALIGNMENTS

RESULT 1

Q93QY5 PRELIMINARY; PRT; 598 AA.
AC Q93QY5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bz10;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157603; AAK68864.1; -
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 100.0%; Score 3042; DB 2; Length 598;
Best Local Similarity 100.0%; Pred. No. 2e-118;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKISRIIWNLSALNAWVVSSELTRNHTKRASATVAVLATLLFATVQANATDDDLYLE 60

Db 1 MNKISRIIWNLSALNAWVVSSELTRNHTKRASATVAVLATLLFATVQANATDDDLYLE 60

Qy 61 PVQRTAVLSFRSDKEGTEGKEDTSNNWAVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120

Db 61 PVQRTAVLSFRSDKEGTEGKEDTSNNWAVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120

Qy 121 NTNENTNDSFTYSLSKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180

Db 121 NTNENTNDSFTYSLSKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180

QY 1 MNKISRIIWSALNAWVVSSELTRNHTKRASATVAVLATLILFATVQANATDDDDLYLE 60
 DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVAVLATLILFATVQANATDDDDLYLE 60
 QY 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
 DB 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
 QY 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
 DB 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
 QY 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
 DB 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
 QY 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
 DB 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
 QY 301 GENGSTDEGGLVTAKEVIDAVNKGWRMKTTTANGOTQADKPFVTSGTKVTFASGN 360
 DB 301 GENGSTDEGGLVTAKEVIDAVNKGWRMKTTTANGOTQADKPFVTSGTKVTFASGN 360
 QY 361 GTTATVSKDDOQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
 DB 361 GTTATVSKDDOQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
 QY 421 KMDETVNIAGNIIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
 DB 421 KMDETVNIAGNIIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
 QY 481 DANKPVRITNAPGVKEGDTNVNQLKGVAQNLNNRIDNVNCGNARAGIAQATATAGLAQA 540
 DB 481 DANKPVRITNAPGVKEGDTNVNQLKGVAQNLNNRIDNVNCGNARAGIAQATATAGLAQA 540
 QY 541 YLPKGSMAIAGGTGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598
 DB 541 YLPKGSMAIAGGTGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598

RESULT 4

QJUPR9 ID QJUPR9 PRELIMINARY; PRT: 598 AA.
 AC QJUPR9;
 DT 01-OCT-2000 (TremBLrel. 15, Created)
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
 DE OUTER MEMBRANE PROTEIN GNA992.
 GN GNA992.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NGH36;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 RT Meningococcus by Whole-Genome Sequencing."
 RL Science 287:1816-1820(2000).
 DR EMBL: AF226382; AAF42531.1.
 SQ SEQUENCE 598 AA; 62718 MW; 9095P8E31AD7C76D CRC64;

Query Match 98.0%; Score 2982; DB 2; Length 598;
 Best Local Similarity 98.0%; Pred. No. 6.1e-116;

Matches 586; Conservative 2; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MNKISRIIWSALNAWVVSSELTRNHTKRASATVAVLATLILFATVQANATDDDDLYLE 60
 DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVAVLATLILFATVQANATDDDDLYLE 60
 QY 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
 DB 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120
 QY 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
 DB 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
 QY 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
 DB 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
 QY 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
 DB 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300
 QY 301 GENGSTDEGGLVTAKEVIDAVNKGWRMKTTTANGOTQADKPFVTSGTKVTFASGN 360
 DB 301 GENGSTDEGGLVTAKEVIDAVNKGWRMKTTTANGOTQADKPFVTSGTKVTFASGN 360
 QY 361 GTTATVSKDDOQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
 DB 361 GTTATVSKDDOQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
 QY 421 KMDETVNIAGNIIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
 DB 421 KMDETVNIAGNIIETRNKGNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
 QY 481 DANKPVRITNAPGVKEGDTNVNQLKGVAQNLNNRIDNVNCGNARAGIAQATATAGLAQA 540
 DB 481 DANKPVRITNAPGVKEGDTNVNQLKGVAQNLNNRIDNVNCGNARAGIAQATATAGLAQA 540
 QY 541 YLPKGSMAIAGGTGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598
 DB 541 YLPKGSMAIAGGTGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598

RESULT 5

QJUPH7 ID QJUPH7 PRELIMINARY; PRT: 594 AA.
 AC QJUPH7;
 DT 01-OCT-2000 (TremBLrel. 15, Created)
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
 GN GNA992 OR NHHA.
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BZ198, AND 297-0;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
 RA Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B
 RT Meningococcus by Whole-Genome Sequencing."
 RL Science 287:1816-1820(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BZ198;
 RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer
 RL membrane protein of *Neisseria meningitidis*.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF226368; AAF42517.1; -
 DR EMBL; AF226358; AAF42507.1; -
 DR EMBL; AF157604; AAK68865.1; -
 SQ SEQUENCE 594 AA; 62361 MW; 436BDDDE68263C5C CRC64;

Query Match	96.9%;	Score 2948;	DB 2;	Length 594;
Best Local Similarity	97.3%;	Pred. NO. 1.5e-114;		
Matches 582;	Conservative	2;	Mismatches 10;	Indels 4;
				Gaps 1;

Qy	1	MNKISRIIWN	SALNANWV	VSSEL	TRNHT	KRASAT	VAT	AVI	LAT	LLF	PAT	VQ	NAT	DDDD	LYLE	60													
Db	1	MNKYIRIWN	SALNANWV	VSSEL	TRNHT	KRASAT	VAT	AVI	LAT	LLF	PAT	VQ	NAT	DDDD	LYLE	60													
Qy	61	PVORTAVV	LSFRSD	KEGT	EGE	TSD	SNNA	VY	FDE	KRV	LKAG	AIT	LKAG	DN	LKIK	QNTNE	120												
Db	61	PVORTAVV	LSFRSD	KEGT	EGE	TSD	SNNA	VY	FDE	KRV	LKAG	AIT	LKAG	DN	LKIK	QNTNE	120												
Qy	121	NTNENT	NDSSFT	YSL	KDL	TDL	TS	VE	T	KL	SF	CANG	KVNI	TSD	T	KGLN	FAKETAG	180											
Db	117	NTNENT	NDSSFT	YSL	KDL	TDL	TS	VE	T	KL	SF	CANG	KVNI	TSD	T	KGLN	FAKETAG	180											
Qy	181	PTVHLN	IGIST	LTD	TLL	NT	GATT	N	VND	N	V	DD	DE	K	RAA	S	V	KD	VLNAG	WNI	KGV	KPG	T	TA	240				
Db	177	PTVHLN	IGIST	LTD	TLL	NT	GATT	N	VND	N	V	DD	DE	K	RAA	S	V	KD	VLNAG	WNI	KGV	KPG	T	TA	240				
Qy	241	SDNVDF	VRTY	DT	VE	FL	SAD	TK	T	T	V	N	V	S	K	D	N	K	R	T	E	V	I	K	E	D	300		
Db	237	SDNVDF	VRTY	DT	VE	FL	SAD	TK	T	T	V	N	V	S	K	D	N	K	R	T	E	V	I	K	E	D	300		
Qy	301	GENGSST	DE	GE	GL	V	T	A	K	E	V	I	D	V	N	K	A	G	R	M	K	T	T	A	N	G	O	360	
Db	297	GENGSST	DE	GE	GL	V	T	A	K	E	V	I	D	V	N	K	A	G	R	M	K	T	T	A	N	G	O	360	
Qy	361	GTTATV	S	K	D	D	G	N	I	T	V	K	Y	D	V	N	G	D	A	L	N	V	O	L	N	G	S	420	
Db	357	GTTATV	S	K	D	D	G	N	I	T	V	K	Y	D	V	N	G	D	A	L	N	V	O	L	N	G	S	420	
Qy	421	KMDETV	NI	NAG	NI	E	T	R	N	K	N	I	D	I	A	T	S	M	A	P	Q	F	S	S	V	S	L	480	
Db	417	KMDETV	NI	NAG	NI	E	T	R	N	K	N	I	D	I	A	T	S	M	A	P	Q	F	S	S	V	S	L	480	
Qy	481	DANKP	V	R	I	T	N	V	A	P	C	V	E	G	D	T	N	V	A	O	L	K	G	V	A	O	L	N	540
Db	477	DANKP	V	R	I	T	N	V	A	P	C	V	E	G	D	T	N	V	A	O	L	K	G	V	A	O	L	N	540
Qy	541	YLPCKS	M	A	T	G	G	T	Y	R	E	A	C	Y	A	I	G	S	I	S	D	T	G	N	W	I	K	T	598
Db	537	YLPCKS	M	A	T	G	G	T	Y	R	E	A	C	Y	A	I	G	S	I	S	D	T	G	N	W	I	K	T	598

RESULT	6	
Q9JPS2		
ID	Q9JPS2	PRELIMINARY; PRT; 594 AA.
AC	Q9JPS2;	
DT	01-OCT-2000 (TrEMBLrel. 15, Created)	
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	OUTER MEMBRANE PROTEIN GNA992.	
GN	GNA992.	
OS	Neisseria meningitidis.	
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=487;	
RN	[1]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=NGE31;	
RC	MEDLINE=PubMed-10710308;	
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,	
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason J., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.,
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
SO SEQUENCE 594 AA: 62114 MW: 1E2A63A78F53D256 CRC64;

Query Match	94.7%	Score 2882;	DB 2;	Length 594;
Best Local Similarity	95.3%;	Pred. No. 8.le-112;		
Matches 570; Conservative	6;	Mismatches 18;	Indels 4;	Gaps
Qy	1	MNKISRIIWN	SALNAWVVVSEL	TRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db	1	MNKIYRIIWN	SALNAWVVVSEL	TRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60
Qy	61	PVQRTAVVL	SRDSKEGTGEKETS	DNMAVYDEKRVLKAGAITLIKAGDNLKIKONTWE 120
Db	61	PVQRTAPVL	SFHADSEGTGEKETS	DNMGVYEDKKGVLTAGTITLIKAGDNLKIKONTDE 120
Qy	121	NTNENTNDS	FETYSLSKDLTDL	SLRSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNGD 180
Db	121	NTNA-----	SSFTYSLSKDLTDL	SLRSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNGD 176
Qy	181	PTVHLNGIG	STLDTLLNTGATT	NVTNDVNTDDEKRAASVKDVLNAGNWKIKVKGPTTA 240
Db	177	TTVHLNGIG	STLDTLLNTGATT	NVTNDVNTDDEKRAASVKDVLNAGNWKIKVKGPTTA 236
Qy	241	SDNVDFVRT	YDTEVEFLSADT	KTTTNNVYESKDNGKRTEVKIGAKTSVIEKDKGLVLTGKK 300
Db	237	SDNVDFVRT	YDTEVEFLSADT	KTTTNNVYESKDNGKKTEVKIGAKTSVIEKDKGLVLTGDK 296
Qy	301	GENGSSDTE	GEGLVTAKEVIDA	NKAGRWKMTTANQOTQOAKFEFVTSGTKVTFASGN 360
Db	297	GENGSSDTE	GEGLVTAKEVIDA	NKAGRWKMTTANQOTQOAKFEFVTSGTKVTFASGN 356
Qy	361	GTTATVSKD	QDGNITVKYDYN	VGDALNVQLNSGNWNLDSKAVAGSSGKVISGNVSPSKG 420
Db	357	GTTATVSKD	QDGNITVKYDYN	VGDALNVQLNSGNWNLDSKAVAGSSGKVISGNVSPSKG 416
Qy	421	KMDETVIN	AGNNIETIRNCK	NDIATISWTPQPSVSSVSLGAGADAPTLSDVDDGALNVGSK 480
Db	417	KMDETVIN	AGNNIETIRNCK	NDIATISWTPQPSVSSVSLGAGADAPTLSDVDDGALNVGSK 476
Qy	481	DANKPVRIT	TVAPGCVKEGDV	TNVAQLKGVAQLNLNRRIDNVGDNARAGIAQAIATAGLAQ 540
Db	477	DANKPVRIT	TVAPGCVKEGDV	TNVAQLKGVAQLNLNRRIDNVGDNARAGIAQAIATAGLQA 536
Qy	541	YLPCKSMA	ATGGGTYRGEAG	YATGYSISDITGNWIKGTASGNSRHFGTSAISVGQW 598
Db	537	YLPCKSMA	ATGGGTYRGEAG	YATGYSISDITGNWIKGTASGNSRHFGTSAISVGQW 594

RESULT	7	
Q9JPI3		
ID	Q9JPI3	PRELIMINARY; PRT; 594 AA.
AC	Q9JPI3:	
DT	01-OCT-2000	(Tremblrel. 15, Created)
DT	01-OCT-2000	(Tremblrel. 15, Last sequence update)
DT	01-MAR-2001	(Tremblrel. 16, Last annotation update)
DE	OUTER MEMBRANE PROTEIN GNA992.	
GN	GNA992.	
OS	Neisseria meningitidis.	
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=487;	
EN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NG3/88, AND BZ232;	
RX	MEDLINE=20175756; PubMed=10710308;	
RA	Pizza M., Scariato V., Masignan V., Giuliani M.M., Arico' B.,	

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT Moxon E.R., Grandi G., Rappuoli R.
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC SPRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -
DR EMBL: AF157608; AAK68869.1; -
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 92.8%; Score 2821.5; DB 2; Length 599;
Best Local Similarity 92.7%; Pred. No. 2.5e-109;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 1 MNKISRIWNSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59
Db 1 MNKIRIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60
QY 60 EPVORTAVLSFRSDKRGTEGKEDTESNNAVYFDEKRVLKAGAITLKAGDNLKIKONTN 119
Db 61 EPVRSALVLOFMIDKRGGENESTGIGWSIYDNNHTLHGATVTLKAGDNLKIKONTN 120
QY 120 ENTNENTNDSSTYSLSKKDLTDLTSVETEKLSFGANGKNYNTSDTKGLNFAKETAGTNG 179
Db 121 KNTNENTNDSSTYSLSKKDLTDLTSVETEKLSFGANGKNYNTSDTKGLNFAKETAGTNG 180
QY 180 DPTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIRKVPKGT 239
Db 181 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIRKVPKGT 240
QY 240 ASDNVDPVRYDYTVFELSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGK 299
Db 241 ASDNVDPVHYDYTVFELSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGK 300
QY 300 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFFETVTSKVTFSAG 359
Db 301 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFFETVTSKVTFSAG 360
QY 360 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419
Db 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
QY 420 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 479
Db 421 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 480
QY 480 KDANKPVRITNPAPGKGVGEGDVTNVAQLKGYAQNLRNIDNVNAGNARAGIAQATAGLAQ 539
Db 481 KDANKPVRITNPAPGKGVGEGDVTNVAQLKGYAQNLRNIDNVNAGNARAGIAQATAGLVO 540
QY 540 AYLPGKSMAIIGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSASVGYQW 598
Db 541 AYLPGKSMAIIGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSASVGYQW 599

RESULT 10

Q9JPS6 PRELIMINARY; PRT; 600 AA.

AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RT Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226371; AAF42520.1; -
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.1%; Score 2772; DB 2; Length 600;
Best Local Similarity 91.4%; Pred. No. 2.8e-107;
Matches 553; Conservative 15; Mismatches 25; Indels 12; Gaps 3;

QY 1 MNKISRIWNSALNANWVVSSELTRNHTKRASATVATVATLTLFAT-----VQANATD 53
Db 1 MNKIRIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQASADNVQASADN 60
QY 54 DDDLYLPVORTAVLSFRSDKRGTEGKEDTESNNAVYFDEKRVLKAGAITLKAGDNLK 113
Db 61 EEEYLEPVPVTVAPVLSFYSDAEDTGEKEVTENTNMGIYFDKNGVKGAGTITLKAGDNLK 120
QY 114 IKONTNENTNDSSTYSLSKKDLTDLTSVETEKLSFGANGKNYNTSDTKGLNFAKE 173
Db 121 IKONTNENTNA----SFSTYSLSKKELTDLTSVGTGKLSFGANGKNYNTSDTKGLNFAKE 176
QY 174 TACTNGDPTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIRK 233
Db 177 TACTNGDPTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNIRK 236
QY 234 VKPGTTASDNVDPRYDYTVFELSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKG 293
Db 237 VKPGTTASDNVDPRYDYTVFELSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKG 296
QY 294 LVTGKKGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFFETVTSK 353
Db 297 LVTGKKGKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFFETVTSK 356
QY 354 VTFASNGTGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 413
Db 357 VTFASNGTGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 416
QY 414 NVSPSKGKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEG 473
Db 417 NVSPSKGKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD- 475
QY 474 ALNVGSKDANKPVRITNPAPGKGVGEGDVTNVAQLKGYAQNLRNIDNVNAGNARAGIA 533
Db 476 ALNVGSKDANKPVRITNPAPGKGVGEGDVTNVAQLKGYAQNLRNIDNVNAGNARAGIA 535
QY 534 TAGLAQAYLPKGSMAIIGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSAS 593
Db 536 TAGLAQAYLPKGSMAIIGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSAS 595
QY 594 VGYQW 598
Db 596 VGYQW 600

RESULT 11

Q9JPS3 PRELIMINARY; PRT; 590 AA.
ID Q9JPS3

Q9JPS3;
01-OCT-2000 (TREMBlrel. 15, Created)
01-OCT-2000 (TREMBlrel. 15, Last sequence update)
01-MAR-2001 (TREMBlrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992.
GNA992.
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
[1]
SEQUENCE FROM N.A.
RC STRAIN=NGE28;
MEDLINE=20175756; PubMed=10710308;
Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL: AF226378; AAF42527.1; -.
SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.0%; Score 2769; DB 2; Length 590;

Best Local Similarity 92.3%; Pred. No. 3.7e-107;

Matches 554; Conservative 9; Mismatches 25; Indels 12; Gaps 3;

QY 1 MKKISRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDDDL-L 59
DB 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDEEDL 60
QY 60 EPVQRTAVVLSRDSKEGTEGEGED-SNWAYVDFEKRVLKAGAITLKAGDNLIKQNT 118
DB 61 DPVQRTAVVLSRDSKEGTEGEGEDSNWAYVDFEKRVLKAGAITLKAGDNLIKQ-- 118
QY 119 NENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 178
DB 119 -----NGTFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 170
QY 179 GQPTVHLNGIGSTLDTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 238
DB 171 GDTTVHLNGIGSTLDTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 230
QY 239 TASDNVDFVRYTYTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEDGKLVTCG 298
DB 231 TASDNVDFVRYTYTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEDGKLVTCG 290
QY 299 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 358
DB 291 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 350
QY 359 GNGTATVSKDDQGNITVYKVDVNVGDALNVNOLQSGWNLDSKAVAGSSGKVISGNVSP 418
DB 351 GNGTATVSKDDQGNITVYKVDVNVGDALNVNOLQSGWNLDSKAVAGSSGKVISGNVSP 410
QY 419 KGKMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVG 478
DB 411 KGKMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVG 470
QY 479 SKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRNIDVNDGNARAGIAIAIATAGLA 538
DB 471 SKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRNIDVNDGNARAGIAIAIATAGLV 530
QY 539 QAYLPCKSMWATGGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 598
DB 531 QAYLPCKSMWATGGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 590

RESULT 12

Q9JPS8
ID Q9JPS8; PRELIMINARY; PRT; 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
OUTER MEMBRANE PROTEIN GNA992.
GNA992.
Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
[1]
SEQUENCE FROM N.A.
RC STRAIN=A22;
MEDLINE=20175756; PubMed=10710308;
Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
Moxon E.R., Grandi G., Rappuoli R.;
"Identification of Vaccine Candidates Against Serogroup B
Meningococcus by Whole-Genome Sequencing.";
Science 287:1816-1820(2000).
EMBL: AF226364; AAF42513.1; -.
SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 90.5%; Score 2752.5; DB 2; Length 599;

Best Local Similarity 91.7%; Pred. No. 1.8e-106;

Matches 551; Conservative 14; Mismatches 31; Indels 5; Gaps 3;

QY 1 MKKISRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD-DDDL-L 59
DB 1 MKKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDDEEYL 60
QY 60 EPVQRTAVVLSRDSKEGTEGEGEDSNWAYVDFEKRVLKAGAITLKAGDNLIKQNTN 119
DB 61 EPVQRTAVVLSRDSKEGTEGEGEDSNWAYVDFEKRVLKAGAITLKAGDNLIKQNTD 120
QY 120 ENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 179
DB 121 ENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 180
QY 180 DPTVHLNGIGSTLDTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 239
DB 181 DPTVHLNGIGSTLDTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 238
QY 240 A--SDNVDFVRYTYTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEDGKLVTC 297
DB 239 TQSGENVDFVRYTYTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEDGKLVTC 298
QY 298 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 357
DB 299 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 358
QY 358 SNGTATVSKDDQGNITVYKVDVNVGDALNVNOLQSGWNLDSKAVAGSSGKVISGNVSP 417
DB 359 SNGTATVSKDDQGNITVYKVDVNVGDALNVNOLQSGWNLDSKAVAGSSGKVISGNVSP 418
QY 418 SKGMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNV 477
DB 419 SKGMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNV 478
QY 478 GSKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRNIDVNDGNARAGIAIAIATAGL 537
DB 479 GSKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRNIDVNDGNARAGIAIAIATAGL 538
QY 538 QAYLPCKSMWATGGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQ 597
DB 539 QAYLPCKSMWATGGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQ 598

```
Qy 598 W 598
Db 599 W 599

RESULT 13
QJUPR7 PRELIMINARY; PRT; 598 AA.
AC QJUPR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SW2107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42534.1; -.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 89.8%; Score 2733; DB 2; Length 598;
Best Local Similarity 90.8%; Pred. No. 1.1e-105;
Matches 545; Conservative 15; Mismatches 36; Indels 4; Gaps 2;

Qy 1 MNKISRIWNSALNANWVVSSELTNRHNTKRASATVATVATLTLFATVQANATDDDLYLE 60
Db 1 MNKIRIWNALNANWVVSSELTNRHNTKRASATVATVATLTLFATVQASANNEDEDL 60
Qy 61 PVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLKAGAITLKAGNLIKQNTNE 120
Db 61 PVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLKAGAITLKAGNLIKQNTNE 120
Qy 121 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 180
Db 121 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 180
Qy 181 PTVHLNGIGSTLTDLTLAGSASHVDAGNQST--HYTRAASIKOVNLNAGWNIKGVKPTTA 240
Db 181 TTVHLNGIGSTLTDLTLAGSASHVDAGNQST--HYTRAASIKOVNLNAGWNIKGVKPTTA 240
Qy 241 --SDNVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLVTK 298
Db 241 --SDNVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLVTK 298
Qy 239 GQSENVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLVTK 298
Db 239 GQSENVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLVTK 298
Qy 299 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEVTSVGTGKVT 358
Db 299 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEVTSVGTGKVT 358
Qy 359 GNGTATVSDDOGNTVYDVNVGDALNVNOLNSGNWLDKSAVAGSGKVTSGNVSPS 418
Db 359 GNGTATVSDDOGNTVYDVNVGDALNVNOLNSGNWLDKSAVAGSGKVTSGNVSPS 418
Qy 419 KGKMDETVNIAGNNIEITRNCKNIDIAATSWTPOFSSVSLGAGADAPTLSDVDEGALNV 478
Db 419 KGKMDETVNIAGNNIEITRNCKNIDIAATSWTPOFSSVSLGAGADAPTLSDVDEGALNV 478
Qy 479 SKDANKPVRITNVAPGVKGDVTNVAOLKGVAQNLRNDRIDVGNAGAGATATATAGLA 538
Db 479 SKDANKPVRITNVAPGVKGDVTNVAOLKGVAQNLRNDRIDVGNAGAGATATATAGLA 538

RESULT 14
QJUPR7 PRELIMINARY; PRT; 591 AA.
AC QJUPR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 89.3%; Score 2716.5; DB 2; Length 591;
Best Local Similarity 90.7%; Pred. No. 5.4e-105;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKISRIWNSALNANWVVSSELTNRHNTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 MNKIRIWNALNANWVVSSELTNRHNTKRASATVATVATLTLFATVQASANNEDEDL 60
Qy 58 YLPPVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLKAGAITLKAGNLIKQ 116
Db 61 YLPPVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLKAGAITLKAGNLIKQ 120
Qy 117 NTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 176
Db 121 -----NGNFTYSLAKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 170
Qy 177 TNGDPTVHLNGIGSTLTDLTLLNTGATTNTVNDVTDDEKRAASVKOVNLNAGWNIKGVK 236
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Qy 237 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLV 296
Db 231 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKRTVEKIGAKTSVIREKDGKLV 290
Qy 297 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEVTSVGTGKVT 356
Db 291 GKDGENSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEVTSVGTGKVT 350
Qy 357 ASNGTTATVSKDDQGNITVYDVNVGDALNVNOLNSGNWLDKSAVAGSGKVTSGNV 416
Db 351 ASGKGTATVSKDDQGNITVYDVNVGDALNVNOLNSGNWLDKSAVAGSGKVTSGNV 410
Qy 417 PSKGMDETNIAGNNIEITRNCKNIDIAATSWTPOFSSVSLGAGADAPTLSDVDEGALN 476
Db 411 PSKGMDETNIAGNNIEITRNCKNIDIAATSWTPOFSSVSLGAGADAPTLSDVDEGALN 469
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QY 477 VGSKDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAG 536
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 QY 537 LAQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDTONWVKGTAAGNSRCHFTSASVGY 596
 Db 530 LVQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDTONWVKGTAAGNSRCHFTSASVGY 589
 QY 597 QW 598
 Db 590 QW 591

RESULT 15
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 AC Q9JRL8;
 DT 01-OCT-2000 (TREMREL. 15, Created)
 DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).
 DE GNA992 OR NMB0992 OR NHHA.
 GN Neisseria meningitidis, and
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487, 491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B, Bz169, Bz83, AND H44/76;
 RX MEDLINE=20175756; PubMed=10710308;
 RA Pizza M., Scarlati L., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galicotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
 RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
 RL Science 287:1816-1820(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tettelin H., Saunders N.J., Herdelberg J., Jeffries A.C., Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A., Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Gill J., Scarlati V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.";
 RL Science 287:1809-1815(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-N.meningitidis; STRAIN-PMC21;
 RA Peak I.R., Srikantha V., Dieckelman M., Moxon R., Jennings M.P.;
 RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF226375; AAF42524.1; -;
 DR EMBL: AE002450; AAF41395.1; -;
 DR EMBL: AF226367; AAF42516.1; -;
 DR EMBL: AF226370; AAF42519.1; -;
 DR EMBL: AF226374; AAF42523.1; -;
 DR EMBL: AF159611; AAK68872.1; -;
 DR TIGR: NMB0992; -;
 KW Complete proteome.
 SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73BC6 CRC64;

Query Match 89.3%; Score 2716.5; DB 16; Length 591;
 Best Local Similarity 90.7%; Pred. No. 5.4e-105;
 Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWNLSALNNAVYSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
 Db 1 MNKIYRIIWNLSALNNAVYSELTRNHTKRASATVATVATLTLFATVQANNEEQEEDL 60
 QY 58 YLEPVORTAVVLSFRSDKEGTGEKGTED-SNNAVYFDEKRVLKAGAITLKGADNLIK 116
 Db 61 YLDPVORTAVVLSFRSDKEGTGEKGTED-SNNAVYFDEKRVLKAGAITLKGADNLIK 120
 QY 117 NTNENTNENTSSFTYSLKDLTDLTSLKFGANGKNVNTSDTKGLNFAKETAG 176
 Db 121 -----NGTNFTYSLKDLTDLTSLKFGANGKNVNTSDTKGLNFAKETAG 170
 QY 177 TNGDPTVHLNGIGSTLTDLTNTGATTNTVNDVNTDDEKKRAASVKDVLNAGNKGVP 236
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 Db 231 GTTASDNVDPVRYDYVEFLSADTKTTTVNVEKDNKGRTEVKIGAKTSVIKEDGKLV 290
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 Db 291 GKCKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVSGTKVTF 350
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 QY 417 PSKGMDETVMINAGNNIEITRNKKNIDIAATSMTPPSSVSLGAGADAPTLSDVDEGALN 476
 Db 411 PSKGMDETVMINAGNNIEITRNKKNIDIAATSMTPPSSVSLGAGADAPTLSDVDEGALN 469
 QY 477 VGSKDANKPVRITNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAG 536
 Db 470 VGSKDNKPVRTNAPGVKEGDTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAG 529
 QY 537 LAQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDTONWVKGTAAGNSRCHFTSASVGY 596
 Db 530 LVQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDTONWVKGTAAGNSRCHFTSASVGY 589
 QY 597 QW 598
 Db 590 QW 591

Search completed: July 3, 2002, 08:48:10
 Job time: 701 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:23 ; Search time 104.77 seconds
(without alignments)

Title: US-09-771-382-9
Perfect score: 3023
Sequence: 1 MNKIYRIIWN3ALNAWTVVS.....TASGNSRGHFGASISVG YOW 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45

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SUMMARIES

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4	2971	98.3	598	22	AAU06177
5	2948	97.5	598	20	AAV23738
6	2948	97.5	598	22	AAU06178
7	2874	95.1	594	20	AAV23740
8	2874	95.1	594	21	AAV57044
9	2874	95.1	594	22	AAU06174
10	2802.5	92.7	599	20	AAV23743
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12	2802.5	92.7	599	22	AAV23743
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16	2733	90.4	592	20	AAV23737	A surface protein	
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42	593	19.6	1116	21	AAB37832	Neisserial conserv	
43	396.5	13.1	2314	22	AAB69136	M. catarrhalis les	
44	385.5	12.8	2123	22	AAE00701	Moraxella catarrha	
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ALIGNMENTS

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ID	AAAY23739 standard; Protein; 594 AA.	
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XX	AAAY23739;	
XX		
XX	08-SEP-1999 (first entry)	
DT		
XX		
XX	A surface protein of <i>Neisseria meningitidis</i> .	
DE		
XX		
XX	Surface protein; surface glycoprotein; infection; vaccine;	
KW	immunoreactive peptide.	
KW		
XX		
XX	<i>Neisseria meningitidis</i> .	
OS		
XX		
XX	WO9931132-A1.	
PN		
PD	24-JUN-1999.	
XX		
XX		
PF	14-DEC-1998; 98WO-AU01031.	
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XX	12-DEC-1997; 97GB-0026398.	
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PA	(ISIS-) ISIS INNOVATION LTD.	
PA	(UYOU) UNIV QUEENSLAND.	
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XX		
PI	Jennings MP, Moxon ER, Peak IRA;	
XX		
XX		
DR	WPI: 1999-418754/35.	
DR	N-PSDB; AAX85791.	
XX		
XX		
PT	<i>Neisseria meningitidis</i> surface proteins useful for treating	
PT	meningitis infections	
XX		

PS Claim 1; Page 95-97; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria meningitidis* which is approximately 62 kDa. The *N. meningitidis* surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of *N. meningitidis* infection in humans. The *N. meningitidis* surface glycoproteins can also be used to prevent or treat *N. meningitidis* infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

XX Sequence 594 AA;

Query Match 100.0%; Score 3023; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKIYRIWNSALNAMYVVSSELTNRHTRKASATVATATLTLFATVQANATDDDDLYLE 60
Db 1 mnkiyriwnsalnawvvsselttrhtrkrasatvatatlifattvqanatdddlyle 60

Qy 61 PVQRTAVVLSFRSDKEGTGEGTSDNNAVYFDEKRVLKAGAITLKAGONLIKQNTNE 120
Db 61 pvgtrtavvlsfrsdkegtgkgtednnavyfdekrvllkagaitllkagdnllkqntne 120

Qy 121 NTNDSSTFYSLKKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180
Db 121 ntndsstfyslkkdltldtsveteklsfgangkvnitstdtkglnfaketagtngdpvh 180

Qy 181 LINGIGSLTDTLTNTGATTNTVNDVDEKRAASVKDVLNAGWNKGVKPGTTASDNV 240
Db 181 lingigsltdtltntgattntvndvdekkraasvkdvlnagwnikgvkpgttasdnv 240

Qy 241 DFVRTYTVFELSADTKTTTVNVEKNGKKEVKGIGAKTSVKEKDGKLVTKGKDGK 300
Db 241 dfvrtvtyvfelsadtktttvnveskngkktvkgigaktsvikekdgklvtgkdgk 300

Qy 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGADKFEVTSCTNVTFAAGKGT 360
Db 301 sstdegeglvtakevidavnkagwrmtttangotgadkfetvtsctnvtfasgkgt 360

Qy 361 TVSKDDGNTIVKYDVNVGDAINYNQNLQNSGWNLDKAVAGSSGKVISGNVSPSKGK 420
Db 361 tvskddgntivkydvnnvgdalinynqlqnsqwnldskavagssgkvvisgnvspskgk 420

Qy 421 TVNINAGNNIEITRNGKNIDIASMAPQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK 480
Db 421 tvninagnnieitrngknidiatsmapqfssvslgagadaptilsvddegalnvsgskdtk 480

Qy 481 PVRTTNVAPGKGDVNTVAQLKGVAONLNNRIDNVDSNARAGTAQATATAGLVQAYLP 540
Db 481 pvrtnnvapgkgdvnvtaqlkgvaonlnnrindnvdsnaragtaqataglvqaylp 540

Qy 541 KSMMAIGDGYRGAGYAIGYSSISDGGNNIIKGTASGNSRGHFGASASGYQW 594
Db 541 ksmmaigdyrgagyaigyssisdggnniikgtasgnsrghfgasasyqgw 594

RESULT 2
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX AAU06179;
AC AAU06179;
XX 24-OCT-2001 (first entry)
DT
DE N. meningitidis B2198 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
QS *Neisseria meningitidis* strain B2198.

XX FH Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT Region 117..126
FT /label= V2
FT /note= "Variable region 2"
FT Region 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT Region 191..212
FT /label= V3
FT /note= "Variable region 3"
FT Region 213..231
FT /label= C4
FT /note= "Conserved region 4"
FT Region 232..238
FT /label= V4
FT /note= "Variable region 4"
FT Region 239..594
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU000069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09169.
XX New NhhA surface antigen polypeptides and polynucleotides from *Neisseria meningitidis*, useful in producing vaccines for treating or preventing broad spectrum of *Neisseria meningitidis* -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel *Neisseria meningitidis* mutant polypeptides of the surface antigen NhhA (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in CC diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of *N. meningitidis*, and in designing and/or screening of CC medicaments. The mutant proteins when used as a vaccine can effectively immunise against a broader spectrum of *N. meningitidis* strains than CC would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen NhhA from *N. meningitidis* strain B2198 is 1 of 10 NhhA polypeptide sequences (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in CC the present invention.
XX Sequence 594 AA;
SQ

Query Match 100.0%; Score 3023; DB 22; Length 594;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULTS

RESULT	3
AAY23742	
ID	AAY23742 standard; Protein; 598 AA.

AA AAY23742;

DT 08-SEP-1999 (first entry)

XX
DE A surface protein of *Neisseria meningitidis*.

XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.

XX
OS *Neisseria meningitidis*.

XX PN WO9931132-A1.

XX
PD 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX
PR 12-DEC-1997; 97GB-0026398.XX
PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.
XX

PI Jennings MP, Moxon ER, peak IRA;
XX

DR WPI; 1999-418754/35.
DR N-PSDB: AAX85794.

PT *Neisseria meningitidis*

PT meningitidis infections

PS Claim 1; Page 108-110; 132pp; English.

CC The present sequence represents a surface protein of *Neisseria*
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

XX	Sequence	598 AA;
SQ		

Query Match	98.3%	Score 2971;	DB 20;	Length 598;
Best Local Similarity	98.0%	Pred. No. 6.1e-172;		
Matches 586:	Conservative	1;	Mismatches	7;
				Indels

Qy	1	MNKYRIIWSALNAWVYVSELTRNHPTKRASATVATAVLATLFLFATVQANATDDDDLYLE	60
Db	1	mnkYriIwSalnawvVvseltrnhckrasatvatavlatlflfatvqanatadddlyle	60
Qy	61	PVQRTAVVLSPRSKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ----	116
Db	61	pvqrtavvlSfrsdektegektedsnwavYfdekrvIkagaitlkagdnIkikqntne	120
Qy	117	NTNENTNDSSPTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAPKETA	176
Db	121	ntnEntndssfTySlkkdlTdltsveteKlsfgangknvnitSdtkglnfaketaCngd	180
Qy	177	PTVHLNGTGSTPLDTLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKPGTTA	236
Db	181	ptvhlngIgstltdllntgattNvTndvntDdekkraasvkdvlNagwnIkvgpgttca	240
Qy	237	SDNVDFVRTYDTVFELSADTKTTTVNVVESKDNCKKTEVKIGAKTSVIEKDKGLVTKGKK	296
Db	241	sDnvdfvrtYdtvfeLsadtKtttvNvveskDngkktevkiGaktsvIekdglvTgkgk	300
Qy	297	DENSGSTDEBGLVTAKEVTDVANKAGWRMKTITANGOTGOADKFEFVTSGTNVTFSAGK	356

RESULT

RESULT 4
AAU06177
ID AAU06177 standard; Protein; 598 AA.

XX
AC AAU06177;XX
DT 24-OCT-2001 (first entry)

DE N. meningitidis H15 surface antigen NhhA polypeptide sequence.

XX Surface antigen NhbA; meningococcal disease; meningitis vaccine.

KW


```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 91-93; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 598 AA;
SQ
Query Match 97.5%; Score 2948; DB 20; Length 598;
Best Local Similarity 97.3%; Pred. No. 1.5e-170;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLALLFATVQANATDDDDLYLE 60
Db 1 mkiisriiwnsalnawvvselttrnhtkrasatvatvatlallfatvqanatdddlyle 60
QY 61 PVQRTAVLSFRSDKRGTEGCEKEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ- --- 116
Db 61 pvqrtavlsfrsdkgtegektedsnwavyfdekrvlikagaitlkagdnlikqntne 120
QY 117 NTNENTNDSFYSYSLKKDITLDTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
Db 121 ntentndsfyslkkdiltltsveteklsfgangkvnitsdtkglnfaketaagngd 180
QY 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGVKPGTTA 236
Db 181 ptvhlngigstltdtllntgattnvtndvtddekkraasvkdvlagnwnikgvpgtta 240
QY 237 SDNVDPRTYDVTVEFLSADTKTTNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296
Db 241 sdnvdprrtydvtveflsadtkttnveskdnkgkrtevkigaktsvikekgklvtgkx 300
QY 297 DENGSSTDEGLVTAKEVIDAVNKAQWRMKTNTTANGOTQADKFETVTSGTNVTFAAGK 356
Db 301 gengsstdeglvtakevidavnkagwrmkntttangqgqadkfetvtsgtktfasgn 360
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
Db 361 gttatvskddqgnitvkydvnvgdalnvqnlgnswnldskavagssgkvisgnvpskg 420
QY 417 KMDETVNIAGNNIETRNKKNIDTATSNAPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 421 kmdevtniagnnnietrnknidtatstnapofssvslgagadaptlsvddegalnvgsk 480
QY 477 DFNKPVRIITNAPGVKREGDVTNVAQLKGVAQLNNRIDNVGNARAGIAQAATAGLVOA 536
Db 481 dnfkpvritnnapgvkregdvtnvvaqlkgvaqlnnridnvgnaragiqaaataglaqa 540
QY 537 YLPKSNMAIGDITYRGEAGYAIQYSSISDGGNWIITKGTASGNSRGRHFGASVGYQW 594
Db 541 ylpkssmnaigdytyrgeagyaigysisdsdgnwniitkgtsngsrgrhfgtsasvgyqw 598
RESULT 6
AAU06178
ID AAU06178 standard; Protein: 598 AA.
XX AC AAU06178;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis B210 surface antigen NhA polypeptide sequence.
```

```
XX Surface antigen NhA; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain B210.
OS
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT Region 117..130
FT /label= V2
FT /note= "Variable region 2"
FT Region 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT Region 195..216
FT /label= V3
FT /note= "Variable region 3"
FT Region 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT Region 236..242
FT /label= V4
FT /note= "Variable region 4"
FT Region 243..598
FT /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09168.
XX
XX New NhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen NhA
XX (AAU06182-AAU06186). The modified or mutant NhA polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen NhA
XX from N. meningitidis strain B210 is 1 of 10 NhA polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 598 AA;
SQ
```

Query Match 97.5%; Score 2948; DB 22; Length 598;
 Best Local Similarity 97.3%; Pred. No. 1.5e-170;
 Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
 DB 1 mnkisiwiwnsalnawvvsselftrnhtkrasatvatvatltilfatvqanatdddddyle 60

QY 61 PVORTAVVLSFRSDKEGTGKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQ--- 116
 DB 61 pvtartavvlsfrsdkegtgkegedtsnwavfdekrvllkagaitlkagdnllkikqntne 120

QY 117 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNPAKTAGTNGD 176
 DB 121 ntntentndssftysllkdltdltsveteklsfgangkvnitsdtkglnfaketagngd 180

QY 177 PTVHLNGIGSTLDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKVGKPGTTA 236
 DB 181 ptvhlngigstltdtllntgattnvdndvlddekkraasvkdvlntagwnikvgkpgtta 240

QY 237 SDNVDFVRYTDFEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDKGLVTCKGK 296
 DB 241 sdnvdfvrytdfevlfsadtkttvnveskdngkrtveikigaktsvikekdglvtgkgl 300

QY 297 DENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFETVTSNTVTFASGK 356
 DB 301 dengssddegglvtakevidavnkagwrmttttangotqadkfetvtsntvtfasng 360

QY 357 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
 DB 361 gttatvskddognitvkvdydvngdalnvqlnsgwnldskavagssgkvvisgnvspkg 420

QY 417 KMDETVNIAGNIEITRNKNIDTSMAPQSSVSLGAGADAPTLISVDEGALNVGSK 476
 DB 421 kmdetvniagnieitrngknidtsmtppqfssvslgagadaptlisvdegalnvsgk 480

QY 477 DTKNRPVITNVAPGKGGDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAIATAGLVQA 536
 DB 481 dtknrvitnvapgkggdvtnvvaqlkgvaqnlrridndvgnaragiaqaiataglaqa 540

QY 537 YLPKSKMAITGGDTRYGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
 DB 541 ylpkksmaigtgdyrgeagyaigyssisdggnwiikgtasgnsrghfgtasasvgyqw 598

RESULT 7
 AAY23740
 ID AAY23740 standard; Protein; 594 AA.
 XX
 AC AAY23740;
 XX
 XX 08-SEP-1999 (first entry)
 DT
 XX
 DE A surface protein of Neisseria meningitidis.
 XX
 KW Surface protein; surface glycoprotein; infection; vaccine;
 KW immunoreactive peptide.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO9931132-A1.
 XX
 PD 24-JUN-1999.
 XX
 PF 14-DEC-1998; 98WO-AU01031.
 XX
 PR 12-DEC-1997; 97GB-0026398.
 XX
 XX (ISIS-) ISIS INNOVATION LTD.
 PA (UYQU) UNIV QUEENSLAND.
 XX
 XX Jennings MP, Moxon ER, Peak IRA;
 PI
 XX

DR WPI; 1999-418754/35.
 XX N-PSDB; AAX85792.
 PT Neisseria meningitidis surface proteins useful for treating N.
 XX meningitidis infections
 XX Claim 1; Page 100-101; 132pp; English.
 XX
 CC The present sequence represents a surface protein of Neisseria
 CC meningitidis which is approximately 62 kDa. The N. meningitidis
 CC surface glycoproteins, nucleic acids, the primers and optionally
 CC a thermostable polymerase, or antibodies are useful in a kit for
 CC the detection or diagnosis of N. meningitidis infection in humans.
 CC The N. meningitidis surface glycoproteins can also be used to
 CC prevent or treat N. meningitidis infection in humans, especially
 CC in the form of vaccines. The proteins and antibodies can also
 CC be used to identify immunoreactive peptides.
 XX
 XX Sequence 594 AA;
 SQ

Query Match 95.1%; Score 2874; DB 20; Length 594;
 Best Local Similarity 95.6%; Pred. No. 4.5e-166;
 Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
 DB 1 mnklyriiwnsalnawvvsselftrnhtkrasatvatvatltilfatvqastdddddyle 60

QY 61 PVORTAVVLSFRSDKEGTGKEGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
 DB 61 pvtartavvlsfrsdkegtgkegedtsnwavfdekrvllkagaitlkagdnllkikqntne 120

QY 121 NTNDSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKTAGTNGDPTVH 180
 DB 121 ntndssftysllkdltdltsveteklsfgangkvnitsdtkglnfaktagtngdptvh 180

QY 181 LNGIGSTLDTLLNTGATTNVDNVDDEKKRAASVKDVLNAGWNIKVGKPGTTASDNV 240
 DB 181 lngigstltdtllntgattnvdndvlddekkraasvkdvlntagwnikvgkpgttasdnv 240

QY 241 DFVRTYDVFELSDTKTTNVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGKGDENG 300
 DB 241 dfvrtydfevlfsadtkttvnveskdngkrtveikigaktsvikekdglvtgkdgend 300

QY 301 SSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFETVTSNTVTFASGKGTTA 360
 DB 301 sstdekglvtakevidavnkagwrmttttangotqadkfetvtsntvtfasgkgtta 360

QY 361 TVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420
 DB 361 tvskddognitvkvdydvngdalnvqlnsgwnldskavagssgkvvisgnvpskgkme 420

QY 421 TVNINAGNIEITRNKNIDTSMAPQSSVSLGAGADAPTLISVDEGALNVGSKDTNK 480
 DB 421 tvninagnieitrngknidtsmtppqfssvslgagadaptlisvdddegalnvsgkdank 480

QY 481 PVRTNVAPGKGGDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAIATAGLVQAYLP 540
 DB 481 pvrtnvapgkggdvtnvvaqlkgvaqnlrridndvgnaragiaqaiataglvqaylp 540

QY 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
 DB 541 ksmaiaiggyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 8
 AAY57044
 ID AAY57044 standard; Protein; 594 AA.
 XX
 AC AAY57044;
 XX
 XX 21-FEB-2000 (first entry)
 DT

XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
XX BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX Nisseria meningitidis.
OS
XX Key Location/Qualifiers
FH Misc-difference 104 /note= "Encoded by AATC"
FT
FT
XX W09958683-A2.
PN
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
PF
XX 13-MAY-1998; 98GB-0010276.
PR
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Ruelle J;
PI
XX WPI; 2000-053103/04.
DR
DR N-PSDB; AAZ39864.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal -
XX
XX Claim 4; Fig 2; 74pp; English.
XX
XX This is the Nisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing BASB029
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of
CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or prophylactic purposes.
CC polynucleotide, and for therapeutic or prophylactic purposes.
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
CC receiving the protein.
XX
SQ Sequence 594 AA;

Query Match 95.1%; Score 2874; DB 21; Length 594;
Best Local Similarity 95.6%; Pred. No. 4.5e-166;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAVWVSELTNRHTRKASATVATVATLTLFATVQANATDDDLYLE 60
DB 1 mnkiyriiwsalnawvavseltrnrhtkrasatvatvatlflfatvqastdddlyle 60
QY 61 PVORTAVWLSFRSDKGTGKGTEDSNWAVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120
DB 61 pvdrtavvlsfrsdkgtegtedsnwgvfydkkgvltagtitlkagdnlkikgntne 120
QY 121 NTNDSSFTYSLLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGNFAKTAGTNGDPTVH 180
DB 121 ntndssftysllkkdltdltsvteklsgangknvntsdtkgnlnfakktagtgngdptvh 180
QY 181 LNGIGSTLTLTLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGKVGKPGTTASDNY 240
XX

DB 181 lngigstltdltlntgattntndvtddekkraasvkdvlnagwnigkvgkpgttasdnv 240
QY 241 DFVRTYDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTCGKGDENG 300
DB 241 dfvrtvdtvfevlfsadtktttvnnveskdngkrtevkigaktsvkekdgklvtgkdgend 300
QY 301 SSTDEGEGLVTAKEVIDAVNKAQWRMKTTTTANGOTGOADKFETVTSGTNVTTFASGKGTTA 360
DB 301 sstdkgeglvtakevidavnkagwrmttttangotgqadkfetvtsgtntvtfasgkgtta 360
QY 361 TVSKDDQGNITVYKVDYVNGDALNVNQLQNSWNLDKAVAGSSGKVISGNVSPSKGKMD 420
DB 361 tvskddqgnitvmydvngdalinvnqlqnswnldskavagssgkvisgnvspskgkmd 420
QY 421 TVNINAGNIEITRNKGNIDDIATSMAPQSSVSLGAGADAPTLSDDEGALNVGSKDNTK 480
DB 421 tvninagnieltrngknidia tsmtpqssvslgagadaptlsvddegalnvsgskdank 480
QY 481 PVRITNVAFVKEGDTNVNAQLKGVANLNNRIDNVDGNARAGIAQAIATPAGLVQAYLPG 540
DB 481 pvrntnvapvkegdvtnvaqlkgvaqnlhndvndgnaragiataglvqaylpg 540
QY 541 KSMMAIGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 ksmmaiggdyrgeagyatgyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 9
AAU06174
ID AAU06174 standard; Protein: 594 AA.
XX
AC AAU06174;
XX 24-OCT-2001 (first entry)
DT
XX N. meningitidis EG327 surface antigen Nhma polypeptide sequence.
DE
XX Surface antigen Nhma; meningococcal disease; meningitis vaccine.
KW
XX Neisseria meningitidis strain EG327.
OS
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX
PN W0200155182-A1.
XX

PD 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09164.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
SQ Sequence 594 AA;

Query Match 95.1%; Score 2874; DB 22; Length 594;
Best Local Similarity 95.6%; Pred. No. 4.5e-166;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLILFATVQANATD-DDDLYLE 60
Db 1 mnkyriiwsalnawvavseltrnhtkrasatvatvatlilfatvqastddldyle 60

Qy 61 PVQRTAVVLSFRSDEKGTGEGTSDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 pvqrtavvlsfrsdekgtegevedtsnwgvyfddkkgvltagttikagdnkikqntne 120

Qy 121 NTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180
Db 121 ntnassfyslkkdltdltsvgtelksfnsankvnitsdtkglnfaktaetngdttvh 180

Qy 181 LNGIGSLTDLTLNTGATTNTNNDVDDERKRAASVKDVLNAGWNKIGVKGPGTTASDNV 240
Db 181 lngigstldtlnltgattntndvtddekrasvkdvlmagwnlkgvkgpgttasdnv 240

Qy 241 DFVRTYDFEFLSADTKTTTNNVSKONGKKEVIGAKTSVKEKDGKLVTKGKDPNG 300
Db 241 dfvrtdydfelsadtkttttnvskongkkrtevigaktsvikekgklyvgkdkngend 300

Qy 301 SSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSNTVTFASGKGTTA 360
Db 301 sstdkgelvtakevidavnkgawrmktttangtqgqdkfetvtsntvtfasgkgtta 360

Qy 361 TVSKDDQGNITVYDVNVGDALNVQNLQNSGWNLDKRAVAGSSKGVISGNVSPSKGKMD 420
Db 361 tvskddqgnitvymvngdnlvngqnlqnsqwnldskavagssgkvvisgnvpskgkmd 420

Qy 421 TVNINAGNIEITRNGKNIDIAATSMAPQFSSVSLGAGADAPTLSVDDGALNVGSKDNTK 480
Db 421 tvninagnieitrngknidiatsmtpqfssvslgagadapltlsvddgalnvsgskdntk 480

Qy 481 PVRITNVAPGVKEGDTNVAQLKGVQANLNINRDNVDGNARAGIAQATAGLVQAYLPG 540
Db 481 pvrntnvgpvkgegdvtnvaqlkgvaqlnnhndvngnragiaqataglvqaylpg 540

Qy 541 KSMMAIGDFTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYQW 594
Db 541 ksmmaig99gtyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 10.
AAI23743
ID AAY23743 standard; Protein; 599 AA.
XX
AC AAY23743;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85795.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 114-115; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 599 AA;

Query Match 92.7%; Score 2802.5; DB 20; Length 599;
Best Local Similarity 92.5%; Pred. No. 9.6e-162;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLILFATVQANATD-DDDLYLE 59
Db 1 mnkyriiwsalnawvavseltrnhtkrasatvatvatlilfatvqanadedeeel 60

Qy 60 EPVQRTAVVLSFRSDEKGTGEGTSDSNWVYFDEKRVLKAGAITLKAGDNLKIKQ--- 116
Db 60 epvrsalvlqfmidkegngengestngwsiyydnhtlbgatvltkagdnkikqntn 120

Qy 117 -NTNENTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
Db 121 kntnentndssftysllkldltsveteklsfgangknvntsdtkglnfaketagtng 180

```
QY 176 DPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNNIKGVKPGTT 235
DB 181 dttvhlngigstltdtllntgattvndvtdckkkaasvkvdlngwngikgvkpgctt 240
QY 236 ASDNVDFVRTYDTVBFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIEKDKGLVTGKG 295
DB 241 asdnvdfvrtvdtvflsadtktttvnnveskdngkrtvkvigaktsvikekdglvtgkg 300
QY 296 KDENGSSDDEGGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSGTNVTFSAG 355
DB 301 kgengsstdegeglvtakevidavnkagwrmtktttcangtgqadkfetvtsgtntvtfasg 360
QY 356 KGTATVSKDDOGNTVTKYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 415
DB 361 kgtatvskddognltvkydyvngdnlvnglqnsqwnldskavagsgkvisgnvpspk 420
QY 416 GKMDETVNTNAGNNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGS 475
DB 421 gkmdetvnnagnnieitrngknidiatsmtpqfssvslgagadapltlsvddkgalnvgs 480
QY 476 KDTNKPVRTNVPAGVKEGDVTNVAQLKGAQNLRNDVNDGNNARAGIAQAIAITAGLVQ 535
DB 481 kdtnkpvrntnvpagvkegdvtnvaqlkgvaqnlrindvndgnnaraglaqalaglvq 540
QY 536 AYLPGKSMMAIGDTRVGEAGYAIGVSSISDGGNWTIKGTASGNSRGHFGASASVGYOW 594
DB 541 aylpgksmmaigdgtrvgeagyaigvssisdggnwnwikgtasgnsrghfgasasvgyow 599

RESULT 11
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX
AC AAU06176;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H38 surface antigen NhhA polypeptide sequence.
XX
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H38.
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..105 /label= V1
FT /note= "variable region 1"
FT Region 106..117 /label= C2
FT /note= "Conserved region 2"
FT Region 118..131 /label= V2
FT /note= "variable region 2"
FT Region 132..195 /label= C3
FT /note= "Conserved region 3"
FT Region 196..217 /label= V3
FT /note= "variable region 3"
FT Region 218..236 /label= C4
FT /note= "Conserved region 4"
FT Region 237..243 /label= V4
FT /note= "variable region 4"
FT Region 244..599 /label= C5
FT /note= "Conserved region 5"
XX
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PN WO20155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYOU ) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
XX
N-PSDB; AAS09166.
XX
New NhhA surface antigen polypeptides and polynucleotides from
Neisseria meningitidis, useful in producing vaccines for treating or
preventing broad spectrum of Neisseria meningitidis -
XX
Claim 9; Fig 1; 91pp; English.
XX
The present invention relates to the isolation of novel Neisseria
meningitidis mutant polypeptides of the surface antigen NhhA
(AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
characterised by deletions of non-conserved amino acids, particularly
the deletion of variable regions. The deletion mutants are useful in
diagnostics, therapeutic and prophylactic vaccines against a broader
spectrum of N. meningitidis, and in designing and/or screening of
medicaments. The mutant proteins when used as a vaccine can effectively
immunise against a broader spectrum of N. meningitidis strains than
would be expected from a corresponding wild-type surface antigen.
XX
The present sequence representing the wild type surface antigen NhhA
from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences
(AAU06171-AAU06180) from 10 different N. meningitidis strains given in
the present invention.
XX
SQ Sequence 599 AA;

Query Match 92.7%; Score 2802.5; DB 22; Length 599;
Best Local Similarity 92.5%; Pred. No. 9.6e-162;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

QY 1 MNKIYRIWNSALNAMYVSELTRNHTKRASATVATVAVLATLFLFATVQANATD-DDDL 59
DB 1 mkiyriwlsalnawvseltrnhtrkrasatvkvavlatllfatvqanadedeeel 60
QY 60 EPVQRTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116
DB 61 epvrsalvlqfmidkeggenestngisyydnhntlhgatvtlkagdnlikqntn 120
QY 117 -NTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNG 175
DB 121 kntnentndssftyslkkdltdltsveteklsfgangknvntsdtkglnfaketagtn 180
QY 176 DPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNNIKGVKPGTT 235
DB 181 dttvhlngigstltdtllntgattvndvtdckkkaasvkvdlngwngikgvkpgctt 240
QY 236 ASDNVDFVRTYDTVBFLSADTKTTTNNVESKDKGKTEVKIGAKTSVIEKDKGLVTGKG 295
DB 241 asdnvdfvrtvdtvflsadtktttvnnveskdngkrtvkvigaktsvikekdglvtgkg 300
QY 296 KDENGSSDDEGGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSGTNVTFSAG 355
DB 301 kgengsstdegeglvtakevidavnkagwrmtktttcangtgqadkfetvtsgtntvtfasg 360
QY 356 KGTATVSKDDOGNTVTKYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 415
DB 361 kgtatvskddognltvkydyvngdnlvnglqnsqwnldskavagsgkvisgnvpspk 420
QY 416 GKMDETVNTNAGNNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGS 475
DB 421 gkmdetvnnagnnieitrngknidiatsmtpqfssvslgagadapltlsvddkgalnvgs 475
```

Db 421 gkmdetvniagnnieitrngknidiatsmtbpqfssvslgagadapltlsvddkgalnvgs 480
QY 476 KDTNKPVRITNVAPGVKRGDVTNVQALKGVAQNLRNIDNVGNARAGIAQAIATAGLVQ 535
Db 481 kdnkpvritnvapgvkegdvtnvaqlkgvaqlnlnridnvdnarnaragiataglvq 540
QY 536 AYLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRHHFGASASVGYQW 594
Db 541 aylpgksmmaiggytyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 599

RESULT 12
AAY57045
ID AAY57045 standard; Protein; 591 AA.
AC AAY57045;
XX
DT 21-FEB-2000 (first entry)
XX
DE BASB029 amino acid sequence from N. meningitidis strain H44/76.
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Misc-difference 90 /note= "Encoded by AAT"
FT Misc-difference 92 /note= "Encoded by GAT"
FT Misc-difference 98 /note= "Encoded by AAC"
FT Misc-difference 108 /note= "Encoded by AATC"
FT Misc-difference 123 /note= "Encoded by ACA"
FT Misc-difference 269 /note= "Encoded by AAA"
FT Misc-difference 389 /note= "Encoded by CGI"
XX
PN W09958683-A2.
XX
PD 18-NOV-1999.
XX
PF 07-MAY-1999; 99WO-EP03255.
XX
PR 13-MAY-1998; 98GB-0010276.
XX
PS (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Ruelle J;
XX
DR WPI; 2000-053103/04.
XX
DR N-PSDB; AA239865.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
PS
PS Claim 4; Fig 2; 74pp; English.
XX
XX This is the Neisseria meningitidis BASB029 amino acid sequence from
CC serogroup B strain H44/76. The BASB029 protein is homologous to the
CC Haemophilus influenzae surface fibril (HSF) protein. The invention
CC relates to BASB029 polynucleotide sequences (AA239864-239865) and
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria
CC meningitidis infection in a mammal. Compositions containing an immune
CC polynucleotides and polypeptides are useful for generating an immune
CC response in an animal. A therapeutic composition comprising an antibody
CC directed against BASB029 is useful in treating humans with Neisseria
CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.
XX
SQ Sequence 591 AA;

Query Match 91.0%; Score 2750.5; DB 21; Length 591;
Best Local Similarity 92.5%; Pred. No. 1.3e-158;
Matches 553; Conservative 8; Mismatches 26; Indels 11; Gaps 4;

QY 1 MNKIYRIWNSALNANVVVSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 mnkiyriwnsalnawvavseltrnhtkrasatvktavlatllfatvgasanneegee 60
QY 58 YLEPVORTAVVLSFRSDKGTGEGT-EDSNWAVFDEKRVLKAGAITLKAGDNLIKIKO 116
Db 61 ylpvortavvllsvrsokegtgekevveedsnwavyfidekgvltareitlkagdnlikiq 120
QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNPAKETAGTNGD 176
Db 121 -----ngsnftysllkldtltsvgteklfsangknvitsdtkglnfaketagngd 174
QY 177 PTVHLNGIGSTLTDLTLLNTGATTNVNDVTDEKRAASVKDVLNAGWNKIKGKPGTTA 236
Db 175 ttvhlngigstltdtllntgattnvndvtddekkraasvkdvltnagwnikgvpqgta 234
QY 237 SDNVDVVRTYDTVEFLSADTKTTNVVESKDNKGKTEVKIGAKTSVKEKDKGLVTGKGK 296
Db 235 sdnvdvrvtydtveflsadtkttvnveskdngkrtevkigaktsvlikekdgkltvgkdk 294
QY 297 DENGSTDEGEGLVTAKEVIDAVNKAQWRMKTNTANGQTQADKFETVTSCTNVTFASGK 356
Db 295 gengsstdegeglvtakevidavnkagwrmtttangqtqadkfetvtsctnvtfasgk 354
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKG 416
Db 355 gttatvskddqgnitvmydvnvgdalnvnqlnsgwnldskavagssgkvisgnvpskg 414
QY 417 KMDETVNIAGNNTETTRNGKNIDIAATSMAPQSSVSLGAGADAPTLSVDEGALNVGSK 476
Db 415 kmdevtninagnniettrngknidiatsmcpqfssvslgagadapltlsvddg-alnvgsk 473
QY 477 DTNKPVRITNVAPGVKRGDVTNVQALKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
Db 474 dtnkpvritnvapgvkegdvtnvaqlkgvaqlnlnridnvdnarnaragiataglvqa 533
QY 537 YLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRHHFGASASVGYQW 594
Db 534 ylpkksmmaiggytyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 591

RESULT 13
AAY27202
ID AAY27202 standard; Protein; 591 AA.
XX
AC AAY27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
XX Neisseria meningitidis.
XX

PN W09936544-A2.
XX 22-JUL-1999.
XX 14-JAN-1999; 99WO-IB00103.
XX 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX (CHTR-) CHIRON SPA.
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
DR WPI: 1999-444400/37.
DR N-PSDB; AAX99124.
XX New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing *Neisseria*
PT meningitidis infections
XX
XX Claim 1; Page 62; 123pp; English.
XX
XX The invention provides proteins (AAY27201-245) from *Neisseria*
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to *Neisseria*
CC bacteria, especially *Neisseria meningitidis*.
XX
XX Sequence 591 AA;
SQ

Query Match 90.7%; Score 2740.5; DB 20; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-158;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;
QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 mnkiyriiwnsalnawvvsseletrnhtkrasatvktavlatllfatvqasannee 60
QY 58 YLEPQVORTAVVLSFRSDKEGTGEGED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
Db 61 yldpqvrtavvlvnsdkegtgekeveensdwavfnekgvltareitlkagdnlikq 120
QY 117 NTWENTNDSSTFYSLKDKLTLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 176
Db 121 -----ngntfyslkkdldtsvgtelksfsangknvntsdtkglnfaketagngd 174
QY 177 PTVHLNGIGSTLTDLTLNTGATTNVTNDVDEKRAASVKDVLNAGWNKGVKPGTTA 236
Db 175 tlvhngigstltdlntgattnvndvndvdekkraasvkdvlagnwnkvgkpgtta 234
QY 237 SDNVDFVRYDTVEFLSADTKTTTVNESKDKGKTEVKIGAKTSVTKERDGLVTKGK 296
Db 235 sdnvdfvrydtveflsadtktttvneskdngkktvkvigaktsvikekgdglvrgkdk 294
QY 297 DENGSTDEGEGLVTAKEVIDAVNKAWRMKTTTANGQTQADKFETVTSGTNVTFSAGK 356
Db 295 gengstdegeglvtakevidavnkagwrmtttangqigqadkfetvtsgtntvtfasgk 354
QY 357 GTTATVSKDDQGNITVKYDVNVDGALNVQNLQNSGWNLSKAVAGSGKVISGNVSPSKG 416
Db 355 gttatvskddqgnitvmydvngvdaInvnqlngsgwnlkskavagsgkvisgnvpskg 414
QY 417 KMDETVNIAGNNIETRNKNDIATSMAPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 415 kmdetvniagnnieltrngknidiatmtlpqfssvslgagadapltlsvdgd-alnvgsk 473
QY 477 DTNKPVRITNVAPGKGVGDVTNVAQLKGVAQNLNNRIDVNGNARAGIAQAIATAGLVQA 536
Db 474 kdnkpvritnvapgvkdvtnvaqlkgvaqnlnnridvngnparagiataqlvqa 533

QY 537 YLPKSMMAIGDGYRGEAGYATGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 594
Db 534 ylpksmmaiggyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 591
RESULT 14
AAY23746
ID AAY23746 standard; Protein; 591 AA.
XX AAY23746;
XX
XX 08-SEP-1999 (first entry)
XX A surface protein of *Neisseria meningitidis*.
DE
XX Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
XX *Neisseria meningitidis*.
OS
XX W09931132-A1.
XX
XX 24-JUN-1999.
PD
XX 14-DEC-1998; 98WO-AU01031.
PF
XX 12-DEC-1997; 97GB-0026398.
PR
XX (ISIS-) ISIS INNOVATION LTD.
PA (UYOU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
XX WPI: 1999-418754/35.
DR N-PSDB; AAX85798.
XX
XX *Neisseria meningitidis* surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 127-128; 132pp; English.
XX
XX The present sequence represents a surface protein of *Neisseria*
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 591 AA;
SQ

Query Match 90.7%; Score 2740.5; DB 20; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-158;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;
QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 mnkiyriiwnsalnawvvsseletrnhtkrasatvktavlatllfatvqasannee 60
QY 58 YLEPQVORTAVVLSFRSDKEGTGEGED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
Db 61 yldpqvrtavvlvnsdkegtgekeveensdwavfnekgvltareitlkagdnlikq 120
QY 117 NTWENTNDSSTFYSLKDKLTLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 176
Db 121 -----ngntfyslkkdldtsvgtelksfsangknvntsdtkglnfaketagngd 174
QY 177 PTVHLNGIGSTLTDLTLNTGATTNVTNDVDEKRAASVKDVLNAGWNKGVKPGTTA 236
Db 175 tlvhngigstltdlntgattnvndvndvdekkraasvkdvlagnwnkvgkpgtta 234

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Db 175 ttvhlngigstldtllntgattntvndvtddekkraasvkdvlhagwnikvqkpgtta 234
QY 237 SDNVDFVRTYDTVEFLSADTKTTNNVESKNGKKTVEKIGAKTSVKEKDGKLVTKGK 296
    |||||
Db 235 sdhvdvrtvdtveflsadtktttnveskngkktvekvigaktsvikekdglvtgkdk 294
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RESULT 15
AAU06171
ID AAU06171 standard; Protein; 591 AA.
XX AC AAU06171;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain PMC21.
XX PH
XX FT Peptide
    1..51 Location/Qualifiers
    1..50 /label= Signal_peptide
    1..50 /label= C1
    51..108 /note= "Conserved region 1"
    51..108 /label= V1
    52..591 /note= "Variable region 1"
    52..591 /label= Mature_Nhha
    52..591 /note= "Predicted mature protein, specifically
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    230..236 /label= V4
    237..591 /note= "Variable region 4"
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FT FT /label= C5
XX XX /note= "Conserved region 5"
PN PN
XX WO200155182-A1.
XX PD 02-AUG-2001.
XX XX
XX 25-JAN-2001; 2001WO-AU00069.
XX XX
XX 25-JAN-2000; 2000US-0177917.
XX XX
XX (UYQU ) UNIV QUEENSLAND.
XX PA
XX PI Peak IRA, Jennings MP;
XX XX
XX WPI: 2001-488774/53.
XX DR N-PSDB; AAS09161.
XX XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX XX
XX Claim 9; Fig 1; 91pp; English.
XX PS
XX CC The present invention relates to the isolation of novel Neisseria
    CC meningitidis mutant polypeptides of the surface antigen Nhha
    CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
    CC characterised by deletions of non-conserved amino acids, particularly
    CC the deletion of variable regions. The deletion mutants are useful in
    CC diagnostics, therapeutic and prophylactic vaccines against a broader
    CC spectrum of N. meningitidis, and in designing and/or screening of
    CC medicaments. The mutant proteins when used as a vaccine can effectively
    CC immunise against a broader spectrum of N. meningitidis strains than
    CC would be expected from a corresponding wild-type surface antigen.
    CC The present sequence representing the wild type surface antigen Nhha
    CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
    CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
    XX the present invention.
XX SQ Sequence 591 AA;
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Query Match 90.7%; Score 2740.5; DB 22; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-158;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

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QY 58 YLEPVPQRTAVVLSPFRSDKEGTGEKTED-SNWAYFDEKRVLKAGAITLKAGDNLKIKQ 116
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QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKUSFGANGKNVITSDTKGLNFAKETAGTNGD 176
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QY 177 PTVHLNGIGSTLTDTLTNTGATTNTVNDTDDKKRAASVKDVLNAGWIKGVKPGTTA 236
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QY 297 DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTttTANGQTGOADKFEFVTSGTNVTFASGK 356
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QY 357 GTTATVSKDDGGNTVKYDYNVGDALVNOLONSGNWLDKAVAGSSGKVISGNVSPSKG 416
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Qy 417 KMDTVNINAGNNIEITRNGKNIDIATSMAPOFSSVSLGAGADAPTLSDDEGALNVGSK 476
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Qy 477 DTNKPVRITNVAPGVKEGDTVNTVAOLKGVQAQNLNRRIDNVGDNARAGIAQAIAATAGLVQA 536
Db 474 kdnkpvrItnvapgvkegdtvntvaqlkgvaqnlrridnvdgnaragiaqaiaataglvqa 533
Qy 537 YLPKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
Db 534 ylpgksmmaigggtyrgeagyaigyssisdggnwiilkgtagnsrgrhfgasasvgyqw 591

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Job time: 321 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:10 ; Search time 39.66 seconds
(without alignments)
365.830 Million cell updates/sec

Title: US-09-771-382-9
Perfect score: 3023
Sequence: 1 MNKIYRIIWSALNAWVVS.....TASGSRGHFGASVGYQW 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3023	100.0	594	4	US-09-377-155-7 Sequence 7, Appli
2	3023	100.0	594	4	US-09-669-974-7 Sequence 7, Appli
3	2971	98.3	598	4	US-09-377-155-13 Sequence 13, Appli
4	2971	98.3	598	4	US-09-669-974-13 Sequence 13, Appli
5	2948	97.5	598	4	US-09-377-155-5 Sequence 5, Appli
6	2948	97.5	598	4	US-09-669-974-5 Sequence 5, Appli
7	2874	95.1	594	4	US-09-377-155-9 Sequence 9, Appli
8	2874	95.1	594	4	US-09-669-974-9 Sequence 9, Appli
9	2802.5	92.7	599	4	US-09-377-155-15 Sequence 15, Appli
10	2802.5	92.7	599	4	US-09-669-974-15 Sequence 15, Appli
11	2740.5	90.7	591	4	US-09-377-155-21 Sequence 21, Appli
12	2740.5	90.7	591	4	US-09-669-974-21 Sequence 21, Appli
13	2733	90.4	592	4	US-09-377-155-2 Sequence 2, Appli
14	2733	90.4	592	4	US-09-669-974-2 Sequence 2, Appli
15	2721.5	90.0	591	4	US-09-377-155-11 Sequence 11, Appli
16	2721.5	90.0	591	4	US-09-669-974-11 Sequence 11, Appli
17	2664	88.1	592	4	US-09-377-155-17 Sequence 17, Appli
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19	2573.5	85.1	589	4	US-09-377-155-19 Sequence 19, Appli
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21	1330.5	44.0	2353	4	US-09-377-155-33 Sequence 33, Appli
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23	1330.5	44.0	2353	4	US-09-669-974-33 Sequence 33, Appli
24	1329.5	44.0	2354	4	US-09-268-347-47 Sequence 47, Appli
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41	1011.5	33.5	679	4	US-08-913-942-15 Sequence 15, Appli
42	1011.5	33.5	679	4	US-09-268-347-26 Sequence 26, Appli
43	757	25.0	1002	4	US-09-268-347-24 Sequence 24, Appli
44	756	25.0	1004	4	US-09-268-347-30 Sequence 30, Appli
45	709	23.5	1104	4	US-09-268-347-28 Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match	100.0%	Score 3023;	DB 4;	Length 594;
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Db	121	NFNDSSFYSLKDLTDLTSVETEKLS	FGANGKNVITSDTKGLNFAKTAGTNGDPTVH	180
QY	181	LANGISTLDTLLNTGATTNVTND	VNVDDEKKRAASVDVLNAGWNIKGVKPGTTASDNV	240
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RESULT 2

US-09-669-974-7
; Sequence 7, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-7

Query Match 100.0%; Score 3023; DB 4; Length 594;
Best Local Similarity 100.0%; Pred. No. 8.7e-236;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNNAWVVSSELTRNHTKRASATVATAVLATLTLFATVQANATDDDDLYLE 60
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Db 61 PVORTAVVLSFRSDKEGTGKEGTEDSNWAVYDEKRVLKAGAITLKAGNLIKQNTNE 120
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Db 121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180
QY 181 LINGISGTLTDLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTASDNV 240
Db 181 LINGISGTLTDLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300
Db 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300
QY 301 SSTDEGELVTAKEVIDAVNKAQWRMTTTTANGOTGOADKFEFVTSGTNTVFASGKGTTA 360

Db 301 SSTDEGELVTAKEVIDAVNKAQWRMTTTTANGOTGOADKFEFVTSGTNTVFASGKGTTA 360
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Db 361 TVSKDDOGNITTVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKGKMD 420
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Db 421 TVNINAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDVDDGALNVGSKDTNK 480
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Db 481 PVRTITNVPAGVKEGDVTNVAQLKGVAQNLANNRIDNVGDNARAGIAQAIAIATAGLVQAYLPG 540
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Db 541 KSMAAIGGDTYRGEAGYAICYSSISDGGNNIIKGTASGNSRGHFGASASVGYOW 594

RESULT 3

US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 98.3%; Score 2971; DB 4; Length 598;
Best Local Similarity 98.0%; Pred. No. 1.4e-231;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

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Db 1 MNKIYRIIWSALNNAWVVSSELTRNHTKRASATVATAVLATLTLFATVQANATDDDDLYLE 60
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Db 61 PVORTAVVLSFRSDKEGTGKEGTEDSNWAVYDEKRVLKAGAITLKAGNLIKQNTNE 120
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Db 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
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Db 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGK 300
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Db 301 DENGSSTDEGEGLVTAKEVIDAVNKAQWRMTTTTANGOTGOADKFEFVTSGTNTVFASG 360
QY 357 GTTATVSKDDOGNITTVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVLISGNVSPSKG 416

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Qy	477	DTNKPVRITVAPGVREGDVTNVAQLKGVAQLNNRINDVGNARAGIAQAATATAGLVA	536
Db	481	DANKPVRITVAPGVREGDVTNVAQLKGVAQLNNRINDVGNARAGIAQAATATAGLAA	540
Qy	537	YLPKSMMAIGGDTYRGEAGYATGYSSISDGGNNIIKGTASGNSRGHFGCASVGYQW	594
Db	541	YLPKSMMAIGGGTYRGEAGYATGYSSISDGTNNWIKGTASGNSRGHFGTSASVGYQW	598

RESULT 6
US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match	97.5%	Score	2948;	DB	4;	Length	598;		
Best Local Similarity	97.3%;	Pred.	No. 9.9e-230;						
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Db	1	MNKYSRIIWN	SALNAVVV	SELTNRH	TKRASAT	VATAVL	ATLLFAT	VOANAT	DDDDLYLE 60
Qy	61	PVQRTAVVLS	SPRSDEGT	GEKGETDS	NWAVYF	FDEKRV	LKAGAT	ITLKAGD	NLKIQQ --- 116
Db	61	PVQRTAVVLS	SPRSDEGT	GEKGETDS	NWAVYF	FDEKRV	LKAGAT	ITLKAGD	NLKIQQNTNE 120
Qy	117	NTNENTND	SSFTYSL	KDLDLT	DSVETEK	LSFGANG	KNVNIT	SDTKGLNF	AKETAGTNGD 176
Db	121	NTNENTND	SSFTYSL	KDLDLT	DSVETEK	LSFGANG	KNVNIT	SDTKGLNF	AKETAGTNGD 180
Qy	177	PTVHLNGIG	STLTD	LLNTGAT	TNTNDNV	TDDK	KRAAS	VKDVL	NAGWNILKGVKPGTTA 236
Db	181	PTVHLNGIG	STLTD	LLNTGAT	TNTNDNV	TDDK	KRAAS	VKDVL	NAGWNILKGVKPGTTA 240
Qy	237	SDNVDFV	RTYDTV	TEFLSAD	TKTTTVN	VESKONG	KKTEVK	IGAKTS	SVIKEKDGLVTGKKG 296
Db	241	SDNVDFV	RTYDTV	TEFLSAD	TKTTTVN	VESKONG	KKTEVK	IGAKTS	SVIKEKDGLVTGKKG 300
Qy	297	DENGSS	TDEB	GGLVTAK	EIVDA	VNKGAK	WRMTT	TANGOT	GQADKFETVTSGTNYTFASGK 356
Db	301	GENGSS	TDEB	GGLVTAK	EIVDA	VNKGAK	WRMTT	TANGOT	GQADKFETVTSGTNYTFASGN 360
Qy	357	GTTATVSK	DDOGNT	IVKYDV	NVGN	DALNV	QNLQ	NSGWN	LDLSKAVAGSSCKVTSGNVSPSKG 416
Db	361	GTTATVSK	DDOGNT	IVKYDV	NVGN	DALNV	QNLQ	NSGWN	LDLSKAVAGSSCKVTSGNVSPSKG 420
Qy	417	KMDET	VNINAG	NNIEIT	RNGKN	IDAT	SMAPQ	FSSV	LSGAGADAPTLISVDDEGALNVGSK 476

Db	421	KMDETVNNAGNIEITRNCKNKNDIATSWTPQSPSSVSLGAGADAPTLSDVDDGALNVGSK	480
QY	477	DTNKPVRITVNPVPGVEGDVTNVAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLVA	536
Db	481	DANKPVRITVNPVPGVEGDVTNVAQLKGVAQNINNRIDNVGNARAGIAQAATATAGLAA	540
QY	537	YLPCKSMWAIIGGDTYRGEAGYAIYGSISIDGGNWIITKGTASGNSRGHFCAASVGYQW	594
Db	541	YLPCKSMWAIIGGDTYRGEAGYAIYGSISIDTGNWIIKGTASGNSRGHFGTASVGYQW	598

```

RESULT      7
US-09-377-155-9
; Sequence 9, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-9

```

Query Match	95.1%	Score 2874;	DB 4;	Length 594;
Best Local Similarity	95.6%;	Pred. No. 9.le-224;		
Matches 568; Conservative	5;	Mismatches 21;	Indels 0;	Gaps 0;
Qy	1	MNKIYRIWNSALNAWVVS	ELTNHTRKRASATVATAVLATLLFATVQANATDDDDLYLE	60
Db	1	MNKIYRIWNSALNAWVVS	ELTNHTRKRASATVATAVLATLLFATVQASITDDDDLYLE	60
Qy	61	PVQRTAVVLSPRSDEGTG	EGTEGDSNWAVYFDEKRVLKAGATITLKAGDNLKIKQNTNE	120
Db	61	PVQRTAVVLSPRSDEGTG	EGTEGDSNWGYFDDKGVLTAGTITLKAGDNLKIKQNTNE	120
Qy	121	NTNDSSTFYSLUKKDLT	LTSTVETBEKLSFGANGKNVNTISDTKGLNFAKETAGTNGDPTVH	180
Db	121	NTNASSFTYSLUKDLT	LTSTVTEKLSFGSANSKNVNTISDTKGLNFAKKTATETNGDPTVH	180
Qy	181	LNGTGSILTDPLLTGAT	TNTVNDVTDDEKKRAASVKDVLNAGWNKIKGVPGGTASDNV	240
Db	181	LNGTGSILTDPLLTGAT	TNTVNDVTDDEKKRAASVKDVLNAGWNKIKGVPGGTASDNV	240
Qy	241	DFVRTYDVEFLSADTK	TTTVNVESKONGKXTEYKVIKAKTSVIEKDGKLVTKGKDBNG	300
Db	241	DFVRTYDVEFLSADTK	TTTVNVESKONGKXTEYKVIKAKTSVIEKDGKLVTKGDKGEND	300
Qy	301	SSTDGEGSLVTAKEVID	AVNKGAGRMKTTTANGQTGQADKFETVTSGTNTVTFASGKGTTA	360
Db	301	SSTDGEGSLVTAKEVID	AVNKGAGRMKTTTANGQTGQADKFETVTSGTNTVTFASGKGTTA	360
Qy	361	TVSKDDOGNITVYKDV	VNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNYSPSKGKWE	420
Db	361	TVSKDDOGNITVYKDV	VNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNYSPSKGKWE	420
Qy	421	TVNINAGNNIEITRNGK	NIDATSMAPQFSSVSLGACADAPTLSDVDEGALNVGSKDNTK	480
Db	421	TVNINAGNNIEITRNGK	NIDATSMTPQFSSVSLGACADAPTLSDVDEGALNVGSKDANK	480
Qy	481	PVRTNTNAPGVKEGDV	TNVNVAOLKGVQNNLNINRINDVNDGNARAGTAAQATATAGLVQAYLP	540

Db 481 PVRITNAPGVKGGDVTNVAQLKGAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540
QY 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594
Db 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

RESULT 8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 6331173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 95.1%; Score 2874; DB 4; Length 594;
Best Local Similarity 95.6%; Pred. No. 9.1e-224;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;
QY 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQASTTDDDDLYLE 60
QY 61 PVQRTAVLSFRSDKGEKTEGSDNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVQRTAVLSFRSDKGEKTEGSDNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
QY 121 NTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
Db 121 NTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
QY 181 LNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
Db 181 LNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
QY 241 DFVRTYDVFELSDTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGKDENG 300
Db 241 DFVRTYDVFELSDTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGKDENG 300
QY 301 SSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTQADKFEFVTSCTNVTFASGKGTGA 360
Db 301 SSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTQADKFEFVTSCTNVTFASGKGTGA 360
QY 361 TVSKDQGNITVYDYNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSKMD 420
Db 361 TVSKDQGNITVYDYNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSKMD 420
QY 421 TVNINAGNIEITRNCKNIDIAATSMAPQSSVSLGAGADAPTLVSDEGALNVGSKDTNK 480
Db 421 TVNINAGNIEITRNCKNIDIAATSMAPQSSVSLGAGADAPTLVSDEGALNVGSKDKANK 480
QY 481 PVRITNAPGVKGGDVTNVAQLKGAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540

Db 481 PVRITNAPGVKGGDVTNVAQLKGAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540
QY 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594
Db 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

RESULT 9
US-09-377-155-15
; Sequence 15, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 92.7%; Score 2802.5; DB 4; Length 599;
Best Local Similarity 92.5%; Pred. No. 5.4e-218;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATD-DDDLYL 59
Db 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATDEDEEL 60
QY 60 EPQRTAVLSFRSDKGEKTEGSDNNAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116
Db 61 EPVRSALVQLFQIDKEGNESTGNIWSIYDHNHTLHGATVTLKAGDNLKIKONTN 120
QY 117 -NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175
Db 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180
QY 176 DPTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGT 235
Db 181 DPTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGT 240
QY 236 ASDNVDFVRYDVFELSDTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGK 295
Db 241 ASDNVDFVRYDVFELSDTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGK 300
QY 296 KDNGSSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTQADKFEFVTSCTNVTFASG 355
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTQADKFEFVTSCTNVTFASG 360
QY 356 KGTATVSKDQGNITVYDYNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 415
Db 361 KGTATVSKDQGNITVYDYNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420
QY 416 GKMDETVNIINAGNIEITRNCKNIDIAATSMAPQSSVSLGAGADAPTLVSDDGALNVGS 475
Db 421 GKMDETVNIINAGNIEITRNCKNIDIAATSMAPQSSVSLGAGADAPTLVSDDGALNVGS 480
QY 476 KDTNKKPVRTNTNAPGVKGGDVTNVAQLKGAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQ 535
Db 481 KDTNKKPVRTNTNAPGVKGGDVTNVAQLKGAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQ 540
QY 536 AYLPGKSMMAIGDVTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

Db 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 599
|||||

RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 92.7%; Score 2802.5; DB 4; Length 599;
Best Local Similarity 92.5%; Pred. No. 5.4e-218;
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
Qy 1 MNKYRIIWSALNANWVVSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLXL 59
Db 1 MNKYRIIWSALNANWVVSELTRNHTKRASATVATVATLTLFATVOANATDDEEEL 60
Qy 60 EPVQRTAVLSFRSDKEGTEGKEDTSNNNAVYDEKRVLKAGAITLTKAGDNLIKQ--- 116
Db 61 EPVVRSALVLOFMIDKEGNGNESTGIGWSIYYDNNHTLHGATVTLKAGDNLIKONTN 120
Qy 117 -NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 175
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 180
Qy 176 DPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 235
Db 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 240
Qy 236 ASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEDGKLVTKGK 295
Db 241 ASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEDGKLVTKGK 300
Qy 296 KDNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGOADKFEFTVSGTNVTFASG 355
Db 301 KGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGOADKFEFTVSGTNVTFASG 360
Qy 356 KGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSK 415
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSK 420
Qy 416 GKMDETVINAGNNIEITRNKNIDTSMAPQFSVSLGAGADAPTLSDVDEGALNVGS 475
Db 421 GKMDETVINAGNNIEITRNKNIDTSMTPQFSVSLGAGADAPTLSDVDDGKALNVGS 480
Qy 476 KDTNKPVRITNAPGVKEGDDVTNVAQLKGAQNLLNNDVGNARAGIAQAATAGLVQ 535
Db 481 KDANKPVRITNAPGVKEGDDVTNVAQLKGAQNLLNNDVGNARAGIAQAATAGLVQ 540
Qy 536 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
|||||

Db 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 599
RESULT 11
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 90.7%; Score 2740.5; DB 4; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-213;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;
Qy 1 MNKYRIIWSALNANWVVSELTRNHTKRASATVATVATLTLFATVOANATD---DDDL 57
Db 1 MNKYRIIWSALNANWVVSELTRNHTKRASATVATVATLTLFATVOANANNEQEEDL 60
Qy 58 YLEPVQRTAVLSFRSDKEGTEGKEDTSNNNAVYDEKRVLKAGAITLTKAGDNLIKQ 116
Db 61 YLDPVQRTAVLSFRSDKEGTEGKEKEVENSNAVYENKGVLTARETLTKAGDNLIKQ 120
Qy 117 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 176
Db 121 -----NGTFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNG 174
Qy 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236
Db 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 234
Qy 237 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEDGKLVTKGK 296
Db 235 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEDGKLVTKGK 294
Qy 297 DENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGOADKFEFTVSGTNVTFASG 356
Db 295 GENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGQTGOADKFEFTVSGTNVTFASG 354
Qy 357 GTTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSK 416
Db 355 GTTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVIISGNVSPSK 414
Qy 417 KMDETVINAGNNIEITRNKNIDTSMAPQFSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 415 KMDETVINAGNNIEITRNKNIDTSMTPQFSVSLGAGADAPTLSDVGD-ALNVGSK 473
Qy 477 DTNKPVRITNAPGVKEGDDVTNVAQLKGAQNLLNNDVGNARAGIAQAATAGLVQA 536
Db 474 KDNKPVRITNAPGVKEGDDVTNVAQLKGAQNLLNNDVGNARAGIAQAATAGLVQA 533
Qy 537 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594
|||||

Db 534 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 591

RESULT 12

US-09-669-974-21
; Sequence 21, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-21

Query Match 90.7%; Score 2740.5; DB 4; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-213;

Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

Qy	1	MNKYRIIWNLSALNAWVYSELTRNHTKRASATVATVAVLATLFLFATVQANATD---DDDL	57
Db	1	MNKYRIIWNLSALNAWVYSELTRNHTKRASATVATVAVLATLFLFATVQASANNEEEDL	60
Qy	58	YLEPVORTAVLSFRSDKEGTEGEGED-SNWAYFDEKRVLKAGAITLKAGDNLKIK	116
Db	61	YLDPVORTAVLVNSDKEGTEGEGEKEVENSOWVYFNEKGVLTAREITLKAGDNLKIK	120
Qy	117	NTNENTNDSFYSLSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	176
Db	121	-----NGTNFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	174
Qy	177	PTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNINIKGVKPGTTA	236
Db	175	TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNINIKGVKPGTTA	234
Qy	237	SDNVDPVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKG	296
Db	235	SDNVDPVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKDK	294
Qy	297	DENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNVTFASG	356
Db	295	GENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNVTFASG	354
Qy	357	GTTATVSKDDQGNITVKYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSPSKG	416
Db	355	GTTATVSKDDQGNITVKYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSPSKG	414
Qy	417	KMDETVINAGNNIETTRNGKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK	476
Db	415	KMDETVINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGSK	473
Qy	477	DINKPVRITNVPAGVKEGDTVNTVAQLKVAQNINRDNVGNARAGIAQAATAGLVQA	536
Db	474	KONKPVRIITNVPAGVKEGDTVNTVAQLKVAQNINRDNVGNARAGIAQAATAGLVQA	533
Qy	537	YLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	594
Db	534	YLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	591

RESULT 13

US-09-377-155-2

; Sequence 2, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-2

Query Match 90.4%; Score 2733; DB 4; Length 592;
Best Local Similarity 91.8%; Pred. No. 2.2e-212;

Matches 550; Conservative 10; Mismatches 27; Indels 12; Gaps 4;

Qy	1	MNKYRIIWNLSALNAWVYSELTRNHTKRASATVATVAVLATLFLFATVQANATDD---DD	56
Db	1	MNKYRIIWNLSALNAWVYSELTRNHTKRASATVATVAVLATLFLFATVQASANNERPRKKD	60
Qy	57	LYLEPVORTAVLSFRSDKEGTEGEGED-SNWAYFDEKRVLKAGAITLKAGDNLKIK	115
Db	61	LYLDPVORTAVLVNSDKEGTEGEGEKEVENSOWVYFNEKGVLTAREITLKAGDNLKIK	120
Qy	116	QNTNENTNDSFYSLSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG	175
Db	121	Q-----NGTNFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG	174
Qy	176	DPTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNINIKGVKPGTT	235
Db	175	DTTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNINIKGVKPGTT	234
Qy	236	ASNDVPVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKG	295
Db	235	ASNDVPVRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVTGKD	294
Qy	296	KDENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNVTFASG	355
Db	295	KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNVTFASG	354
Qy	356	KGTTATVSKDDQGNITVKYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSPSK	415
Db	355	KGTTATVSKDDQGNITVKYDVNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSPSK	414
Qy	416	GRKDETVINAGNNIETTRNGKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGS	475
Db	415	GRKDETVINAGNNIETTRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVGD-ALNVGS	473
Qy	476	KDINKPVRITNVPAGVKEGDTVNTVAQLKVAQNINRDNVGNARAGIAQAATAGLVQ	535
Db	474	KDINKPVRITNVPAGVKEGDTVNTVAQLKVAQNINRDNVGNARAGIAQAATAGLVQ	533
Qy	536	AYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	594
Db	534	AYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW	592

RESULT 14

US-09-669-974-2
; Sequence 2, Application US/09669974
; Patent No. 6333173

GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-2

Query Match 90.4%; Score 2733; DB 4; Length 592;
Best Local Similarity 91.8%; Pred. No. 2.2e-212;
Matches 550; Conservative 10; Mismatches 27; Indels 12; Gaps 4;

Qy 1 MNKIYRIIWSALNANVVSSELTRNHTKRASATVATVATLTLFATVQANATDD---DD 56
Db 1 MNKIYRIIWSALNANVVSSELTRNHTKRASATVATVATLTLFATVQASANNPRKKD 60

Qy 57 LYLEPQVORTAVVLSFRSDEKTEGEGED- SNNAVYFDEKRVKAGAITLKAGDNLKIK 115
Db 61 LYLEPQVORTAVVLSFRSDEKTEGEGED- SNNAVYFDEKRVKAGAITLKAGDNLKIK 120

Qy 116 QNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 175
Db 121 Q-----NGTNYFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 174

Qy 176 DPTVHLNIGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 235
Db 175 DPTVHLNIGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 234

Qy 236 ASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 295
Db 235 ASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 294

Qy 296 KDENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFETVTSGTNVTFAAG 355
Db 295 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFETVTSGTNVTFAAG 354

Qy 356 KGTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 415
Db 355 KGTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 414

Qy 416 GKMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSVDDEGALNVGS 475
Db 415 GKMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSVDGD-ALNVGS 473

Qy 476 KDTNKPVRITNVAPGVKEGDTNVAQLKGAQNINNRIDNVGNARAGIAQAIAATAGLVQ 535
Db 474 KDTNKPVRITNVAPGVKEGDTNVAQLKGAQNINNRIDNVGNARAGIAQAIAATAGLVQ 533

Qy 536 AYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594
Db 534 AYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 592

RESULT 15
US-09-377-155-11
; Sequence 11, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-11

Query Match 90.0%; Score 2721.5; DB 4; Length 591;
Best Local Similarity 91.6%; Pred. No. 1.8e-211;
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

Qy 1 MNKIYRIIWSALNANVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57
Db 1 MNEILRIIWSALNANVVSSELTRNHTKRASATVATVATLTLFATVQASANNEEQEEDL 60

Qy 58 YLEPQVORTAVVLSFRSDEKTEGEGED- SNNAVYFDEKRVKAGAITLKAGDNLKIK 116
Db 61 YLEPQVORTAVVLSFRSDEKTEGEGED- SNNAVYFDEKRVKAGAITLKAGDNLKIK 120

Qy 117 QNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
Db 121 -----NGTNYFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 174

Qy 177 PTVHLNIGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236
Db 175 TTVHLNIGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 234

Qy 237 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 296
Db 235 SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 294

Qy 297 DENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFETVTSGTNVTFAAGK 356
Db 295 GENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFETVTSGTNVTFAAGK 354

Qy 357 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 416
Db 355 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 414

Qy 417 KMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSVDDEGALNVGSK 476
Db 415 KMDETVINAGNIEITRNKNIDIAATSMPTQFSSVSLGAGADAPTLSVDGD-ALNVGSK 473

Qy 477 DTKNKPVRITNVAPGVKEGDTNVAQLKGAQNINNRIDNVGNARAGIAQAIAATAGLVQA 536
Db 474 KDNKPVRITNVAPGVKEGDTNVAQLKGAQNINNRIDNVGNARAGIAQAIAATAGLVQA 533

Qy 537 YLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594
Db 534 YLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 591

Search completed: July 3, 2002, 08:37:11
Job time: 337 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:24 ; Search time 58.79 Seconds
(without alignments)
970.863 Million cell updates/sec

Title: US-09-771-382-9
Perfect score: 3023
Sequence: 1 MNKIYRIIWNLSALNAWVVS.....TASGNSRGHGASASVGYQW 594

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2740.5	90.7	591	2	G81133	adhesin NMB0992 [i
2	2552	84.4	592	2	A81888	probable surface f
3	635	21.0	298	2	I64138	adhesin homolog Hi
4	404	13.4	2059	2	D82671	surface protein XF
5	392.5	13.0	1190	2	A82615	surface protein XF
6	371	12.3	1107	2	AC0976	probable autotrans
7	356	11.8	1588	2	A86036	probable adhesin Z
8	356	11.8	1588	2	H91188	probable adhesin E
9	338	11.2	658	2	AH0110	probable surface p
10	260	8.6	1004	2	C82672	surface-exposed ou
11	240	7.9	1091	2	G64964	hypothetical prote
12	230	7.6	1286	2	S28634	adhesin AIDA-I pre
13	221.5	7.3	1910	2	A80394	probable adhesin h
14	217.5	7.2	3705	2	A00123	probable autotrans
15	216	7.1	949	2	D90803	Aida-I adhesin-lik
16	216	7.1	1005	2	H85611	probable adhesin Z
17	213.5	7.1	4919	2	T31105	hypothetical prote
18	211	6.9	5291	2	F90696	hypothetical prote
19	207.5	6.9	1343	2	D85724	hypothetical prote
20	207	6.8	5188	2	B95547	probable RTX fami
21	206.5	6.8	1109	2	A56143	surface-array prot
22	206.5	6.8	1325	2	A64905	ydek protein - Esc
23	204.5	6.8	1343	2	E90893	hypothetical prote
24	204.5	6.8	1417	2	A83080	hypothetical prote
25	204	6.7	1536	2	A43855	high-molecular-wei
26	203	6.7	1018	2	H83135	probable adhesin P
27	201	6.6	2551	2	B98047	hypothetical prote
28	200.5	6.6	961	2	A00548	puative autotransp
29	199	6.6	1361	2	T03415	S-layer protein -

RESULT 1
G81133
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TE>
A:Cross-references: GB:AE002450; GB:AE0020598; NID:g7226229; PIDN:AAF1395.1; PID:g722 A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

ALIGNMENTS

Query Match 90.7%; Score 2740.5; DB 2; Length 591;
Best Local Similarity 92.1%; Pred. No. 4.8e-131;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;
QY 1 MNKIYRIIWNLSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQANATD---DDDL 57
DB 1 MNKIYRIIWNLSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQASANNEEQEEDL 60
QY 58 YLEPQVORTAVLVNLSKDKSGTGEKTEGD-SNWAIFYDEKRVLKAGAITLKAGDNLIKIK 116
DB 61 YLDPQVORTAVLVNLSKDKSGTGEKTEKVEENSDWAVYFNEKGVLTAREITLKAGDNLIKIK 120
QY 117 NTNENTNDSFFYSLSKDLTDLTSVETKLSFGANGKNYNTSDTKGLNFAKTAGTNGD 176
DB 121 -----NGNFTYSLSKDLTDLTSVETKLSFGANGKNYNTSDTKGLNFAKTAGTNGD 174
QY 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIKVKPGTTA 236
DB 175 TTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKIKVKPGTTA 234
QY 237 SDNVDFRVYDYVEFLSADTKTTTVNVESKDNKKTEVIGAKTSVIKEDGKLVTKGKG 296
DB 235 SDNVDFRVYDYVEFLSADTKTTTVNVESKDNKKTEVIGAKTSVIKEDGKLVTKGDK 294
QY 297 DENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTNVTASGK 356
DB 295 GENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSCTNVTASGK 354
QY 357 GTTATVSKDDOIGNITVKYDVNVGDALNVQLQNSGNLDSKAVAGSSGKVISGNVSPSKG 416

Db 355 GTTATVSKDDQGNITVYDYNVGVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
QY 417 KMDTVMNAGNNEITRNKGNIDATSMAPQSSVSLGAGADAPTLSDVDEGLNVGSK 476
Db 415 KMDTVMNAGNNEITRNKGNIDATSMPTQSSVSLGAGADAPTLSDVGD-ALNVGSK 473
QY 477 DTNKPVRITTVAPGKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
Db 474 KDNKPVRTTVAPGKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 533
QY 537 YLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
Db 534 YLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 591
RESULT 2
A81888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain Z249
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgels, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:20222556
A:Accession: A81888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match 84.4%; Score 2552; DB 2; Length 592;
Best Local Similarity 86.8%; Pred. No. 1-5e-121;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLXL 59
Db 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60
QY 60 EPVORTAVLVSFRSDEKGTGEGE-TEDSNWAY--YFDEKRVLKAGAITILKAGDNL 112
Db 61 ESQVOR-SVSGSIQASMEGSGELEFISLMTNDSKEFVDPYI-----VVTLLKAGDNL 110
QY 113 KIKONTNENTNDSFTYSLKKDLTSLVETEKLSFGANGKNVITSDTKGLNFAKETAG 172
Db 111 KIKONTNENTNASSFTYSLKKDLTLINVTETEKLSFGANGKNVITSDTKGLNFAKETAG 170
QY 173 TNGDPTVHLNGIGSTLTPDVTLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKGVKP 232
Db 171 TNGDPTVHLNGIGSTLTPDVTLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKGVKT 228
QY 233 GTTA--SDNVDFRTYDTVEFLSADTKTTVNVESKDKGKTEVKIGAKTSVKEKDGKL 290
Db 229 GSTTGQSENDFRTYDTVEFLSADTKTTVNVESKDKGKRTVEVKIGAKTSVKEKDGKL 289
QY 291 VTGKGDENGSSDTDEGEGLVTAKEVIDAVNKGWRMKTITTANGQTGOADRFETVTSCTNV 350
Db 289 VTGKKGENGSSDTDEGEGLVTAKEVIDAVNKGWRMKTITTANGQTGOADRFETVTSCTNV 348
QY 351 TFASGKGTATVSKDDGNTITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGN 410
Db 349 TFASGKGTATVSKDDGNTITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGN 408
QY 411 VSPSKGKMDTVMNAGNNEITRNKGNIDATSMAPQSSVSLGAGADAPTLSDVDEGA 470
Db 409 VSPSKGKMDTVMNAGNNEITRNKGNIDATSMAPQSSVSLGAGADAPTLSDVDEGA 468

QY 471 LNVGSKDTNKPVRITTVAPGKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAT 530
Db 469 LNVGSKDANKPVRTTVAPGKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAT 528
QY 531 AGLVQAYLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASV 590
Db 529 AGLVQAYLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASV 588
QY 591 GYQW 594
Db 589 GYQW 592
RESULT 3
I64138
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64138
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 21.0%; Score 635; DB 2; Length 298;
Best Local Similarity 47.8%; Pred. No. 2.9e-25;
Matches 151; Conservative 42; Mismatches 88; Indels 36; Gaps 9;
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDLYLE 60
Db 1 MNKIFKVIWNVVTQTVVVSSELTRAHTKRTSATVATVATLTLFATVQANATVQVQ----- 49
QY 61 PVORTAVLVSFRSDEKGTGEGEEDSNWAYVDEKRVLKAG-AITLKAGDNLKIKONTN 119
Db 50 -INDAGTFVVKVQSTDEDDIEDSAATKDDN-----KQALKAGDPTLTKAGKNLAKL--- 99
QY 120 ENTNDSFTYSLKKDLTSLVETEKLSFGAN-----GNKNVITSDTKGLNFAKETAG 172
Db 100 -DOGGKSVTFLAKDLVDVKAKVSDTLTIGNTPAAGATPKVTSITTAGDKLAK---G 155
QY 173 TNGDPTVHLNGIGSTLTPDVTLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKGVKP 232
Db 156 TNGDPTVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTRAATIKDVLNAGWNKGVK 214
QY 233 GTTASDNVDFRTYDTVEFLSADTKTTVNVESKDKGKTEVKIGAKTSVKEKDKGLVT 292
Db 215 AGGNTENVLDVAGYDVFITGDKNTLDVVLTAKEGKTEVKTPKTSVIKNNGLLT 274
QY 293 GKQ-KDEN-GSSDDEGE 307
Db 275 GKQLKDANTGTATNATE 291

RESULT 4
D82671
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 405, 151-157, 2000
A:Title: the genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below


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Db 963 ----NVADAKEAT--DAVNLRQLDRVAODANRYVDNKTIESLSEGQTF----- 1003
Qy 421 TVNINAGNIEITRNGKNIDIATSMAPQFSSVSLCAGADA-----PTLSVDDEG 469
Db 1004 -VKVNSLNN-----SATPIAGVATAIGVGATASCADSIAMGNKASASADNAV 1051
Qy 470 AL-----NVGSKDNKPKVRITNVAPGVKEGVDVTVNAQLKGVAQNLRNDRDND 517
Db 1052 AIGNHSVADRANTVSGSAGSER--QVTVNAAGTADTDAVNVSQLNQGLITAKQYTDGV 1109
Qy 518 GNAR-----AGTAAQTATAGLQVAYLPKSMMAIGDTRYGEAGYAGVSSYSDGNGWLIK 573
Db 1110 GSLRDTDGGVAAATATANLPQATIPGRGMTSVGVSYRGOSATAVGVSSVSEGRWVFK 1169
Qy 574 GTASGNSRGHFCASASVGYQW 594
Db 1170 FSGSANTSVQVIGAGVGYQW 1190

RESULT 6
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhi
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
  S.; Moule, S.; O'Gaora, P.
  Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
  A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 12.3%; Score 371; DB 2; Length 1107;
Best Local Similarity 22.0%; Pred. No. 3.2e-11;
Matches 184; Conservative 105; Mismatches 263; Indels 286; Gaps 31;

Qy 27 TKRASATVAT---AVLATLTFAT---VQANATDDDLLEFPVQRTAVVLSFRSDKEGTG 79
Db 286 TNLAAGTAAADSTDAVNGSQLYETNQKVDQNTSAIADINTSITNLSSDNLSSWNETTNSFS 345

Qy 80 EKEGTEDSNWAVYFDEKRVLKAGAITLKAGD-----NLKIKONT----- 118
Db 346 ASHGSSSTN-----KITNVAAGELSESTDAVNGSQLFETNEKRVQDNTTIAANTTNIT 399

Qy 119 -----NENTNDSFTYSLKKDLTD---LFSVTEKLSFGANGKNVNTSDTKGLNPAK 168
Db 400 QNSAIEANLNTSVSDINTESI-TGLTDNALLWDEDTGAFSANHGGSTSKITNVAAGALSED 458

Qy 169 ETAGTNGDPTVHLNGICSTLTDL--LNTGATTNVTNDVTDDEKKRAASVKVDVLNAGWN 226
Db 459 STDAVNGSQLYETNQKVDQNTSAIADINT-SITNLGTDALSMDDEEGAFSAHSGTSGTNK 517

Qy 227 IKGVKPGTASDNDVDFV---RTYDT-----VEFLSADTKTTTVN-----VES 265
Db 518 ITNVAAGEIASDSTDAINGSQLYETNMLISOYNESISQAGDTSETYITENGTVGKYIRT 577

Qy 266 KDNKKTE-----VKIGAKTSVKEK-----DGKLVYTGKGDEN----- 299
Db 578 NDNGLEGODAYATGATAGVADAVASAGCALQCNSSSSIEGSIALGSGSTSNRAITT 637

Qy 300 ----GSSTDEGEL--VTAKEVIDAVNKA---GWRMKTITANGQTCQADKFFETVTSGT 348
Db 638 GIRETSATSDGVWIGYNTTDRLLGAUSLGTDGSGYRQITNWADG--SEADAVTVRQLQ 695
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Qy 349 NVTFASCKGTTATYSKDDQGNIT-----VKYDVNVGDALNVNQLQN 389
Db 696 NAIGA-----VTTTPTKYYHANSTEEDSLAVGCTDSLAMGAKTIVNADAGIGLNTLVWAD 751
Qy 390 --SGWNLDKAVAGSSGKVISGNVSP-----SKGMD---E 420
Db 752 AINGIATGNSNARANHANSIAMNGSQTTTRGAQTDYTAYNMDTPQNSVGEFSVSGSDGQOR 811
Qy 421 TVTNINAGN-----NIEITRNGKNI-----DIATFS 444
Db 812 ITNVAAGSADTDAVNVGOLKYTDQAQVSRNTOSIITNLNTQVSNLDRVTNIEINGDITVT 871
Qy 445 MAPOF-----SSVSLGAGADAP-----TSLVDDE-GALNVGSKDKTNK 480
Db 872 GSTKYFKTNTDGDANAGGADSVAGISGSGIAAAEENSVALGTSNVADEANTVSGSSTQOR 931
Qy 481 PVRITNVAPGVKEGDVTNVAOLK----- 503
Db 932 --RITNVAAGVNTDVAVNVAOLKASEAGSVRYETNADGSVNVSVNLNLGDGSGGTTTRIGNV 989
Qy 504 -----GVAO-----NLNRIIDVGNARAGIAQAIAATAGLVQA 536
Db 990 SAAVNDTDAVNVYAQLKRSVEEANTYTDOKMGEMSKIKGIENKMSGGSIASAMAGLPOA 1049
Qy 537 YLPKSMMAIGDTRYRGAGYAGVSSISDGGNWIILKGTASGNSRGHFGASASVGYQW 594
Db 1050 YAPGANMTSIAGGTFCGESAVAGVSMVYSEGSGVWYKLGQTSNCGDYSAALGAGFQW 1107

RESULT 7
A86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
  iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
  Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1598 <STO>
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:
  A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 25029

Query Match 11.8%; Score 356; DB 2; Length 1588;
Best Local Similarity 25.8%; Pred. No. 2.9e-10;
Matches 149; Conservative 81; Mismatches 240; Indels 108; Gaps 21;

Qy 111 NLKIKONT---NENTNDSFTYSLKKDLTDLTSVET---EKLSE-----GANGKNKVNITS 159
Db 1025 NMWIEQNTQIIINQLAGNTDAY-IQENGAGINYVVRTNDGLAENDASQAQGVGATAGVNS 1083

Qy 160 DTGKLNFAKETAGTNGDPTVHLNGIGSTLTDLTNTGA-TTNVTNDNV-----TDDEKK 212
Db 1084 VAKGDSVAIQGGSYSVDVTGIALGSSSVSRVIAKGRSDTSITENGVIYDITDTEGELL 1143

Qy 213 RAASVKD-----VLNAGWNKGVKPGCTASDNDVDFVRYTDTVEFLSADTKTTTVNVESK 266
Db 1144 GALSIGDDGKYRQIIN-----VADGSEADAVT-VRLQNAICAVATTTKTFHANST 1195

Qy 267 DNGK-----KTEVKICAKTSVKEKDGKLVTKGDKDENGSSSTDEGEGLVTAKEVIDAVNKA 322
Db 1196 EEDSLAVGCTDSLAMGAKTIVNGDKGIGIGYGAIVDANALN---GTAIGSNAQVIVHNSIA 1252

Qy 323 GWRMKTITANGQTCQADKFFETVTSFGKSG---GQAD-----KFEVTYSGTNVTYFASGK--- 357
```

Db 1253 I G N S T T T R G A O T N T A Y N M D A P Q N S V G E F S V G S A D C Q R Q I T N V A A G S A D T D A V N V G Q L K 1312
QY 358 - T T A T V S K D Q G N I T - - - - - V K Y D V N V G D A L - - - - - N V N O L Q N S G W N 393
Db 1313 V T D A Q V S Q N T Q - S I T N L D N R V T N L D S R V T N I E N G I G D I V T T G T K Y F K T N T D G V D A S A Q 1371
QY 394 L D S K A V A G S G K V I S G N V S P S K G M - - - D E T V N I N A G N N I E I T R N - - - G N I D I A T S M A P 447
Db 1372 K D S V A I G S G S I A A D N S V A L G T G S V A T E E N T I S V G S T N O R R I T N V A A G K N A T D A V N V A Q 1431
QY 448 Q P S S V S L G A G A D A P T L S V D D E G A L N V G S K D T N K P V R I T N V A P G V K E G D Y T N V A Q L K G V A Q 507
Db 1432 L K S S E A G G V R Y D T K A D G S I D Y S N I T L G G - G N G T T R I S N V S A G V N N D V N V Y A Q L K Q S V Q 1490
QY 508 - - - - - N L N N R I D N V D G N A R I A Q A T A G L V O A Y L P G K S M A I G G D T Y R G E A G 556
Db 1491 E T K Q Y T D Q R M V E M D N K L S T E S K L S G I A S A M A M T G L P Q A Y T P G A S M A S I G G G T Y N G E S A 1550
QY 557 Y A I G Y S S I D G G N W I I K T A S G N S R G H F G A S A S V G Y Q W 594
Db 1551 V A L G V S M V S A N G R W Y K L O G S T N S Q G E Y S A A L G A G I Q W 1588

RESULT 8

H91188
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: H91188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4480

Query Match 11.8%; Score 356; DB 2; Length 1588;
Best Local Similarity 25.8%; Pred. No. 2.9e-10;
Matches 149; Conservative 81; Mismatches 240; Indels 108; Gaps 21;
QY 111 N L K I K O N T - - - N E N T N D S P T Y S L K K D L T D L T S V E T - - E K L S F - - - - - G A N G K N Y N I T S 159
Db 1025 N M M I E Q N T O I I N O L A G N T D A T Y - I O E N G A G I N V R T N D D G L A E N D A S A Q G V G A T A I G Y N S 1083
QY 160 D T K G L N F A K E T A G N D P T V H L N G I G S T L T D L L N T G A - T T N V T N D N V - - - - - T D E K K 212
Db 1084 V A K G D S V A I G O G S Y D V D T G I A L G S S V S S R V I A K G S R D T S I T E N G V I G Y D T D G E L L 1143
QY 213 R A A S V D - - - - - V L A N A G N I K V K P G T T A S D N V D F V R I Y D T V E F L S A D T K T T V N V E S K 266
Db 1144 G A L S I G D G K Y R O I N - - - - - V A D G S E A H D A V T - V R O L Q N A I G A V A T T P T K Y F H A N S T 1195
QY 267 D N G K - - - - - K T E V R I G A K T S V I K E D K L V T G K G D E N G S T D E G L V T A K E I D A V N K A 322
Db 1196 E E D S L A V G T D S L A M A K T I V N G K I G I G V A Y V D A N A L N - - - G I A I G S N A Q V I H V N S I A 1252
QY 323 G W R M K T T T A N G O T - - - - - G Q A D - - - - - K F E T V T S G T N V T F A S G K G - - - 357
Db 1253 I G N S T T T R G A O T N T A Y N M D A P Q N S V G E F S V G S A D C Q R Q I T N V A A G S A D T D A V N V G Q L K 1312
QY 358 - T T A T V S K D Q G N I T - - - - - V K Y D V N V G D A L - - - - - N V N O L Q N S G W N 393
Db 1313 V T D A Q V S Q N T Q - S I T N L D N R V T N L D S R V T N I E N G I G D I V T T G T K Y F K T N T D G V D A S A Q 1371
QY 394 L D S K A V A G S G K V I S G N V S P S K G M - - - D E T V N I N A G N N I E I T R N - - - G N I D I A T S M A P 447

Db 1372 K D S V A I G S G S I A A D N S V A L G T G S V A T E E N T I S V G S T N O R R I T N V A A G K N A T D A V N V A Q 1431
QY 448 Q P S S V S L G A G A D A P T L S V D D E G A L N V G S K D T N K P V R I T N V A P G V K E G D Y T N V A Q L K G V A Q 507
Db 1432 L K S S E A G G V R Y D T K A D G S I D Y S N I T L G G - G N G T T R I S N V S A G V N N D V N V Y A Q L K Q S V Q 1490
QY 508 - - - - - N L N N R I D N V D G N A R I A Q A T A G L V O A Y L P G K S M A I G G D T Y R G E A G 556
Db 1491 E T K Q Y T D Q R M V E M D N K L S T E S K L S G I A S A M A M T G L P Q A Y T P G A S M A S I G G G T Y N G E S A 1550
QY 557 Y A I G Y S S I D G G N W I I K T A S G N S R G H F G A S A S V G Y Q W 594
Db 1551 V A L G V S M V S A N G R W Y K L O G S T N S Q G E Y S A A L G A G I Q W 1588

RESULT 9
AH0110
probable surface protein (partial) YPO0902 [imported] - Versinia pestis (strain CO92)
C:Species: Versinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Versinia pestis, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 11.2%; Score 338; DB 2; Length 658;
Best Local Similarity 23.8%; Pred. No. 7.5e-10;
Matches 154; Conservative 84; Mismatches 236; Indels 174; Gaps 28;
QY 27 T K R A S A T V A T - - - - - A V L A T L L F A T V Q - - - - - A N A T D D D D L Y L E P V Q R T A V - - - - - 67
Db 105 T N L A P A T I S T S T D A V V G S Q L Y N L V O D G T R Y F H A N S V N P T D S L A S G L E T I A V G P A T V V S G 164
QY 68 - - - - - V L S F R S D K E G T G - - - - - E K E G T E D S N W A V F D E K R V L 99
Db 165 D N G V G I G N T A L V G A A A T G G I A I G F Q V T A A G A T A I G S A A Q A G A - - - - - Q S L A L 214
QY 100 K A G A I T L K A D N L K I K O N T N E N T N D S S F T - Y S L K K D L T D L T S V E T E K L S F G - A N G N K V N I 157
Db 215 G A G A V T S Q A N S I A L G A A S I N T V G A Q S S Y S A Y A L - - - - - T A P Q A S V G E L G I G T A L G N R - K I 268
QY 158 T S D T K G L N F A K E T A G N D P T V H L N G I G S T L T D L T L T G A T T N V T N - D N V T D D E K K R A A 215
Db 269 T G V A A G - - - - - S A S S D A V N V A Q L T A V G D Q V Q N - - - - - T A N I T S L G R V T T I E - - - - - G 312
QY 216 S V K D V L N A G N I K V K P G T T A S D N V D F V R I Y D T V E F L S A D T K T T V N V E S K D N G K K T - - - 272
Db 313 S M A S I A N G G - G V K Y F H A N S T Q P D S V - - - - - A S G T N S V A I G P A S L A S N A A L S 359
QY 273 - - - - - E V K I G A K T S V I K E D K L V T G K G D E N G S T D E G L V T A K E I D A V N K A G W R M K T T 329
Db 360 G A G A V A I G - - - - - D G A A A S A D G S V A I G Q G S D G N R G V E N I G - - - - - K Y S N 400
QY 330 T A N G O T Q A D K F E T V T S G T N V T F A S G K T T A T V S K D D Q G N I T V K Y D V N V G D A L N V Q L Q N 389
Db 401 A S N T S S G - - - - - T V S V G N T A T - - - - - G E T R T V S N V A D G - - - - - L Q A T D A V N L R Q L D G 442
QY 390 S G W N L D S K A V A G S G K V I S G N V S P S K G M D E T V N I N A G N N I - E I T R N K K I D I - - - A T S M A 446
Db 443 - - - - - I A A S I V V E N N V S L Q N G T D G M F Q V N N S S G L A K P S A T G A N S A T G G A G S V A 492

Query Match	7.9%;	Score 240;	DB 2;	Length 1091;
Best Local Similarity	23.7%;	Pred. No. 0.00013;		
Matches 149;	Conservative 57;	Mismatches 210;	Indels 212;	Gaps
Qy	1	MNKYRIIWNALNANWVVSSELTRNHTTKRASATVATAVIATLTLFATVQANATDDDDLLYLE	60	
Db	57	LNTCYRLVNMHMTGAFVVASELARAGKRGGVAVALSAAVTSLPVLLA-----DIVVH	110	
Qy	61	PVQRTAVVLSFRSDKECTGEKETSNSNAWVYDFEKRVLKAGAITLKAGDNLKIKONTNE	120	
Db	111	P-----GE-----TVNGG--TLAHNDNQIVFGTTG	134	
Qy	121	NTNDSSFTYSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH	180	
Db	135	MTISLTGLEYPDNE---ANTGGQWQDGGTANKTIVTSG--CLQ--RVNPGGSVSDTVI	186	
Qy	181	LNIGIGSTL-----TDTLLNTG-----ATTWNTDNDVTDEKKRAASVKVDVNLNAGWNI	227	
Db	187	SAGGGQSLOGRAVNTTNGGEQNMHFGATGTGVINDK-----GWQV	228	

QY 228 KGVKPGTASNDVDFVRT-----YDTVEFLSADTKTTTNNVESKDNKKTEVKIG 277
 Db 229 --VKPGTATDTV--VNTGAEGGPDENGDTGQFVRGDAVRTTIN-----KNGRQIVRAEG 280
 QY 278 -AKTSVIKEDGKLVTGKKDE--NGSSDDEGLVTAKEVIDAVNKAGWRM-----K 327
 Db 281 TANTTVYAGGDTQVHGHADLTTLNGGYQYVHNG-GTASDTV--VNSDQWQIVKNGGVAG 337
 QY 328 TTTTANGOTGQADFEVTVTSGTNTVTFASG---KGTATATVSKDDQGNITVKYDYNVGDALN 383
 Db 338 NTVTVN-QKGR-LQVDAAGGTATNTLTKQGGALVTSTATVT-----G 376
 QY 384 VNQLNSGNWLDKAVAGSSGKVISGNVSPSKGMDETNINAGNNTIETRNKNIDIAF 443
 Db 377 INRL-----GAFSVVECKADNVV-----LENGRDLVLT 405
 QY 444 SMAPQSSVSLGAGADAPLTVSDGALNVGSKDTPKPKVITWVAPGVKRGDVTNVAQLK 503
 Db 406 -----GHTATNTRVDGGLDVRNGGTATTVSMGN--GGVLLAD-----S 443
 QY 504 GVAQNLRNDRIDVGNARAGIAQAIATAGILVQAYL--PGKSMMAIGGDT-----Y 551
 Db 444 GAA-----VSGFRSDGKAFSIG-GGQADALMLEKSSFTLNAGDTATDTTVNGGLF 493
 QY 552 RGPAGYAIGYSSISDGGNWIIGKTASGN 579
 Db 494 TARGGTLAGTTTLNNGAILTSLGKTVNN 521

RESULT 12

adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
 C:Species: Escherichia coli
 C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
 C:Accession: S28634; S22680; S28881; S72657
 R:Benz, I.
 submitted to the EMBL Data Library, March 1992
 A:Reference number: S28634
 A:Accession: S28634
 A:Molecule type: DNA
 A:Residues: 1-1286 <BE2>
 A:Cross-references: EMBL:X65022; NID:g42254; PIDN:CAA46156.1; PID:g42255
 R:Benz, I.; Schmidt, M.A.
 Mol. Microbiol. 6, 1539-1546, 1992
 A:Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeagenic Escherichia coli serotype O157:H7
 A:Reference number: S22680; MUID:92326638
 A:Accession: S22680
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 839-1286 <BE2>
 A:Cross-references: EMBL:X65022
 A:Experimental source: strain 2787
 A:Accession: S28881
 A:Molecule type: protein
 A:Residues: 50-56 <BE3>
 A:Experimental source: strain 2787
 R:Suhr, M.; Benz, I.; Schmidt, M.A.
 Mol. Microbiol. 22, 31-42, 1996
 A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence for the outer
 A:Reference number: S72657; MUID:97055419
 A:Accession: S72657
 A:Molecule type: protein
 A:Residues: 847-856 <SUH>
 A:Experimental source: DAEC strain 2787
 C:Genetics:
 A:Genome: plasmid pIB6
 C:Keywords: membrane protein
 F:1-49/Domain: signal sequence #status predicted <SIG>
 F:50-1286/Product: adhesin AIDA-I #status predicted <MAT>

Query Match 7.6%; Score 230; DB 2; Length 1286;
 Best Local Similarity 17.0%; Pred. No. 0.0005;

Matches 156; Conservative 106; Mismatches 291; Indels 364; Gaps 31;
 QY 1 MNKIYRIINNSALNANVWVSELTRNH-----TKRASATVATA--VLATLLFATVOANA 51
 Db 1 MNKAYSIIISHSHSQAWIVASELARGHGFVLAKNTLLVLAVVSTIGNAFVAVNSGTVSSGG 60
 QY 52 TDDDDLLLEPVQRTAVVLSFRSDKEGTGEKGT----- 85
 Db 61 TVSSG-----ETQIVYSGRGNATVNSGGTQIVNNGGKTTATTVNSSSGSNVGTSGA 113
 QY 86 -----DSNNAVYFDEKRVLKAGAIT--- 105
 Db 114 TISTIVNSGGIQRVSSGVSATNLSSGAQNIYNLGHASNTVIFSGNQIFSGGIDTST 173
 QY 106 -LAKGDLNLIKQN--TNENTNDSSFTYSLKQD--LTDLTSVETKLSFGANGKNVIT 158
 Db 174 NISSGGQORVSSGGVASNTTINSAGQNIILSEGAISTHISGGNQIISAGANATEIIVN 233
 QY 159 SDTKGLNFARAKETAGTNGDPTVHLNG-----IGSLTLDTLN 194
 Db 234 SG---GFQRVNSGAVATGTVLSGGTONVSSGSAISTSVYNSGVQTVFAGATVDTTVN 289
 QY 195 TGATTVTNDNVDDDEKKRAASVKDVLNAG---WNKIG----- 229
 Db 290 SGCNQNISSGGIVSETTVNVSGTQNIYSGGSALSANIKGSQIVNSECTAINTLVDSGGYQ 349
 QY 230 -VKPGTTASDNVDFRTYDVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVIRE--K 286
 Db 350 HIRNGGIASGTIVNQSGY-----VNISGGYAESTIINSGGTLRVLSDGYA 395
 QY 287 DGKLVTKGKGD--ENG-----STDEGGLVTAKEVIDAVNKAG----- 323
 Db 396 RGIIILNSGRVNSGGVSYNAMINTGGNOYIYSDGEATAIIVNTSGFORINSGGTAPVQ 455
 QY 324 -----WRMKTITTTANGQ-----TG 336
 Db 456 NSVVVTRTVSSAAKPDAAEVYSGGKQTVYLWRGIWYSNFLTAVNMFPGGTASGANVLSG 515
 QY 337 QADKFEVTVSGTNTV-----FASGKGTATATVSKDDGNTVYKVDVNVGALNVNQLO-- 388
 Db 516 RLNAFAGNVVGTILNQEGROYVYSGATATSTVGNREGREYVLSGGITDGTVLNSGGLOAV 575
 QY 389 NSGNWLDKSAVAGSSGKVI--SGNVSPSKGMDETNINAGN---NIEITRNKNIDIAF 443
 Db 576 SSGKASATVINEGGAQFVYDGGQVGTCTNKNGGTIRVDSGASALNIALSSGNLFTSTG 635
 QY 444 SMAPQFSSV-----SLGAGD-----APTLSDVDEGALN-- 472
 Db 636 ATLPELTTMAALSVSQNHASNIVLENGGLLRVTSGGTATDTTVNSAGRLRIDDGGTINGT 695
 QY 473 -----VGSKDTNKPVRITWAP----- 489
 Db 696 TTINADGIVAGTNIQNDGNFILNLAENYDFETELSSGVLVKDNTGIMTYAGTLTQAGV 755
 QY 490 GVKEG-----DVTNVAQLKGVAQN-----LNNRDNVDGNARAG 523
 Db 756 NVRNGGIIFDSAVVNMADMAVNQNNAYINISQATINGSVNNNGSIVINNSI--INGNTND 813
 QY 524 IQAIAITAGIVQAYLPKSM-----MAIGGDT-----YRGEAGYAIGYSSISDGG 568
 Db 814 ADLSFGTKALLSATVNSGLVNNKNIILNPKESAGNTLTVSNYTGTPGVSILSGVLEGD 873
 QY 569 N-----WIIKGTASGNS 580
 Db 874 NSLTDRLVVRKNTSGQS 890

RESULT 13

AF0394
 Probable adhesin hmwa [imported] - Yersinia pestis (strain C092)
 C:Species: Yersinia pestis
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
 C:Accession: AF0394

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N. Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0394
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1910 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:gl5981183; GSPDB:GN00175
C:Genetics:
A:Gene: hmwA

```
Query Match          7.3%; Score 221.5; DB 2; Length 1910;
Best Local Similarity 21.5%; Pred. No. 0.0022;
Matches 153; Conservative 86; Mismatches 271; Indels 201; Gaps 30;

Qy 14 NAWVVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLEPVQ-----R 64
Db 898 NATITANNISNN---GNITANDAVLMTNTFLTAKGDIKTD---LTSPTKGLWFRNGGM 950

Qy 65 TA---VWLSFRSDKEGTEGSDSNWVYFDEKRV-LKAGATLKGADNLKIKQNTNE 120
Db 951 TAANNILLVANSTSGGETVKINASSSNKNMTAGKDIIAGNSKTATGPNINI-ENVNI 1009

Qy 121 NTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNCDDPVH 180
Db 1010 ETNNGNFT-----TNGITSTWLSGVNVASNG--VDITSNTG-----TGIVLDNTNI 1055

Qy 181 LINGISTLTLANTGATTNTNDVTDDEKRAASVKDV-----LNAGNIKGV--KPGT 234
Db 1056 LTTVGD-----INT-IVTNSSGKIWIKNSTLNSNKDITLVGVSAGQN-EGVLIQSS 1107

Qy 235 TASDNDVPRYDVVEFLSADTKTTTVNVESKDKGKTEVKIG--AKTSVIKEKDGKLV 292
Db 1108 DASRN-----NISAQGNITLIGKMGNGSGQHSILNLGNVSLTS-----S 1146

Qy 293 GKGDKENGSSDDEGBGLVTAKEVIDAVNKAGWRMKTFTA-----NGOTGQADK 340
Db 1147 GRNDINGSAGTGDVYFTNVELNATAGNVSIYAEKTLSTLNAVLSLGGNNSIKAQN 1206

Qy 341 FETVSGTNVTFAGKGTATVSKDDQGNITVK-----YDYNVGDAKNV 385
Db 1207 GWLIGKAFNTQAGIGFRANSSLSVDGNIILKGETGVGATRGIDFYGANTLNIKGS 1266

Qy 386 QLQNSGNLDSKAVAG----- 401
Db 1267 QLSLGLENKGAQDTAGGNGISYTSIAKLTVNNGSLKMEGRSTSGTGINFPSSNNTLVFN 1326

Qy 402 -----SSGKVIISGNVSPSKCKMD-----ETVNIINAGN 428
Db 1327 GDGDTLKGSSVAGTGAISGVVNNSTGPMTEIGISTDCAGVHIFSABHRIDRINVTGSS 1386

Qy 429 ----NIEITRNKNIDIA-TSMAPQFSSVSLGA--GADAPTLSDDEGALNVGSKDNTKP 481
Db 1387 THAEGRLISGNAIIVDTTLTKSINGSQVKIDSLPGSSVVRVSLDNATLN-GSSSSCKG 1445

Qy 482 VRITNAPGVKEGDTVWVAQLKGAQNLNRRIDNVGDNARAG--IAQAIATAGLVQVAYLP 539
Db 1446 VEITSDINGIHSSINGTTGTGTGIDIGEN-SNVITGTSEADLLILQGVATTG-----T 1498

Qy 540 GKSMAIGGDYRGEA-----GVAIGYSS-ISDGGNWIIGKTASGNSRG 582
Db 1499 GTGIKLGNNDLSNTSLNSSAVDGIADITGPLANQGNVILNGTASGSGIG 1549
```

RESULT 14
AD0123

probable autotransporter protein yaph [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C:Accession: AD0123
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N. Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3705 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89847.1; PID:gl5979073; GSPDB:GN00175
C:Genetics:
A:Gene: yaph

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Query Match          7.2%; Score 217.5; DB 2; Length 3705;
Best Local Similarity 20.6%; Pred. No. 0.0083;
Matches 164; Conservative 85; Mismatches 272; Indels 277; Gaps 36;

Qy 2 NKIYRIIWNLSALNAWVVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLEP 61
Db 364 NVIYNLGTGSLKA-----TWGTILAT-----KNANNASDIYRS 398

Qy 62 VORTAVVLSFRSDKEGTG-----EKEGTEDSNWVYFDEKRVLKA-----GATLKGAD 110
Db 399 AGDITAAATGATGTHGTGTVKIKNDGTTTSTAGTATISSASIKSIVSDTGTATATAGT 458

Qy 111 NLKTKQ-----NTNENTNDSSTFYSL-KKDLTDLTSVETEKLSFG---ANGNKV 155
Db 459 GVNVLASAILNLFGGTINTSATANGITFAGTEGGHTLTDLT---INLGTGIALSNVAGV 515

Qy 156 NITSDTKGLNFAKETA-----GTNGDPTVHLN--GIGSTLDTLLNT----- 195
Db 516 NLTLNVTNLNTALNSLTGLTLDVSLNGRNTINIBGAGIGIAANTELNTFDAREALD 575

Qy 196 -----GATTNVTNDNVTDDEKRAASVKOVLNAGWNI-KGVKPGTTRASDNVDF-VRTYD 247
Db 576 INVNAGIGIQTGGVNLASNLIIINVANTLGTALQITDGTIDNTTTIGNEIQLNAENAT 635

Qy 248 TVEFLSADTKTTTVNVEKONG--KKTEVKITGAKTSVIKEK---DGKLVTCGKDE---- 298
Db 636 AINFLGSSSKTL-----NNGTIGKSVIFAGVADHIIINNNGTLDTGTLTTGAGNDTLVLD 689

Qy 299 -----NGSSTDEGEGLVTAKEVIDAVNKAGWRM 326
Db 690 SSSQSDNVINLGDGNNSVTIONGATVSSIITGNGNDFTINGMSVGSYLGSLD-ACGTGL 748

Qy 327 KTTTANGOTGO-----ADKFTVTSQTNV----- 350
Db 749 NTLNPNASTDELAATAATSLQGFTNINLVDSHITLVSDDNIGSGMVNIDSSSELLFGSTPDG 808

Qy 351 ----TFASGKGT-----TATVSKDDQGNITVKYDVNVGDAL---NVNQLQNS-----GW 392
Db 809 ILHATLGAAGTGSATLVNNSANVSLQASMFAGTQVWNOGAGLTASNOLGSAKIGLDGTL 868

Qy 393 NLDSKAVAGSGKVIISGNVSPSKGMDETVINAGNNTIETRNKNIDIA-TSMAPQFSSV 452
Db 869 NLDNAL---FNHVLGTNGT-----LNVAKNLATTA---PDFGSTVGGAFTSGI 910

Qy 453 -----SLGAGAD-----APTLSDDEGALNVGSKD----- 477
Db 911 VNLTKTTTFALSDANAAALASATLKLSDDSVTGTTGTRTLHGLDLSGCTLIFDGAVPQSQ 970

Qy 478 TNKPVRTNTPVAPVKEGDV-----TNYAQLK-----GVAQNLRNIDNDVGG 518
Db 971 TSGVVTYTDLA--LNSGTVNITGSGWDNTDPLATNVSIILEODRAGSTLELIN-ATNVTG 1027

Qy 519 NARA-----CIAQAIATAGLVQVYLPCKSMMA-----IGGDTYRCEAGYAGYS--- 562
Db 1028 DIDALDLLVNGTATISGTQGVQSAIQOQGSIVANAIHNVGLASSNSGDSGLVYNTLSA 1087

Qy 563 --SISDGGNWIIGKTASG 578
```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:58 ; Search time 29.79 seconds
(without alignments)
772.051 Million cell updates/sec

Title: US-09-771-382-9

Perfect score: 3023
Sequence: 1 MNKIYRIINNSALNANWVVS.....TASGSRGHFGASASVGYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	240	7.9	1039	1 AG43_ECOLI	P39180 escherichia
2	230	7.6	1286	1 AIDA_ECOLI	Q03155 escherichia
3	206.5	6.8	1325	1 YDEK_ECOLI	P32051 escherichia
4	198	6.5	1608	1 HLYA_SERMA	P15320 serratia ma
5	197.5	6.5	2249	1 OMPA_RICRI	P15921 rickettsia
6	190	6.3	2003	1 YDBA_ECOLI	P33666 escherichia
7	189.5	6.3	1654	1 OMPB_RICRI	Q53047 r outer mem
8	188.5	6.2	1655	1 OMPB_RICCN	P98ka3 r outer mem
9	188	6.2	1567	1 ICEN_XANCT	P18127 xanthomonas
10	184	6.1	1577	1 HLYA_PROMI	P16466 proteus mir
11	182	6.0	2021	1 OMPA_RICCN	Q52657 rickettsia
12	180.5	6.0	1645	1 OMPB_RICRY	P96989 r outer mem
13	179.5	5.9	933	1 SLAP_CAMPE	P35827 campylobact
14	175.5	5.8	1300	1 120K_RICRI	P14914 rickettsia
15	175.5	5.8	1861	1 APG_THETU	P38536 t amylopull
16	175	5.8	1953	1 BIGA_SALTY	P25927 salmonella
17	173.5	5.7	918	1 YMTB_CAEEL	P34487 caenorhabdi
18	170.5	5.6	1656	1 OMPB_RICJA	Q06653 r outer mem
19	170	5.6	550	1 FLIC_SHIFL	Q08860 shigella fl
20	169.5	5.6	1025	1 SLAP_CAUCR	P35828 caulobacter
21	168	5.6	1569	1 YPTA_ECOLI	P52143 escherichia
22	168	5.6	2334	1 WAPA_BACSU	Q07833 bacillus su
23	166.5	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
24	162.5	5.4	671	1 ALYS_ENTFA	P37710 enterococu
25	162	5.4	1148	1 ICEK_PSESK	O30611 pseudomonas
26	161.5	5.3	1200	1 ICEN_PSESY	P06620 pseudomonas
27	161	5.3	1007	1 Y741_CHLMU	Q9p1t6 chlamydia m
28	161	5.3	1034	1 ICEN_PANAN	Q47879 pantoea ana
29	161	5.3	1258	1 ICEN_ERWHE	P16239 erwinia her
30	160.5	5.3	1210	1 ICEN_PSEFL	P09815 pseudomonas
31	159.5	5.3	642	1 FLID_CAMJE	Q9phw6 campylobact
32	159.5	5.3	948	1 HP11_DEIRA	P56867 deinococcus
33	159	5.3	1322	1 ICEA_PANAN	P20469 pantoea ana

RESULT 1
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT: 1039 AA.
AC P39180; P76360; P75614; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizohata K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded

Q01837 listeria iv
O33479 pseudomonas
P19570 bacillus sp
P13390 bacterioph
P13345 caulobacter
P04949 escherichia
Q01714 rattus norv
P45508 escherichia
O84462 chlamydia t
P80544 staphylococ
P44969 haemophilus
P45384 haemophilus

ALIGNMENTS

CC	EMBL; X65022; CAA46156.1; -	
DR	PIR; S28634; S28634.	
KW	Cell adhesion; Signal; Outer membrane; Plasmid.	
FT	SIGNAL 1 49	
FT	CHAIN 50 ? ADHESIN AIDA-I.	
FT	PROPEP ? 1286	
SQ	SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;	
Query Match 7.6%; Score 230; DB 1; Length 1286;		
Best Local Similarity 17.0%; Pred. No. 0.00027;		
Matches 156; Conservative 106; Mismatches 291; Indels 364; Gaps 31;		
QY	1 MNKIYRIIWNLSALNANWVSELTNRH-----TKRASATVATA--VLATLLFATVQANA 51	
DB	1 MNKAYSIIINSHSQAWIVASELARGHGFVLAKNTLLVAVVSTIGNAFVAVNISGTVSSGG 60	
QY	52 TDDDLLEPVPQRTAVLVLSFRSDEKGTGEKETE----- 85	
DB	61 TVSSG-----ETQIVYSGRGSNATVNSGGTQIVNNGGKTATTAVNSGSONVCTSGA 113	
QY	86 -----DSNWAVYFDEKRVLKAGAIT--- 105	
DB	114 TISTIVNSGGIORVSSGGVASATNLSSGAQNIYNLGHASNTVIFSGNQTFISGGITDST 173	
QY	106 -LKAGDNLKIQN---TNEFTNDSSFTYSLKKD---LTDLTSVETEKLSFGANGKVNIT 158	
DB	174 NTSSGQQRVSSGGVASNTINSSGAQNLSEGAISTHSSGNGQYISAGANATTIYN 233	
QY	159 SDPKGLNFAKETAGTNDPTVHLNG-----IGSTLTDTLLN 194	
DB	234 SG---GFQVNSGAVATGTVLSGGTQNVSSGSAISTSVYNSGVQTVFAGATVTDTTVN 289	
QY	195 TGATTNVTNDVTDDEKRAASVKDVLNAG---WNIGK----- 229	
DB	290 SGGNQNISSGGIVSETVNVSGTQNIYSGGSALSANIKGSQIVNSEGTINTLVSDGGYQ 349	
QY	230 -VKPGTTASDNVDVFTYDTVFEVLSADTKTTVNVEKDKGKTEVKIGAKTSVIRE--K 286	
DB	350 HIRNGIAGSTVINOQSGY-----VNISGGYAESTIINSGLTVLSDGYA 395	
QY	287 DGLVTKGKD--ENGSS-----STDEGEGLVTAKEVIDAVNKAG----- 323	
DB	396 RGTILNNSGRNVNGSVSNAMINTGGQYIYSDGEATAIVNTSGFORINSGGTAPVQ 455	
QY	324 -----WRMKTITANQ-----TG 336	
DB	456 NSYVVTRTVSSRAKPPDAEYVSGGKQTVYIWRGIWYSNFLTAVWMSFPFGTASGANVLSG 515	
QY	337 QADKFEVTVSGTNVT-----FASGKGTATVSKDOGNITVKYDYNVGDALNVNOLQ-- 388	
DB	516 RLNAPAGNVVGTLLNDEGRQYVYSGATATSTVGNNGREYVLSGGITDGTVLNSSLGQAV 575	
QY	389 NSGNWLDKSAVAGSSGKVI--SGNVSPSKGMDETVINAGN---NIEITRNKNIDIAI 443	
DB	576 SSGGKASATVINBGAQFVYDGGQVGTGKNGKGTIRVDSGASALNALSSGGLNSTG 635	
QY	444 SNAQPFSSV-----SLAGAD-----APTLSVDDEGALN-- 472	
DB	636 ATLPELTMAALSVSQNHASNIIVLENGLLRVTSSTGATDTTNSAGRLRIDGGTINGT 695	
QY	473 -----VGSKDTNKPVRITNAP----- 489	
DB	696 TTNADGIVAGTNIQDNGFILNLAENYDFETELSSGVLVKDNTGIMTYAGFLYTAQGV 755	
QY	490 GVKGE-----DVTNVNQLKVAQN-----LNNRIDNVNDRAG 523	
DB	756 NVKNGGIIFDSAVVNADMAVNQININISDOATINGSVNNNGSIVNINSI--INGNITND 813	
QY	524 IAQAIATAGLVQAYLPKSKM-----MATGGDT-----YRQBAGYAIGYSSISDGG 568	
DB	814 ADLSFGTAKLLSATVNGSLVNNKNIILNPTKESAGNTLTVSNYTGTPGVSISLGGVLEGD 873	

QY	569 N-----WIIKGTASGNS 580	
DB	874 NSLTDLRLVVKGNSTSGOS 890	
RESULT 3		
ID	YDEK_ECOLI STANDARD; PRT; 1325 AA.	
AC	P32051; P76140; P77168;	
DT	01-OCT-1993 (Rel. 27, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Hypothetical lipoprotein ydek precursor (ORET).	
GN	YDEK OR ORF OR B1510.	
OS	Escherichia coli.	
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC	Escherichia.	
OX	NCBI_TaxID=562;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12 / MG1655;	
RX	MEDLINE=97426617; PubMed=9278503;	
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,	
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	
RA	Mau B., Shao Y.;	
RT	"The complete genome sequence of Escherichia coli K-12.";	
RL	Science 277:1453-1474(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12;	
RX	MEDLINE=97251357; PubMed=9097039;	
RA	Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,	
RA	Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,	
RA	Makino K., Mikii T., Mizobuchi K., Mori H., Mori T., Motomura K.,	
RA	Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,	
RA	Sampel G., Seki Y., Silvasundaram S., Tagami H., Takeda J.,	
RA	Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;	
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome	
RT	corresponding to the 28.0-40.1 min region on the linkage map.";	
RL	DNA Res. 3:363-377(1996).	
RN	[3]	
RP	SEQUENCE OF 595-1325 FROM N.A.	
RX	MEDLINE=94100243; PubMed=8274505;	
RA	Cartwright P.J., Timms M.W., Lithgow T., Hoef P.B., Hoogenraad N.J.;	
RT	"An Escherichia coli gene showing a potential ancestral relationship	
RT	to the genes for the mitochondrial import site proteins ISP42 and	
RT	MOM38.";	
RL	Biochim. Biophys. Acta 1153:345-347(1993).	
CC	-I- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor	
CC	(potential).	
CC	-I- SIMILARITY: TO E.COLI YFAL.	
CC	-I- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS	
CC	ISP42 AND MOM38.	
CC	-I- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A	
CC	FRAMESHIFT IN POSITION 653.	
CC	-----	
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CC	or send an email to license@isb-sib.ch).	
CC	-----	
DR	EMBL; AE000248; AAC74583.1; -	
DR	EMBL; D90793; BAA15190.1; ALT_INIT.	
DR	EMBL; D90794; BAA15197.1; ALT_INIT.	
DR	EMBL; X73295; CAA51730.1; ALT_FRAME.	
DR	PIR; S34315; S34315.	
DR	EcoGene; EG11780; ydek.	
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.	

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X16353; CAA34403.1; -
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.3%; Score 189.5; DB 1; Length 1654;
Best Local Similarity 21.7%; Pred. No. 0.035;
Matches 148; Conservative 85; Mismatches 284; Indels 165; Gaps 34;

QY 15 AWVVSELTNRHFKRA-----SATVATAVLATL-----LFATVQA-NATDDD 55
Db 181 ASTLVENLANPTTQKAPLILGDNAVANGVNGTLNVTNGFIQVSNKSFATVKAINIADGQ 240
QY 56 DYLEVPQRTAVVLSFR-----SDKEGTGEK-----EGTESDNVAVYF 93
Db 241 GIIFNTDANNANFLNIQAGGTTINFTGDTGRLVLLSKHAAATNFNITGSLGNLKGVI 300
QY 94 DEKRVLKAGAITLKAGDNLKIKONTENTNDSSFTYSLKLDLTLSVETEKLSFGANGN 153
Db 301 EFNVAVDGOLTNAGANAANAVICNGAGRAAGFVVSVD-----NGK 342
QY 154 KVNITSDTKGLNFAKETAGTNGDPTV-HLNGIGSTLTDTLLTGATTNVTNDN--VTDDE 210
Db 343 VATIDGQVYAKDMVIOQSANATGOVNFRRHVDVGADGTAPKTAASKVTITQDSNFGNTDF 402
QY 211 KKAASVK--DVLNAGWNIGK--VKPGTTRASDNVDFVRYD--TVEFLSADKTTTVN- 262
Db 403 GNLAQIKVFNATLTGNETGDSNFGNTAG-----VITFDANGTLESADANVAVTNN 457
QY 263 ---VESKDNG-----KKEVEIGAKTSVKEKDGKLVTK-----GKDENGSSTD 304
Db 458 ITAIEASGAGVQVLSGTHAEELRGNAGSIFKLADGTVINGKYNQVALVGALAAAGTITL 517
QY 305 EGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETV-SGTNVTFASG-----K 356
Db 518 DGSATITGD--IGNAGGAALQRITLAN-----DAKKTTLTGANIIGAGGTTIDLQAN 569
QY 357 GTTATVSKDDQGNITVYKDYVNVG-DALNVNQLONGNWLDSKAVAGSSGKVISGNVSPSK 415
Db 570 GGTIKLT-STQNIVVDFDLAIATDQTV-----VDASLTNAQTLLTINGKGT-TI 618
QY 416 GKMDTV-NINAGNTEITRNG-----KNIDIATSMAPQF-----SSVSLGAGA--- 458
Db 619 GANNKTLGQFNIGSSKTVLSNGVAINELVIGNDGAVQFAHDYLYLTRTNAAGQKLIIF 678
QY 459 -----DAPTLSDVEGALNVGSKDTNPKVRITNVAFGVKBCDVTNVAQLKGVAQNLNRI 513
Db 679 NPVVNNTTLA---AGTNLGS-A-TNPLAEINFGSGVNVVDVLNVGE--GVNLXATN-I 730
QY 514 DNVDGHNARAGIAQAIAT---AGLV-----QAYLPKSKMAATGGDYYRGEAGYAG 560
Db 731 TTTDANYGSFVFVAGGTNIVSGTVGGQGNKFNFTVALENGTTVKFLGNATFNGNTTAA 790
QY 561 YSSISDGSNNIIGKTASGNSRG 582
Db 791 -STLIQGGNTYADCVASADGTG 811

RESULT 8

OMPB_RICCN STANDARD; PRT; 1655 AA.
ID OMPB_RICCN 09KX98; 09XC45;
AC O9KX98; 09KX98; 09XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RA MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT Mechanisms of evolution in Rickettsia conorii and R. prowazekii.;
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rOmpB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL: AF008659; AAL03623.1; -
DR EMBL: AF123721; AAF34124.1; -
DR EMBL: AF123726; AAF34129.1; -
DR EMBL: AF149110; AAD39533.1; -
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).


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Db 1162 LIAGYGTGTAGYNSILITGGYSTQTQAQSSSITAGYGTST--STAGYDSTLTAGYGTST 1219
QY 567 GG--NWIKGTAGSNRHH-----FGASASVGQ 593
Db 1220 AGYKSTLTAGYGSNSTAGHSSLIAGYGTQIAGYE 1255

RESULT 10
HLIA_PROMI
ID HLIA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpma and hpmb) reveals sequence similarity with the Serratia marcescens hemolysin genes (shla and shlb).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140;
KW Hemolysin; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match
Best Local Similarity 6.1%; Score 184; DB 1; Length 1577;
Matches 142; Conservative 80; Mismatches 253; Indels 186; Gaps 30;

QY 22 LTRNHTKRASATVATVATLFLATVQANATD--DDDLLEPQVQRTAVLSPRSDEKGTG 79
Db 317 LFKTELKGNITLVAS-----SHNQIKASDLMGDDITLQAGDLTI-----DGKQLQ 362
QY 80 EKEGTDSNW-----AVYDEKRVLLKAG-----AITLRAGDNL 112
Db 363 QKETDIDNWFYSWKYDVTKKEKEIQIGSQIDAKNNATLTATKGVDTLDAKINAGN 422
QY 113 KI-----KQNTNENNTNDSSTYSLLK-----DLTDLT----- 139
Db 423 AINANKDIHINGLVEKESRSENGKRNHTRSLESGSWNSHOTETLKASELTAGKDLGD 482
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QY 140 ---SVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN-----GIGSTLTDT 191
Db 483 AOGSTTAQAGAKLHANENVLVNAKDNLNVQK-----TNNDKTVTDHNVWVGIGGQGNK 538
QY 192 LLNTGATTNVTNDVTDDEKKRAASVKDYLNAGWNKIG-----VKPGTTASDNVDFVRTY 246
Db 539 NNNQOVSHAT--QLTADGQLLLAADNNVNITGSQVKGNOGAFVK--TTQGDVVIDNALS 594
QY 247 DTVEFLSAD-----TKTTTVNVEKDKNGKTEVKIGAKTSVIREKD-----GKLVYTKG 295
Db 595 ETISKIDERTGTAFTNITKSHKNETNKSTGSELISDAQLTVVSGNDVNVIGSLIKSAD 654
QY 296 K-----DENGST-----DEGGLVT---AKEVIDAVNKAAGWRMKTITANGTGOA 338
Db 655 KLGIIHSLGDINVKSAQOVTKIDDEKTSLAITGHAKVEDEKQYSAGPHIHTTNKNTSTET 714
QY 339 DKFETVTSCTNVTTFASGKGTATTVS--KDOGQNTVYKDVNVGDALNVNQLQNSGNW 396
Db 715 EQANSTISCANVDLQANKDVTTFAGSDLKTTAGNASITGD--NVAFVSTENKKQTD--NTDT 771
QY 397 KAVAGSSGKVISGNVSPSKGMD-----ETVNNAGNNIEIT----- 433
Db 772 TISGGFS---YTGVDKVGSKADFYDKQHTQTEVTNKRGSQTEVAGDLTITANKDLLHE 828
QY 434 -----RNGKNID-IATSMAPQFSVSLGACADAPTILSVDDDEGALNVGSKDNTKP 481
Db 829 GASHHVEGGRYQSGENIIQHLAVNDSETSKYDLSNVGIDV-----GVNLDYSGVTKP 879
QY 482 VR-----ITNVPAGYKGEQDVNTNAQLKGAQVQNNLRIDNVGNARAGIAQAIATAGLVQ 535
Db 880 VKKATIEDGVNTTKPG--NNTDLTKKVTARDAIANLAN--LSNLE--TPNVGVEVGKGGSQ 936
QY 536 A 536
Db 937 S 937

RESULT 11
OMPA_RICCN
ID OMPA_RICCN STANDARD; PRT; 2021 AA.
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOMPA) (rOMPA).
GS OMPA OR RC1273.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=94171067; PubMed=8125327;
RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
RL Gene 140:115-119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [3]
RP SEQUENCE OF 8-204 FROM N.A.
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
RX MEDLINE=97015921; PubMed=8862558;
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RESULT 12
OMP_RICHY STANDARD; PRT; 1645 AA.
AC OMPB_RICHY
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON; PubMed=8224886;
RX MEDLINE=94040787; PubMed=1370573;
RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=WILMINGTON;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNBr fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: Identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL; L04661; ABA48987.1; -
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
FT CONFLICT 657 657 H -> N (IN REF. 2).
FT CONFLICT 842 842 V -> I (IN REF. 2).
FT CONFLICT 1071 1071 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

Query Match 6.0%; Score 180.5; DB 1; Length 1645;
Best Local Similarity 21.1%; Pred. No. 0.097;
Matches 145; Conservative 90; Mismatches 265; Indels 187; Gaps 35;

QY 28 KRASATVATAVLATLFA-----TVQANATDDDLYLE-----PVORT 65
DB 10 KIISAGLVTTASTATIVAGFSGVAMGVMQYRNTTAAATVVDGAGFDQTGAGVNLPVATN 69
QY 66 AVVLSFRSKEGEGEGEDSNWVYFDEKRVLKAGAITLKAGDNLKIKQNTNENTNDS 125
DB 70 SVITANSNNAITNTPNGLNS---LFLDTANTL---AVTINENTTTLGFTVNTVKQGNFF 123
QY 126 SFTYSLSKDLT-----DLTSTVETEKLSFGAN-GNKVNT-----TSDTKGLNAFAKETAGTNG 175
DB 124 NFIGAGKSLTITGHGITAQAATTKSAQNVSVKNAGAAINDNDLSGVCSIDFTRAAPS- 182
QY 176 DPTVHLNGIGSTLTDLNLTGATNTVND-----NVTDDKKRAASVKVDNLNAGWNKGV 230
DB 183 --VLEFNLIINPTTQEAPLTLGDNAKIVNGANGILNITNGEVK---VSDKTFAG--IKTI 234
QY 231 KPGTTASDNVDVFTYDTVEFLSADTKTTTVNVESKD-----NGKKEVKI----- 276
DB 235 NIGD--NQGLMFTNTPDAANALNQQGGNTINFNGRGTGKLVLSKNGNATEFNVTGSL 292
QY 277 GAKTSVIKED-----GKLVTKGK-----DENGs-----STDEG-----EGLVTA 312
DB 293 GGNLKGVIEDTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSDVNGNAATISQVYA 352
QY 313 KEVIDAVNKGWRMKTITANGOT-----GQADKFETVSGTNVTVFASGKGTTATV 362
DB 353 KDIV-----IQSANAGQGVTFEHLVDVGLGGTKNFKTADSKVITIENASFGST--- 400
QY 363 SKDDQGNITVKYDVN-----VGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSP 413
DB 401 ---DFGNLAVQIVVPPNNKILTNFGIDG-----KNGG-NTAGVITFNANGTLVSGNTDP 450
QY 414 S-----KGKMDETVNI-----NAGNNEITRNGKNIDIAATSMAPQFSVS 453
DB 451 NIVVTNKATEVEGAGIVQLSGIHGAELRGNAGSIFKLA-DGTVINGPVNQNLVNNNA 509
QY 454 LGAGA---DAPTLISVD--EGALNVGSKDTNKPVRITNPVAPGVKGDVTVNQALKGVAQN 508
DB 510 LAAGSIQDLSGSAITIGDIGNAVNAALQD---ITLAN-----DASKILTLSGA--- 554
QY 509 LNNRIDNVDCNARAGIAQAATAGLVQAYLPKGSMAA-IGDITYRGAGYAIGVSSISDG 567
DB 555 -----NIIGANAGGAHFOANGGTIQLTSTQNNILVDFLDVTDQTG-VVDASSLTNN 607
QY 568 GNNIIRGT-----ASGNSRHFSGAS 589
DB 608 QTLTNGSIGTICANTKTLGRFNVGSS 634

RESULT 13
SLAP_CAMEE
ID SLAP_CAMEE STANDARD; PRT; 933 AA.
AC R35827;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE S-layer protein (Surface array protein) (SAP).
GN SAPA.
OS Campylobacter fetus.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=196;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=84-32 / 23D;
RX MEDLINE=90354448; PubMed=2387868;
RA Blaser M.J., Gotschlich E.C.;
RT "Surface array protein of Campylobacter fetus. Cloning and gene
RT structure.";
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RL J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RP ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
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CC -----
DR EMBL; J05577; AAA23032.1; ..
KW Cell wall; S-layer.
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match          5.98; Score 179.5; DB 1; Length 933;
Best Local Similarity 22.98; Pred. No. 0.055;
Matches 149; Conservative 89; Mismatches 251; Indels 163; Gaps 30;

QY 11 SALNA-----WVYSELTRNTRKRASATVATVATLFLFATVQANATDDDLYLEPVQRT 65
DB 228 STLSAFDKTRMSVLGRDTLN-----AIFTAI-----TRAALLTDQAEILITIKRTN 273
QY 66 AVVLSFSDKDEGTG-----EKEG-----TEDSNAAVDFDEKRVLKA-----G 102
DB 274 VENINISDLTSGDFVNGEYKGFVNLGDIVSFADDSKSNVETGTTTATAGTG 333
QY 103 AITLKAG--DNLIKQNTNEN---TND-----SFTYSLK---KDLTDLTSVETEK 145
DB 334 KVDVVGAKISALTADSRTSVNLATNTDITLTSANAATSVNLKQKQAKDAT-ITSAMQOK 392
QY 146 LSFGANQKV-NIISDTKGLNFAKETAGTGDPTVHLN-GTGSVLTDTL-----L 193
DB 393 ---YNNRRNRIATISATAVENLTVKHA-TN---VALNGMDKLTATVTLDNAALTAADI 445
QY 194 NTGATVNTDNDVTDDEK-----KRAASVKDVLNAGWNIKGVKPGCTTASDNVDF 242
DB 446 KSAFTLNLSNVGPHLYSKRRYCKFKRAA-----VKVLNTTA-----487
QY 243 VRTYDTVEFLSADTKTTVNVNYESKNGKTEVKIGAKTSVIKEDKGLVTGKRGDENGSS 302
DB 488 -----ATDOTVTLKANATDNSLEFDSATAKTTSVTASGSKTLVIKA-----530
QY 303 TDEGEGLTAKEVIDAVNKAQWRMKTITANGCQTQADKFETVSGTNVTFASGKGTATV 362
DB 531 ---EVEVLN-----IDTTAFNALQSVSGFKTGQGGKF-SVKTGTDGDKTFEFGVTTL 580
QY 363 SK--DDOQNTVKYDVNVGDALNVQLNSGWNLDKSAVAG---SSGKVISGNSVSPSKGK 417
DB 581 GSVIDAFGNDTIAMKSAALTSANTFMKNENVAISDAVATADLSSAFNSVLIITKEA 640
QY 418 MDEVTVNAGNIEITRNGKNIDIATSMAPQFSSVSLGAGADPTLSVDDREGALNVGSKD 477
DB 641 ADTTLTINKDQVI-----NFTAADAGSVKLITVKLN---DVTALMIVKIVLDAADAK 690
QY 478 TNKPV-----RITNAPGVKEGDTVWVAQL---KVAQNLNINRDNVDGNARAGIAQAI 528
DB 691 TNIALGTAADAKALVIDTIGTIELTSLVKATSPETTATVNAKLTDVTSIIIDGMQITL 750
QY 529 ATAGLVQAYLPKSMMAIGGDTYRGEAGYAGYSSISDGGNWIILKGTASGNS 580
DB 751 GHAGTAGTDYSKVSWI-----DASALKAGLFDASAILGANATIKGGSGADS 798
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RESULT 14
120K_RICRI
ID 120K_RICRI STANDARD; PRT; 1300 AA.
AC P14914;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 120 kDa surface-exposed protein.
GN P120.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
[1]
RP SEQUENCE FROM N.A.
SR STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES
CC CONFERRING ANTIGENICITY TO THE PROTEIN
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16353; CAA34402.1; ..
PIR; S07575; S07575.
DR InterPro; IPR003858; rompa_ompb.
DR Pfam; PF02708; rompa_ompb; 1.
KW Antigen; Glycoprotein; Cell wall; S-layer.
FT CARBOHYD 66 66 N-LINKED (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (POTENTIAL).
FT CARBOHYD 655 655 N-LINKED (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (POTENTIAL).
FT CARBOHYD 710 710 N-LINKED (POTENTIAL).
FT CARBOHYD 799 799 N-LINKED (POTENTIAL).
FT CARBOHYD 800 800 N-LINKED (POTENTIAL).
FT CARBOHYD 826 826 N-LINKED (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (POTENTIAL).
FT CARBOHYD 861 861 N-LINKED (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (POTENTIAL).
FT CARBOHYD 920 920 N-LINKED (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (POTENTIAL).
FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).
FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).
FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).
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FT	CARBOHYD	1146	1146	N-LINKED (POTENTIAL).
FT	CARBOHYD	1211	1211	N-LINKED (POTENTIAL).
SQ	SEQUENCE	1300	AA; 132801	MW; E09E52C3F647243D CRC64;

Query Match 5.8%; Score 175.5; DB.1; Length 1300;
Best Local Similarity 20.8%; Pred. No. 0.13;
Matches 153; Conservative 93; Mismatches 282; Indels 207;

Qy	30	ASATVATAVLATLLEATVQAN--ATDDDDLLLEPVORTAVVL--SFRSDKSGTGEKGE	85
Db	1	: :	
Db	22	ADGTAFTAAASKVTITQDSNFGNFTDEGNLAAQIKVPNAITLTGNTGTDASNPGNTAG--	79
Qy	86	DSNAVVFDEKRVLKAGAILKAGDNLIKONTNENTNDSFTYSLKKDLTDLTSVETEK	145
Db	80	---VITFDANGTLESAS-----ADANVAV-----TNNTAISAGAGVVOLSGTHAAE	124
Qy	146	LSFGANGKNVNITSDTKGLNPAKETA---GTNGDPTVHLNGIGSTLTDLTLNLTGATTVT	202
Db	125	LRLNAGSIFKLADGTVYNGKVTALVGGALAAAGTITLDG-SATITGDIGNAGGAALQ	183
Qy	203	NDNVTDEKKRAASVKOVNLNAGNIKWVKPQT-----TASN-----VDF---VR	244
Db	184	RITLANDAK-----KTLITLGGANIAGGCTIDLOANGGTIKLTSTQNNIWWDFDLAIA	237
Qy	245	TYDF-----VEFLSADTKTTVNVEKDNCK-----KT-----EVKIGA	278
Db	238	TDQFGVVDASLTVNAOHLTINGKITGIGANNKTLGQFNIGSSKTVLSNGNVAINELVTGN	297
Qy	279	KTSVIKEKDGKLVT-----GKKG-----DENGSSD-----EGE	307
Db	298	DGAVQFAHDTVLTIRTTNAAQGGKIIFNPVYNGTTLAAGTNLGSATNPLAEINFGSKGV	357
Qy	308	GLVTAKEVIDAVNAGHMKMTTAN-----GQTG--QADKEETV--SGT	348
Db	358	NVDTVLNVGEGVNIYATNITTTDANGSFVFNAGGTNIVSGTVGGQQGQNKENTVALENGT	417
Qy	349	NVTF---ASGKGTTATYSKDD---QGNITVYDVNVGDALNVQLNSG---WNLDSKA-	398
Db	418	TVKFLGNATFNMGNTIIAANSTLQJGGNTADC-VASADGCTGIVEFVNTGPTVTLNKQAA	476
Qy	399	-----VAGSSGKVIS--GNVSPSKGKMDETVNI-----NAGNN	429
Db	477	PVNALKQITVSGPCNVVINEIGNAGNHGAVTDTIAFENSSLGAVVFLPGCIPENDAGNT	536
Qy	430	IEIT-----RNKNNDIAT-----SMAQFSSVSLGAGAD-----APT	462
Db	537	MPLTIKSTVGNKTKAGFDVPVWVLGVDSVIADGGVIGDQNNIVGLGLSGDNGIIVNAT	596
Qy	463	LSV-----DDEGALNVGSKDTNKPVRTNVPAGVKEGDTVNTVAQLKGAQNLRNDRNV	516
Db	597	LYAGISTLNNQGVTVTLSSGGVPNTPGTVYIGLTGIGASKFKQVOT-----FTTDDNGLNII	652
Qy	517	DGNRAGTAQAIATAGVLQVAILPGKSMMAIGGDTYRGEAGVAYIGYSISDCGNIIKGTGA	576
Db	653	ATNATINDGVTVTGGIAGIGFDCG--ITLGSVNGNGVRFADGILSNSTS---MIGTTK	707
Qy	577	SGNSRGHFHASASVG	591
Db	708	ANNCTVTVYLGNAFVG	722

RESULT 15

APU_THETU	STANDARD;	PRT; 1861 AA.
ID APU_THETU		
AC P38536;		
DT 01-OCT-1994 (Rel. 30, Created)		
DT 01-NOV-1995 (Rel. 32, Last sequence update)		
DT 01-MAR-2002 (Rel. 41, Last annotation update)		
DE Amylopullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase		
DE type II) [includes: Alpha-amylase (EC 3.2.1.1) (1,4-alpha-D-glucan		
DE glucanohydrolase); Pullulanase (EC 3.2.1.41) (1,4-alpha-D-glucan		
DE glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].		

AMVB.
 Thermoanaerobacter thermosulfurogenes (Clostridium
 thermosulfurogenes).
 Bacteria; Firmicutes; Bacillus/Clostridium group;
 Thermoanaerobacter group; Thermoanaerobacterium.
 NCBI_TaxID=33950;
 [1]
 SEQUENCE FROM N. A.
 STRAIN=DSM 3896 / EM1;
 MEDLINE=94252998 / PubMed=8195085;
 Matuschek M., Burchhardt G., Salm K., Bahl H.;
 "Pullulanase of Thermoanaerobacterium thermosulfurogenes EM1
 (Clostridium thermosulfurogenes): molecular analysis of the gene,
 composite structure of the enzyme, and a common model for its
 attachment to the cell surface.";
 J. Bacteriol. 176:3295-3302(1994).
 -I- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 linkages in oligosaccharides and polysaccharides.
 -I- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
 linkages in pullulan and in amylopectin and glycogen, and the
 alpha- and beta-limit dextrins of amylopectin and glycogen.
 -I- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
 S-LAYER ANCHOR.
 -I- PTM: GLYCOSYLATED.
 -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 KNOWN AS THE ALPHA-AMYLASE FAMILY.
 -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 -I- SIMILARITY: CONTAINS 3 S-LAYER HOMOLGY (SLH) DOMAINS.

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 the European Bioinformatics Institute. There are no restrictions on its
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 or send an email to license@isb-sib.ch).

EMBL; M57692; AAB00841.1; -.	
HSP; Q08751; IBVZ.	
InterPro: IPR000461; Alpha_amyase.	
InterPro: IPR003961; FN_III.	
InterPro: IPR001119; SLH.	
InterPro: IPR004185; alpha-amyase_N.	
InterPro: IPR004193; isoamyase_N.	
Pfam; PF001128; alpha-amyase; 1.	
Pfam; PF02806; alpha-amyase_C; 1.	
Pfam; PF02903; alpha-amyase_N; 1.	
Pfam; PF00041; fn3; 2.	
Pfam; PF02922; isoamyase_N; 1.	
Pfam; PF00395; SLH; 3.	
SMART; SM00060; FN3; 1.	
PROSITE; PS01072; SLH_DOMAIN; 3.	
HydroLase; GlycoSIDase; Carbohydrate metabolism; Signal; Repeat;	
MW Multifunctional enzyme; Glycoprotein.	
FT SIGNAL 1 35	POTENTIAL.
FT CHAIN 36 1861	AMYLOPULLULANASE.
FT DOMAIN 928 1018	FIBRONECTIN TYPE-III 1.
FT DOMAIN 1157 1248	FIBRONECTIN TYPE-III 2.
FT ACT_SITE 628 628	BY SIMILARITY.
FT ACT_SITE 657 657	BY SIMILARITY.
FT ACT_SITE 734 734	BY SIMILARITY.
FT DOMAIN 1681 1739	SLH 1.
FT DOMAIN 1740 1803	SLH 2.
FT DOMAIN 1804 1861	SLH 3.
FT CONFLICT 1734 1734	D -> E (IN REF. 1; AAB00841).
FT SEQUENCE 1861 AA: 206104 MW: 06C23070E453B574	CRC64.

Query Match 5.8%; Score 175.5; DB 1; Length 1861;
Best Local Similarity 19.6%; Pred. No. 0.2;
Matches 131; Conservative 94; Mismatches 219; Indels 223; Gaps 32;
Qv 2 NKIYRIWNSALNA-----WVVGSELTRNHTKRASATVAVLATLLEATVQA----- 49

Db 1208 NEVNYIDTSVINGTYNYKVVAVDLSFNRTESNVVTVIKPDVWPVKVIFNVTVPDYTPDA 1267
QY 50 -----NAT-DDDLVLEPVQRTAVVLSFRSDEGT-----GEKEGTEDSNNAVY 92
Db 1268 VNLAGTFPNAIWDPSAOQMTKIDNNTYSITLTD-EGTQIEYKARGSWDKVEDEYEGNE 1326
QY 93 FDEKRVLKAGAILKAGDNLKIKONTNENT-NDS-----SFTYSLKKDLTDLTSVET 143
Db 1327 FASNR-----KVTI-----VNGGNEMTINDTVYWRDIPFIYSPSSNMTVDSNIST 1374
QY 144 EKLSEGA-NGKNVNTSDT-----KGLNFAKETA---CTN-----GDPVHLNGIGST 187
Db 1375 MEVKNGTYKGAKVINGDSFQDKNGVFTKDVSLNYGVNKKIHVEPNDSGVYGN----- 1429
QY 188 LTDPLNLTGATTNVTND---NVTDERKKRAASV--KDVLNAGWNIKGVPCTTASDNV-- 240
Db 1430 -----DQGRITELTKDIEIDVIRQENNSGGTGNNTSTSGSNSSTGSGTGSTITS 1483
QY 241 DFVETVDFEFLSADTKTTTVNVESKDKKTEVKIGAKTSVKEKDKGLVTKGKDGENG 300
Db 1484 NISNTSNTSNTIGVITKNGNVITLTDAGK-----AKDLIVNSKDKKVVF----- 1528
QY 301 SSTDEGEG-----LVTAKEVIDAVNKAGWRMKTTFANGOTGOADKFEFTVSGTNVTFASGK 356
Db 1529 DITITIGEGQOKVQVQISKILD-----TSAANGKD----- 1557
QY 357 GTTATVSKDDOGNTTVKYDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVSPSKG 416
Db 1558 -----IVIKSDNASIAL-----TKDALNQIQON-GVNVSIK-----DNG 1591
QY 417 KMDFTVINAGNNTIEITRNKNIDDIATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSK 476
Db 1592 KPNVTNVVSLSNVVDITISGISGNV-----TLAKPVEVTINISKA 1631
QY 477 DTNKPVRI-----TNVAPGVKEGDTVNAQLKGAQNALNNRIDNVDGNA 520
Db 1632 NDKPKVAVYYNPTTNQWEXYGVGKVDASSGTITFNATHFSQY--AAPEYDKTFENDIKDNW 1689
QY 521 RAGIAQAIATAGLYOA-----YLPKGS-----MMAIGGDTYRGFAGYAGYSS 563
Db 1690 AKDVIEVLASRHHIVEGMDTQYEPNKTVTTRAETAMILRLNLINIKDEYISGE-----FSD 1743
QY 564 ISDGGNW 570
Db 1744 VK-SGDW 1749

Search completed: July 3, 2002, 08:49:07
Job time: 713 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:10 ; Search time 100.13 seconds
(without alignments)
1026.256 Million cell updates/sec

Title: US-09-771-382-9
Perfect score: 3023
Sequence: 1 MNKYRIIWSALNAWVVS.....TASGSRGFGASASVGYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_l9:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3023	100.0	594	2 Q9JPH7	Q9Jph7 neisseria m
2	2997	99.1	598	2 Q9JPS9	Q9Jps9 neisseria m
3	2971	98.3	598	2 Q9JPS0	Q9Jps0 neisseria m
4	2957	97.8	598	2 Q9JPT0	Q9Jpt0 neisseria m
5	2948	97.5	598	2 Q9JQY5	Q9Jqy5 neisseria m
6	2948	95.5	594	2 Q9JPS2	Q9Jps2 neisseria m
7	2884	95.4	594	2 Q9JPI3	Q9Jpi3 neisseria m
8	2874	95.1	594	2 Q9JQY4	Q9Jqy4 neisseria m
9	2802.5	92.7	599	2 Q9JPS8	Q9Jps8 neisseria m
10	2800	92.6	600	2 Q9JPS6	Q9Jps6 neisseria m
11	2782	92.0	590	2 Q9JPS3	Q9Jps3 neisseria m
12	2740.5	90.7	591	2 Q9JPS7	Q9Jps7 neisseria m
13	2740.5	90.7	591	16 Q9JRI8	Q9Jri8 neisseria m
14	2734.5	90.5	599	2 Q9JPS8	Q9Jps8 neisseria m
15	2733	90.4	592	2 Q9AQF0	Q9aqf0 neisseria m
16	2721.5	90.0	591	2 Q9JQY3	Q9Jqy3 neisseria m

17	2715	89.8	598	2 Q9JPR7	Q9Jpr7 neisseria m
18	2694	89.1	592	2 Q9JPS9	Q9Jps9 neisseria m
19	2664	88.1	592	2 Q9JQY2	Q9Jqy2 neisseria m
20	2661	88.0	600	2 Q9JPS5	Q9Jps5 neisseria m
21	2656.5	87.9	595	2 Q9JPH0	Q9Jph0 neisseria m
22	2584.5	85.5	589	2 Q9JPI0	Q9Jpi0 neisseria m
23	2573.5	85.1	589	2 Q9JQY1	Q9Jqy1 neisseria m
24	2552	84.4	592	16 Q9JQW4	Q9Jqw4 neisseria m
25	2484.5	82.2	526	2 Q9JPS4	Q9Jps4 neisseria m
26	2482.5	82.1	530	2 Q9JPS1	Q9Jps1 neisseria m
27	1330.5	44.0	2353	2 P71401	P71401 haemophilus
28	1050	34.7	1098	2 Q48152	Q48152 haemophilus
29	442	14.6	1299	16 Q9F3X6	Q9f3x6 pasteurella
30	404	13.4	2059	16 Q9PD50	Q9pd50 xylella fas
31	392.5	13.0	1190	16 Q9PC04	Q9pc04 xylella fas
32	371	12.3	1107	2 Q9F2D8	Q9f2d8 salmonella
33	363	12.0	2712	16 Q9F3X5	Q9f3x5 pasteurella
34	260	8.6	1004	16 Q9PD63	Q9pd63 xylella fas
35	253.5	8.4	1291	16 Q92KQ7	Q92kq7 rhizobium m
36	244.5	8.1	1953	16 Q98HJ2	Q98hj2 rhizobium l
37	240.5	8.0	2276	2 Q93TY6	Q93ty6 staphylococ
38	240	7.9	1039	2 Q9L6T7	Q9l6t7 escherichia
39	234.5	7.8	1265	2 Q9FDA0	Q9fda0 xanthomonas
40	232.5	7.7	1039	2 Q9L6T8	Q9l6t8 escherichia
41	230.5	7.6	989	2 Q9XD84	Q9xd84 escherichia
42	228	7.5	1040	2 Q9AL50	Q9al50 shigella fl
43	226	7.5	3930	16 Q98E20	Q98e20 rhizobium l
44	218.5	7.2	945	2 Q93F03	Q93f03 shigella fl
45	218	7.2	1557	2 Q9RNI2	Q9rni2 haemophilus

ALIGNMENTS

RESULT 1

Q9JPH7 PRELIMINARY; PRT; 594 AA.

AC Q9JPH7: 01-OCT-2000 (TREMREL. 15, Created)

DT 01-OCT-2000 (TREMREL. 15, Last sequence update)

DT 01-DEC-2001 (TREMREL. 19, Last annotation update)

DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).

GN GNA992 OR NHHA.

OS Neisseria meningitidis.

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI_TaxID=487;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BZ198, AND 297-0;

RX MEDLINE=20175756; PubMed=10710308;

RA Pizsa M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarcelli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;

RT Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.;

RL Science 287:1816-1820(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=BZ198;

RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;

RT Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF226358; AAF42517.1; -

DR EMBL: AF226358; AAF42507.1; -

DR EMBL: AF157604; AAK68865.1; -

SQ SEQUENCE 594 AA; 62361 MW; 436BDDDED6263C5C CRC64;

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Query Match 100.0%; Score 3023; DB 2; Length 594;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60
QY 61 PVQRTAVVLFRSDKECTGEGTSDNSWAVYFDEKRVLKAGAITLTKAGDNLIKQNTNE 120
DB 61 PVQRTAVVLFRSDKECTGEGTSDNSWAVYFDEKRVLKAGAITLTKAGDNLIKQNTNE 120
QY 121 NTNDSSTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180
DB 121 NTNDSSTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180
QY 181 LKNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGYPGTTASDNV 240
DB 181 LKNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGYPGTTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGKGDENG 300
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGKGDENG 300
QY 301 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFFASGKGTTA 360
DB 301 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFFASGKGTTA 360
QY 361 TVSKDDGNTVTKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
DB 361 TVSKDDGNTVTKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420
QY 421 TVTNAGNNTIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480
DB 421 TVTNAGNNTIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480
QY 481 PVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQATAGLQVAYLPG 540
DB 481 PVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQATAGLQVAYLPG 540
QY 541 KSMMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 541 KSMMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594

RESULT 2
QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
DR EMBL; AF226382; AAF42531.1; -.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 99.1%; Score 2997; DB 2; Length 598;
Best Local Similarity 99.0%; Pred. No. 1.3e-117;
Matches 592; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60
QY 61 PVQRTAVVLFRSDKECTGEGTSDNSWAVYFDEKRVLKAGAITLTKAGDNLIKQNTNE 116
DB 61 PVQRTAVVLFRSDKECTGEGTSDNSWAVYFDEKRVLKAGAITLTKAGDNLIKQNTNE 120
QY 117 NTNENTNDSSTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 121 NTNENTNDSSTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
QY 177 PTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGYPGTTA 236
DB 181 PTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKGYPGTTA 240
QY 237 SDNVDFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGCK 296
DB 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGCK 300
QY 297 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFFASGK 356
DB 301 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFETVTSCTNVTFFASGK 360
QY 357 GTTATVSKDDGNTVTKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDDGNTVTKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVINAGNNTIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476
DB 421 KMDETVINAGNNTIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480
QY 477 DTNKPVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDVNDGNARAGIAQATAGLQV 536
DB 481 DTNKPVRTITNAPVKGEGDVTNVAQLKGVAQNLRNIDVNDGNALAGIAQATAGLQV 540
QY 537 YLPKGSMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 541 YLPKGSMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 598

RESULT 3
QJUPSO PRELIMINARY; PRT; 598 AA.
AC QJUPSO;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH15;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RL Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
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RA [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H15;
RA Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RL membrane protein of *Neisseria meningitidis*.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226381; AAF42530.1; -;
DR EMBL: AF157607; AAK68868.1; -;
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 98.3%; Score 2971; DB 2; Length 598;
Best Local Similarity 98.0%; Pred. No. 1.6e-116;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEGTEGDSNNAVYFDEKRVLKAGAITLKAGDNLKIQ---- 116
DB 61 PVORTAVVLSFRSDKEGTGEGTEGDSNNAVYFDEKRVLKAGAITLKAGDNLKIQNTNE 120
QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
QY 177 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236
DB 181 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
QY 237 SDNVDFVRTYDTEFFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG 296
DB 241 SDNVDFVRTYDTEFFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG 300
QY 297 DENGSSDDEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGK 356
DB 301 DENGSSDDEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGN 360
QY 357 GTTATVSKDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
DB 421 KMDETVINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 477 DTNKPVRITNVAPGVKEGDTNVNQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
DB 481 DANKPVRITNVAPGVKEGDTNVNQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540
QY 537 YLPCKSMATGGDTYRGEAGYAGYSSISDGNWIKGTASGNSRGRHFGASASVGYQW 594
DB 541 YLPCKSMATGGDTYRGEAGYAGYSSISDGNWIKGTASGNSRGRHFGASASVGYQW 598

RESULT 4
Q9JPT0 PRELIMINARY; PRT; 598 AA.
ID Q9JPT0
AC Q9JPT0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tetelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT *Meningococcus* by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226359; AAF42508.1; -;
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 97.8%; Score 2957; DB 2; Length 598;
Best Local Similarity 97.5%; Pred. No. 6.2e-116;
Matches 583; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEGTEGDSNNAVYFDEKRVLKAGAITLKAGDNLKIQ---- 116
DB 61 PVORTAVVLSFRSDKEGTGEGTEGDSNNAVYFDEKRVLKAGAITLKAGDNLKIQNTNE 120
QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
QY 177 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236
DB 181 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
QY 237 SDNVDFVRTYDTEFFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG 296
DB 241 SDNVDFVRTYDTEFFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG 300
QY 297 DENGSSDDEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGK 356
DB 301 DENGSSDDEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGN 360
QY 357 GTTATVSKDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
DB 421 KMDETVINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
QY 477 DTNKPVRITNVAPGVKEGDTNVNQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
DB 481 DANKPVRITNVAPGVKEGDTNVNQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540
QY 537 YLPCKSMATGGDTYRGEAGYAGYSSISDGNWIKGTASGNSRGRHFGASASVGYQW 594
DB 541 YLPCKSMATGGDTYRGEAGYAGYSSISDGNWIKGTASGNSRGRHFGASASVGYQW 598

RESULT 5
Q93QY5 PRELIMINARY; PRT; 598 AA.
ID Q93QY5
AC Q93QY5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN-BZ10;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RL membrane protein of *Neisseria meningitidis*."
DR EMBL; AF157603; AAK6884.1; -
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 97.5%; Score 2948; DB 2; Length 598;
Best Local Similarity 97.3%; Pred. No. 1.5e-115;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLALLFATVOANATDDDDLLYLE 60
Db 1 MNKISRIIWSALNAWVVSSELTRNHTKRASATVATVATLALLFATVOANATDDDDLLYLE 60
Qy 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 116
Db 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Qy 117 NTNENTNDSSTYSLLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
Db 121 NTNENTNDSSTYSLLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Qy 177 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236
Db 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240
Qy 237 SDNVDFVRYDVFELSDTKTTTVNVESKONGKTEVKIGAKTSVKEKDKGLVTGK 296
Db 241 SDNVDFVRYDVFELSDTKTTTVNVESKONGKTEVKIGAKTSVKEKDKGLVTGK 300
Qy 297 DNGSSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKPEVTSCTNVTFSAGK 356
Db 301 GENGSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKPEVTSCTNVTFSAGN 360
Qy 357 GTTATVSRDQGNITVKYDVNVGDALNVQNSGWNLDKRAVAGSSGKVISGNVSPSKG 416
Db 361 GTTATVSRDQGNITVKYDVNVGDALNVQNSGWNLDKRAVAGSSGKVISGNVSPSKG 420
Qy 417 KMDVTNINAGNIEITRNGKNIDIATSMAPQSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 421 KMDVTNINAGNIEITRNGKNIDIATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSK 480
Qy 477 DTNKPVRTNVPAGVKEGDTVNTVAOLKGVQNLNHNIDVGNARAGIAQAATAGLVAQA 536
Db 481 DANKPVRTNVPAGVKEGDTVNTVAOLKGVQNLNHNIDVGNARAGIAQAATAGLVAQA 540
Qy 537 YLPCKSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
Db 541 YLPCKSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 598

RESULT 6
Q9JPS2
ID Q9JPS2 PRELIMINARY; PRT; 594 AA.
AC Q9JPS2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.R., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT *Meningococcus* by Whole-Genome Sequencing."
RL Science 287:1816-1820(2000).
DR EMBL; AF226379; AAF42528.1; -
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 95.5%; Score 2888; DB 2; Length 594;
Best Local Similarity 96.0%; Pred. No. 4.6e-113;
Matches 570; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLALLFATVOANATDDDDLLYLE 60
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLALLFATVOASTDDDDLLYLE 60
Qy 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Qy 121 NTNDSSTYSLLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
Db 121 NTNDSSTYSLLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
Qy 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDV 240
Db 181 LNGIGSTLTDLLNTGATTNTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDV 240
Qy 241 DFVRTYDVFELSDTKTTTVNVESKONGKTEVKIGAKTSVKEKDKGLVTGKDKENG 300
Db 241 DFVRTYDVFELSDTKTTTVNVESKONGKTEVKIGAKTSVKEKDKGLVTGKDKENG 300
Qy 301 SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKPEVTSCTNVTFSAGKGTTA 360
Db 301 SSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGQADKPEVTSCTNVTFSAGKGTTA 360
Qy 361 TVSKDDQGNITVKYDVNVGDALNVQNSGWNLDKRAVAGSSGKVISGNVSPSKGKDE 420
Db 361 TVSKDDQGNITVKYDVNVGDALNVQNSGWNLDKRAVAGSSGKVISGNVSPSKGKDE 420
Qy 421 TVNINAGNIEITRNGKNIDIATSMAPQSSVSLGAGADAPTLSDVDEGALNVGSKDNK 480
Db 421 TVNINAGNIEITRNGKNIDIATSMTPQSSVSLGAGADAPTLSDVDEGALNVGSKDNK 480
Qy 481 PVRTNVPAGVKEGDTVNTVAOLKGVQNLNHNIDVGNARAGIAQAATAGLVAQYLP 540
Db 481 PVRTNVPAGVKEGDTVNTVAOLKGVQNLNHNIDVGNARAGIAQAATAGLVAQYLP 540
Qy 541 KSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
Db 541 KSMMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 7
Q9JPI3
ID Q9JPI3 PRELIMINARY; PRT; 594 AA.
AC Q9JPI3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NG3/88, AND B232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -;
DR EMBL: AF226369; AAF42518.1; -;
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D004B46 CRC64;

Query Match 95.4%; Score 2884; DB 2; Length 594;
Best Local Similarity 95.8%; Pred. No. 6.7e-113;
Matches 569; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
DB 61 PVORTAVVLSFRSDKSGTGEKGTEDSNWGVYFDKKGVLTAITLKAGNLKIKONTDE 120
QY 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
DB 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
QY 181 LNGIGSTLDTLTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
DB 181 LNGIGSTLDTLTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKLVTKGKDENG 300
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKLVTKGKDENG 300
QY 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEFTVSGTNTVFASGKTGA 360
DB 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEFTVSGTNTVFASGKTGA 360
QY 361 TVSKDDQGNITVYKVDVNVGDALNVQNSLQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420
DB 361 TVSKDDQGNITVYKVDVNVGDALNVQNSLQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420
QY 421 TVNINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480
DB 421 TVNINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDKANK 480
QY 481 PVRTITVAPGVKGGDVTNVAQLKGAQNLLNNDVNDGNARAGIAQAIATAGLVQAYLPG 540
DB 481 PVRTITVAPGVKGGDVTNVAQLKGAQNLLNNDVNDGNARAGIAQAIATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 8
Q930Y4 ID Q930Y4 PRELIMINARY; PRT; 594 AA.
AC Q930Y4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=EG327;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157605; AAK68866.1; -;
SQ SEQUENCE 594 AA; 62297 MW; 9DD448B04B3A8EA2 CRC64;

Query Match 95.1%; Score 2874; DB 2; Length 594;
Best Local Similarity 95.6%; Pred. No. 1.7e-112;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQASTTDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGNLKIKONTNE 120
DB 61 PVORTAVVLSFRSDKSGTGEKGTEDSNWGVYFDKKGVLTAITLKAGNLKIKONTNE 120
QY 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
DB 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180
QY 181 LNGIGSTLDTLTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
DB 181 LNGIGSTLDTLTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKLVTKGKDENG 300
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKGKTEVKIGAKTSVKEKDKLVTKGKDENG 300
QY 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEFTVSGTNTVFASGKTGA 360
DB 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEFTVSGTNTVFASGKTGA 360
QY 361 TVSKDDQGNITVYKVDVNVGDALNVQNSLQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420
DB 361 TVSKDDQGNITVYKVDVNVGDALNVQNSLQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420
QY 421 TVNINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480
DB 421 TVNINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDKANK 480
QY 481 PVRTITVAPGVKGGDVTNVAQLKGAQNLLNNDVNDGNARAGIAQAIATAGLVQAYLPG 540
DB 481 PVRTITVAPGVKGGDVTNVAQLKGAQNLLNNDVNDGNARAGIAQAIATAGLVQAYLPG 540
QY 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 9
Q9JPR8 ID Q9JPR8 PRELIMINARY; PRT; 599 AA.
AC Q9JPR8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH38;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Moxon R., Jennings M.P.;
RA Broeker M., Hufnagel E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP226383; AAF42532.1; -;
DR EMBL: AF157608; AK68869.1; -;
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match		92.7%;	Score 2802.5;	DB 2;	Length 599;				
Best Local Similarity		92.5%;	Pred. No. 1.7e-109;						
Matches 554;		Conservative 12;	Mismatches 28;	Indels 5;	Gaps 2;				
Qy	1	MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLXL	59						
Db	1	MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL	60						
Qy	60	EPVORTAVLSFRSDKCTGKCTGKEDTSNNAVYFDEKRVLKAGAITLKAGDNLIKIKO--	116						
Db	61	EPVRSVALVQFMIDKKGNGENESTGIGWSIYDNNHTLHGATVTLKAGDNLIKIKONTN	120						
Qy	117	-NTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG	175						
Db	121	KNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG	180						
Qy	176	DPTVHLNGIGSTLTDLLNTGATTNVDNVTDDKRAASVKDVLNAGWNKIKVKGCTT	235						
Db	181	DTTVHLNGIGSTLTDLLNTGATTNVDNVTDDKRAASVKDVLNAGWNKIKVKGCTT	240						
Qy	236	ASDNVDVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG	295						
Db	241	ASDNVDVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG	300						
Qy	296	KDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSCTNVTFA	355						
Db	301	KGENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSCTNVTFA	360						
Qy	356	KGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK	415						
Db	361	KGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK	420						
Qy	416	GKMDETVNIAGNNIEITRNCKNIDTATSMAPQFSSVSLGAGADAPTLSDDEGALNVGS	475						
Db	421	GKMDETVNIAGNNIEITRNCKNIDTATSMAPQFSSVSLGAGADAPTLSDDEGALNVGS	480						
Qy	476	KDTPKPVRIITNAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQ	535						
Db	481	KDANKPVRIITNAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQ	540						
Qy	536	AYLPCKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASASVGYQW	594						
Db	541	AYLPCKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASASVGYQW	599						
RESULT 10									
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ID	Q9JPS6	PRELIMINARY;	PRT;	600	AA.				
AC	Q9JPS6;								
DT	01-OCT-2000 (TrEMBLrel. 15, Created)								
DF	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)								
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)								
DE	OUTER MEMBRANE PROTEIN GNA992.								
GN	GNA992.								

OS	Neisseria meningitidis.				
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=487;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=E26;				
RX	MEDLINE=201757556; PubMed=10710308;				
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,				
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,				
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,				
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,				
RA	Broeker M., Hufnagel E., Knapp B., Blair E., Mason T., Tettelin H.,				
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,				
RA	Moxon E.R., Grandi G., Rappuoli R.;				
RT	"Identification of Vaccine Candidates Against Serogroup B				
RT	Meningococcus by Whole-Genome Sequencing.";				
RL	Science 287:1816-1820(2000).				
DR	EMBL: AF226371; AAF42520.1; -;				
SQ	SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;				
Query Match		92.6%;	Score 2800;	DB 2;	Length 600;
Best Local Similarity		92.7%;	Pred. No. 2.1e-109;		
Matches 557;		Conservative 13;	Mismatches 23;	Indels 8;	Gaps 2;
QY	1	MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASADNVQASDN	53		
DB	1	MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASADNVQASDN	60		
QY	54	DDDLLEPVORTAVLSFRSDKCTGKCTGKEDTSNNAVYFDEKRVLKAGAITLKAGDNLK	113		
DB	61	EEBEYFPVVRTAVLSFYSDAEDTGEKTEVTENWGIYDKNGVIRAGITLKAGDNLK	120		
QY	114	IKQNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGT	173		
DB	121	IKQNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGT	180		
QY	174	NGDPTVHLNGIGSTLTDLLNTGATTNVDNVTDDKRAASVKDVLNAGWNKIKVKGPG	233		
DB	181	NGDPTVHLNGIGSTLTDLLNTGATTNVDNVTDDKRAASVKDVLNAGWNKIKVKGPG	240		
QY	234	TTASDNVDVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG	293		
DB	241	TTASDNVDVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG	300		
QY	294	KGKDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSCTNVTFA	353		
DB	301	KGKDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTTTANGQTQADKFETVTSCTNVTFA	360		
QY	354	SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP	413		
DB	361	SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP	420		
QY	414	SKGRMDETVNIAGNNIEITRNCKNIDTATSMAPQFSSVSLGAGADAPTLSDDEGALNV	473		
DB	421	SKGRMDETVNIAGNNIEITRNCKNIDTATSMAPQFSSVSLGAGADAPTLSDDEGALNV	479		
QY	474	GSKDTNKPVRITNAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGL	533		
DB	480	GSKDTNKPVRITNAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGL	539		
QY	534	VOAYLPCKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASASVGYQ	593		
DB	540	VOAYLPCKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFHGASASVGYQ	599		
QY	594	W 594			
DB	600	W 600			
RESULT 11					
Q9JPS3					
ID	Q9JPS3	PRELIMINARY;	PRT;	590	AA.

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AC Q9JPS3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 92.0%; Score 2782; DB 2; Length 590;
Best Local Similarity 93.3%; Pred. No. 1.2e-108;
Matches 556; Conservative 9; Mismatches 23; Indels 8; Gaps 3;

QY 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLLEATVQANATDDDL-L 59
DB 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLLEATVQANATDEDEDL 60
QY 60 EPIQRTAVVLSRDKGEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQT 118
DB 61 DPVQRTAVVLIIVNSDKGEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ-- 118
QY 119 NENTNDSFTYSLKKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGDPT 178
DB 119 -----NGTFTYSLKKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGDPT 174
QY 179 VHLNGIGSLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTASD 238
DB 175 VHLNGIGSLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTASD 234
QY 239 NVDFVRYTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGKGE 298
DB 235 NVDFVRYTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGKGE 294
QY 299 NGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEFTVSGTNTVFASGKT 358
DB 295 NGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEFTVSGTNTVFASGKT 354
QY 359 TATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 418
DB 355 TATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 414
QY 419 DETVNIINAGNNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDT 478
DB 415 DETVNIINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSKDA 474
QY 479 NKPVRTINVAPGVKGGDVTVNVAQLKGVAQNLRIDNVNAGNARAGIAQAIAATAGLVQAYL 538
DB 475 NKPVRTINVAPGVKGGDVTVNVAQLKGVAQNLRIDNVNAGNARAGIAQAIAATAGLVQAYL 534
QY 539 PKGSMAAIGGDTYRGAGYAGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 594
DB 535 PKGSMAAIGGDTYRGAGYAGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 590
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RESULT 12

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Q9JPS7
ID Q9JPS7 PRELIMINARY; PRT; 591 AA.
AC Q9JPS7;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B2147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizzo M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226366; AAF42515.1; -.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 90.7%; Score 2740.5; DB 2; Length 591;
Best Local Similarity 92.1%; Pred. No. 6.2e-107;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

QY 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLTLLEATVQANATD---DDDL 57
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QY 58 YLEPQRTAVVLSRDKGEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
DB 61 YLDPQRTAVVLIIVNSDKGEGTEGEGED-SNWAVYFDEKRVLKAGAITLKAGDNLKIKQ 120
QY 117 NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGD 176
DB 121 -----NGTFTYSLKKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGD 174
QY 177 PVHNLGIGSLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236
DB 175 PVHNLGIGSLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 234
QY 237 SDNVDFVRYTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGKCK 296
DB 235 SDNVDFVRYTYDTVEFLSADTKTTTNNVESKDKGKTEVKIGAKTSVKEKDKGLVTGKCK 294
QY 297 DENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEFTVSGTNTVFASGK 356
DB 295 DENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEFTVSGTNTVFASGK 354
QY 357 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 355 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414
QY 417 KDETVINAGNNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476
DB 415 KDETVINAGNNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDG-ALNVGSK 473
QY 477 DTKNKPVRTINVAPGVKGGDVTVNVAQLKGVAQNLRIDNVNAGNARAGIAQAIAATAGLVQA 536
DB 474 KDNKPVRTINVAPGVKGGDVTVNVAQLKGVAQNLRIDNVNAGNARAGIAQAIAATAGLVQA 533
QY 537 YLPKGSMAAIGGDTYRGAGYAGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 594
DB 534 YLPKGSMAAIGGDTYRGAGYAGYSSISDGGNNIIKGTASGNSRGRHFGASASVGYOW 591
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OSJR18	
ID Q9JR18	PRELIMINARY; PRT; 591 AA.
AC Q9JR18;	
DT 01-OCT-2000 (TremBLrel. 15, Created)	
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)	
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)	
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE	
DE PROTEIN)	
DE GNA992 OR NMB0992 OR NHHA.	
GN	
OS Neisseria meningitidis, and	
OS Neisseria meningitidis (serogroup B).	
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
OX NCBI_TaxID=487, 491;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;	
RX MEDLINE=20175756; PubMed=10710308;	
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,	
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,	
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
RA Moxon E.R., Grandi G., Rappuoli R.;	
RT "Identification of Vaccine Candidates Against Serogroup B	
RT Meningococcus by Whole-Genome Sequencing.";	
RL Science 287:1816-1820(2000).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=MC58 / SEROGROUP B;	
RX MEDLINE=20175755; PubMed=10710307;	
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,	
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,	
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,	
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,	
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,	
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,	
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,	
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;	
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain	
RT MC58.";	
RL Science 287:1809-1815(2000).	
RN [3]	
RP SEQUENCE FROM N.A.	
RC SPECIES=N.meningitidis; STRAIN=PMC21;	
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;	
RT "Identification and characterization of a gene encoding a novel outer	
RT membrane protein of Neisseria meningitidis.";	
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AF226375; AAF42524.1; -	
DR EMBL; AE002450; AAF41395.1; -	
DR EMBL; AF226367; AAF42516.1; -	
DR EMBL; AF226370; AAF42519.1; -	
DR EMBL; AF226374; AAF42523.1; -	
DR EMBL; AF157611; AAK68872.1; -	
DR TIGR; NMB0992; -	
KW Complete proteome.	
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAEF7F73EC6 CRC64;	
Query Match 90.7%; Score 2740.5; DB 16; Length 591;	
Best Local Similarity 92.1%; Pred. No. 6.2e-107;	
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;	
QY 1 MNKYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57	
DB 1 MNKYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANNEEQEEDL 60	
QY 58 YLEPQRTAVVLSFRSDEKGEKTEGDSNNAVYFDEKRVLKAGAITLKAGDNLIKQ 116	
DB 61 YLDPQRTAVVLSFRSDEKGEKTEGDSNNAVYFNEKGVLTAREITLKAGDNLIKQ 120	

QY 117 NTNENTNDSSFTYSLKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176	
DB 121 -----NCTNETYSLKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 174	
QY 177 PTVHLNGIGSTLTDLTLLNGATTNTVNDDEKRAASVKDVLNAGWNIGKVPKGTGA 236	
DB 175 TVVHLNGIGSTLTDLTLLNGATTNTVNDDEKRAASVKDVLNAGWNIGKVPKGTGA 234	
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIKEKDKLVTKGK 296	
DB 235 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDKNGKTEVKIGAKTSVIKEKDKLVTKGK 294	
QY 297 DENGSTDEGLVTAKEVIDAVNAGRMKTTTANGOTGQADKFTVTSNTVTFASKG 356	
DB 295 GENGSTDEGLVTAKEVIDAVNAGRMKTTTANGOTGQADKFTVTSNTVTFASKG 354	
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 416	
DB 355 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVIISGNVSPSKG 414	
QY 417 KMDETVINAGNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSK 476	
DB 415 KMDETVINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDGD-ALNVGSK 473	
QY 477 DTNKPVRITNVAPGKEGDVTNVAQLKGVANLNINRDNVDGNARAGIAQAATATAGLVQA 536	
DB 474 KDNKPVRIITNVAPGKEGDVTNVAQLKGVANLNINRDNVDGNARAGIAQAATATAGLVQA 533	
QY 537 YLPGKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFSGASASVGYQW 594	
DB 534 YLPGKSMMAIGGDTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFSGASASVGYQW 591	
RESULT 14	
Q9JPS8	PRELIMINARY; PRT; 599 AA.
ID Q9JPS8	
AC Q9JPS8;	
DT 01-OCT-2000 (TremBLrel. 15, Created)	
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)	
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)	
DE OUTER MEMBRANE PROTEIN GNA992.	
GN GNA992.	
OS Neisseria meningitidis.	
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
OX NCBI_TaxID=487;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=A22;	
RX MEDLINE=20175756; PubMed=10710308;	
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,	
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,	
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
RA Moxon E.R., Grandi G., Rappuoli R.;	
RT "Identification of Vaccine Candidates Against Serogroup B	
RT Meningococcus by Whole-Genome Sequencing.";	
RL Science 287:1816-1820(2000).	
DR EMBL; AF226364; AAF42513.1; -	
SQ SEQUENCE 599 AA; 62693 MW; 46C2E97A7F7F78E9 CRC64;	
Query Match 90.5%; Score 2734.5; DB 2; Length 599;	
Best Local Similarity 91.5%; Pred. No. 1.1e-106;	
Matches 550; Conservative 13; Mismatches 29; Indels 9; Gaps 4;	
QY 1 MNKYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDL 59	
DB 1 MNKYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANTDEEYL 60	
QY 60 EPQRTAVVLSFRSDEKGEKTEGDSNNAVYFDEKRVLKAGAITLKAGDNLIKQ--- 116	

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|||||
Db 61 EPVKRTAVVLSFRSDKEGTGEKVEYTESDHWGVLKAGITLTKAGDNLIKQNTD 120
Qy 117 -NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175
Db 121 ENTIDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180
Qy 176 DPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTT 235
Db 181 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTT 238
Qy 236 A--SDNVDFVRYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVIEKDGKLVGTG 293
Db 239 TQSENVDVRYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVIEKDGKLVGTG 298
Qy 294 KGKDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKFEVTSCTNVTFA 353
Db 299 KGKDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKFEVTSCTNVTFA 358
Qy 354 SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 413
Db 359 SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 418
Qy 414 SKGMDETVNIAGNNIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDDGALNV 473
Db 419 SKGMDETVNIAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDGALNV 478
Qy 474 GSKDTNKPVRITNVAPGKVEGDTNVAQLKGVAQNLRNIDNVGNARAGTAQAIATAGL 533
Db 479 GSKDANKPVRITNVAPGKVEGDTNVAQLKGVAQNLRNIDNVGNARAGTAQAIATAGL 538
Qy 534 VQAYLPKGSMAIIGGDTYRGAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 593
Db 539 VQAYLPKGSMAIIGGDTYRGAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 598
Qy 594 W 594
Db 599 W 599

RESULT 15
Q9AQFO PRELIMINARY; PRT; 592 AA.
AC Q9AQFO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RL membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1; -.
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

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Query Match 90.4%; Score 2733; DB 2; Length 592;
Best Local Similarity 91.8%; Pred. No. 1.3e-106;
Matches 550; Conservative 10; Mismatches 27; Indels 12; Gaps 4;

Qy 1 MNKIYRIITNSALNAWVVSSELTRNHTKRASATVATATLTLFATVQANATDD---DD 56
Db 1 MNKIYRIITNSALNAWVVSSELTRNHTKRASATVATATLTLFATVQANPRPKKD 60
Qy 57 LYLEPVQRTAVVLSFRSDKEGTGEKVEYTESDHWGVLKAGITLTKAGDNLIK 115

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Db 61 LYLEPVQRTAVVLIYNSDKEGTGEKVEYTESDHWVYFNEKGVLTAREITLTKAGDNLIK 120
Qy 116 QNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175
Db 121 Q-----NGTFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 174
Qy 176 DPTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTT 235
Db 175 DTTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGKPGCTT 234
Qy 236 ASDNVDFVRYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVIEKDGKLVGTG 295
Db 235 ASDNVDFVRYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVIEKDGKLVGTG 294
Qy 296 KDENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKFEVTSCTNVTFA 355
Db 295 KGKDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKFEVTSCTNVTFA 354
Qy 356 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 415
Db 355 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKRAVAGSSGKVISGNVSP 414
Qy 416 GKMDETVNIAGNNIEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDDGALNV 475
Db 415 GKMDETVNIAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDG-ALNVGS 473
Qy 476 KDTNKPVRITNVAPGKVEGDTNVAQLKGVAQNLRNIDNVGNARAGTAQAIATAGL 535
Db 474 KDKNKPVRITNVAPGKVEGDTNVAQLKGVAQNLRNIDNVGNARAGTAQAIATAGL 533
Qy 536 AYLPKGSMAIIGGDTYRGAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 594
Db 534 AYLPKGSMAIIGGDTYRGAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQ 592

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Search completed: July 3, 2002, 08:48:11
Job time: 702 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:25 ; Search time 104.77 seconds
(without alignments)
627.619 Million cell updates/sec

Title: US-09-771-382-10
Perfect score: 2988
Sequence: 1 MNKYRIWNSALNNAWVAVS.....TASGNSRGHFGASVGYQW 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

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11: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*

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22: /SIDSL1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2988	100.0	592	22 AAU06180	N. meningitidis 22
2	2942	98.5	592	20 AAY27203	Amino acid sequenc
3	2779	93.0	592	20 AAY23744	A surface protein
4	2626.5	87.9	592	22 AAU06172	N. meningitidis H4
5	2626.5	87.9	589	20 AAY23745	A surface protein
6	2626.5	87.9	589	22 AAU06173	N. meningitidis P2
7	2587.5	86.6	599	20 AAY23743	A surface protein
8	2587.5	86.6	599	22 AAU06176	N. meningitidis H3
9	2552	85.4	594	20 AAY23739	A surface protein
10	2552	85.4	594	22 AAU06179	N. meningitidis B2
11	2533	84.8	594	20 AAY23740	A surface protein

12	2533	84.8	594	21	AAU57044	BASB029 amino acid
13	2533	84.8	594	22	AAU06174	N. meningitidis EG
14	2524	84.5	598	20	RAY23742	A surface protein
15	2524	84.5	598	22	AAU06177	N. meningitidis H1
16	2521	84.4	598	20	RAY23738	A surface protein
17	2521	84.4	598	22	AAU06178	N. meningitidis B2
18	2478.5	82.9	591	21	AAU57045	BASB029 amino acid
19	2464.5	82.5	591	20	RAY27202	Amino acid sequenc
20	2464.5	82.5	591	22	RAY23746	A surface protein
21	2464.5	82.5	591	20	AAU06171	N. meningitidis PM
22	2445.5	81.8	591	20	RAY23741	A surface protein
23	2445.5	81.8	591	22	AAU06175	N. meningitidis EG
24	2443	81.8	592	20	RAY23737	A surface protein
25	2351.5	78.7	513	22	AAU06183	N. meningitidis H4
26	2351	78.7	502	22	AAU06186	N. meningitidis PM
27	2289	76.6	512	22	AAU06182	N. meningitidis PM
28	2221	74.3	604	22	AAU06181	N. meningitidis su
29	2009.5	67.3	433	22	AAU06185	N. meningitidis PM
30	1893.5	63.4	407	22	AAU06184	N. meningitidis PM
31	1135	38.0	1098	17	AAU99392	Haemophilus adhesi
32	1132.5	37.9	2353	17	AAU99393	Haemophilus influe
33	1102.5	36.9	2411	21	AAU23860	Haemophilus adhesi
34	1000.5	33.5	679	17	AAU99394	Haemophilus adhesi
35	1000.5	33.5	679	21	AAU23855	Haemophilus influe
36	975	32.6	1094	21	AAU23858	Haemophilus influe
37	750	25.1	245	20	RAY27201	Amino acid sequenc
38	730	24.4	1002	21	AAU23854	Haemophilus influe
39	721	24.1	1004	21	AAU23857	Haemophilus influe
40	666	22.3	1104	21	AAU23856	Haemophilus influe
41	666	22.3	1104	21	AAU23859	Haemophilus influe
42	600	20.1	116	21	AAU37832	Neisserial conserv
43	398	13.3	1778	22	ABU52677	Escherichia coli p
44	396.5	13.3	2123	22	AAU00701	Moraxella catarrha
45	393.5	13.2	1992	17	AAU04505	Moraxella 200 kda

ALIGNMENTS

RESULT 1
AAU06180
ID AAU06180 standard; Protein; 592 AA.
XX AC AAU06180;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis 22491 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain 22491.
XX FH Key Location/Qualifiers
XX FT Region 1..50
XX FT /label= C1
XX FT /note= "Conserved region 1"
XX FT Region 51..102
XX FT /label= V1
XX FT /note= "Variable region 1"
XX FT Region 103..114
XX FT /label= C2
XX FT /note= "Conserved region 2"
XX FT Region 115..124
XX FT /label= V2
XX FT /note= "Variable region 2"
XX FT Region 125..188
XX FT /label= C3
XX FT /note= "Conserved region 3"
XX FT Region 189..208
XX FT /label= V3
XX FT /note= "Variable region 3"
XX FT Region 209..227

FT FT /label= C4
FT FT /note= "Conserved region 4"
FT FT 228..236
FT FT /label= V4
FT FT /note= "Variable region 4"
FT FT 237..592
FT FT /label= C5
FT FT /note= "Conserved region 5"
XX WO200155182-A1.
XX PN
XX PD
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.
XX PF 25-JAN-2000; 2000US-0177917.
XX PA (UYOU) UNIV QUEENSLAND.
XX PI
XX PI Peak IRA, Jennings MP;
XX DR
XX DR WPI: 2001-488774/53.
XX DR N-PSDB; AAS09170.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain 22491 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 592 AA;

Query Match 100.0%; Score 2988; DB 22; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-166;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKTYRIWNSALNANWAVAVSELTRNHTKRASAVKTAVALTLATLFAVQANATDEDEEL 60
DB 1 mnklyriwnsalnawavavseltrnhckrasatvktavlatllfavlqanatdedeeel 60

QY 61 ESVQSVVGSIQASMEGSGELETISLMTNDSKEFDYPIYVVTLKAGDNLKIKQNTNMENT 120
DB 61 esvqsvvgsiqasmeegsgeletislsmtndsksfedpyivvtlkagdnlikikqntnment 120

QY 121 NASFFYSLKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nasfyslkkdlgtgliinveteklsfgangkkniiisdtkglnfaketagngdtttvhl 180

QY 181 GIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGWNKIKVYKGTGTGQSENVDF 240
DB 181 gigtstltdtlagssashvhdagnosthytraasikdvlnagwnkikvykgtgtgqsenvdf 240

QY 241 VRYDVTVEFLSADTKTTVNVEKSDNGKRTEVKIGAKTSVIKEKDGKLVTKGKGENGSS 300
DB 241 vrydvtveflsadtktttvnveskngkrtevkigaktsvikekdgklvtgkkgengss 300

QY 301 TDEGEGLVTAKEVIDAVNKAQWRMKTITTANGQTQADKFFETVSGTNVTFASGKGITATV 360

DB 301 tdegeglvtakevidavnkagwrmktttangqtqgadkfetvtsgnvtfasgkgittatv 360
QY 361 SKDDQGNITVMYDYNVGDALNVNQLQNSGWNLDLSKAVAGSSGKVIISGNVSPSKGMDTV 420
DB 361 skddqgnitvmydvnvvgdlnvnqlqnsqwnldskavagssgkvisgnvspskgmdetv 420
QY 421 NINAGNNIELSRGNKIDITATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPV 480
DB 421 ninagnnielsrngknidiatsmapqfssvslgagadaptlsvddegalnvsgskdankpv 480
QY 481 RITNVAPGVKEGDTNVAOLKGVQNLNRRIDNVDGNARAGIAQAATATAGLVOAYLPKGS 540
DB 481 ritnvapgvkegdvtnvaqlkgvaqlnnrldnvdgnaraglaqataglvqaylpqks 540
QY 541 MMAIGGTYRGEGAGYAGYSSISDGGNWIITKGTASGNSRGHFGASASVGYQW 592
DB 541 mmaiggytyrgeagyaigyssisdggwniikgtasngsrghfgasasvgyqw 592

RESULT 2
AAY27203
ID AAY27203 standard; Protein; 592 AA.
XX
AC AAY27203;
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40a.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
KW bacterial infection; treatment.
XX
OS Neisseria meningitidis.
XX
PN WO9936544-A2.
PD 22-JUL-1999.
PF 14-JAN-1999; 99WO-IB00103.
PR 09-OCT-1998; 98GB-0022143.
PR 14-JAN-1998; 98GB-0000760.
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
DR WPI: 1999-444400/37.
DR N-PSDB; AAX99125.
XX
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 63; 123pp; English.
XX
CC The invention provides proteins (AAY27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 592 AA;

Query Match 98.5%; Score 2942; DB 20; Length 592;
Best Local Similarity 98.8%; Pred. No. 2.8e-163;
Matches 585; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mnkiyriiwsalnawavseltrnrhtkrasatvktavlatllfatvqanatede 60
QY 61 ESVQSVVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120
DB 61 esvqsvvgsioasmegeletislsmtndskfvdpyivvtlkagdnlikqntn 120
QY 121 NASSFTYSLSKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nassftryslskdlgtlinveteeklsfgangkkvniisdtkglnfaketagtdttvhl 180
QY 181 GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIKGVTGSGTQSENVD 240
DB 181 gigtstltdtlaassashvdagnxsthytraasikdvlagnwnikvgvsgtsgsenvdf 240
QY 241 VRTYDTVEFLSADTKTTVNVEKDKNGKRTVEVKIGAKTSVIKEKDKGLVTGKKGENGSS 300
DB 241 vrttdtveflsadtktttvnveskdngkrtevkigaktsvikekdglvtgkgkengss 300
QY 301 TDEGELVTAKEVIDAVNKAQWRMKTITTTANGOTGOADKFETVTSNTVTFASGKTATV 360
DB 301 tdegeglvtakevidavnkagwrmttttangotgoadkfetvtsntvtfasgkttatv 360
QY 361 SKDDQGNITVMYDVNVGDALNVQNLQNSGWNLDKXAVAGSSGKVISGNVSPSKGMDETV 420
DB 361 skddqgnitvmydvnvgdalnvqlnsgwnldskavagssgkvlsnvspsgkmdetv 420
QY 421 NINAGNNIEISRNKNKIDATSMAPQFSVSLGAGADAPTLSDVDEGALNVGSKDANKPV 480
DB 421 ninagnnieisrngnkidiatsmapqfsvslgagadaptlsdvddegalnvgskdankpv 480
QY 481 RTTNVAPGVKEGDVTNVAQLKVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLPKGS 540
DB 481 rttnvapgvkxgdvtnvaqlkvagvaqlnrdnvgnaraglaqaiataglvqaylpkgs 540
QY 541 MMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592
DB 541 mmaigggyrgeagyaigyssisdgnwliikgtasngsrghfgasasvgyqw 592

RESULT 3

AAU06172
ID AAU23744 standard; Protein; 592 AA.
XX
AC AAU23744;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DE WPI; 1999-418754/35.
DR N-PSDB; AAX85796.
XX
PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX Claim 1; Page 118-120; 132pp; English.

CC The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. CC The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

XX Sequence 592 AA;

Query Match 93.0%; Score 2779; DB 20; Length 592;
Best Local Similarity 93.9%; Pred. No. 8.4e-154;
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

DB 1 mnkiyriiwsalnawavseltrnrhtkrasatvktavlatllfatvqanatede 60

QY 61 ESVQSVVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNTNENT 120

DB 61 esvqsvvgsioasmegeletislsmtndskfvdpyivvtlkagdnlikqntn 120

QY 121 NASSFTYSLSKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180

DB 121 nassftryslskdlgtlinveteeklsfgangkkvniisdtkglnfaketagtdttvhl 180

QY 181 GIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIKGVTGSGTQSEN 238

DB 181 gigtstltdmlntgattntvndvtddekkraasvkdvlagnwnikvgkpgtta--sdnv 238

QY 239 DFRVRYDTVEFLSADTKTTVNVEKDKNGKRTVEVKIGAKTSVIKEKDKGLVTGKKGENG 298

DB 239 dfrvrydtveflsadtktttvnveskdngkrtevkigaktsvikekdglvtgkgeng 298

QY 299 SSTDEGELVTAKEVIDAVNKAQWRMKTITTTANGOTGOADKFETVTSNTVTFASGKTATV 358

DB 299 sstdegeglvtakevidavnkagwrmttttangotgoadkfetvtsntvtfasngtta 358

QY 359 TVSKDDQGNITVMYDVNVGDALNVQNLQNSGWNLDKXAVAGSSGKVISGNVSPSKGMD 418

DB 359 tvskddqgnitvmydvnvgdalnvqlnsgwnldskavagssgkvlsnvspsgkmd 418

QY 419 TVNINAGNNIEISRNKNKIDATSMAPQFSVSLGAGADAPTLSDVDEGALNVGSKDANK 478

DB 419 tvninagnnieisrngnkidiatsmapqfsvslgagadaptlsdvddegalnvgskdank 478

QY 479 PVRITNVAPGVKEGDVTNVAQLKVAQNLRNIDNVGNARAGIAQAIAATAGLVQAYLP 538

DB 479 pvrntnvapgvkxgdvtnvaqlkvagvaqlnrdnvgnaraglaqaiataglvqaylp 538

QY 539 KSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592

DB 539 ksmmaigggytlygeagyaigyssisaggnwliikgtasngsrghfgasasvgyqw 592

RESULT 4

AAU06172
ID AAU06172 standard; Protein; 592 AA.
XX
AC AAU06172;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H41 surface antigen NHA peptide sequence.
XX
KW Surface antigen NHA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H41.
XX FH Key Location/Qualifiers
FT Peptide 1..51
FT Region /label= Signal_peptide
FT 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..102
FT /label= V1
FT /note= "Variable region 1"
FT 52..592
FT /label= Mature_Nhha
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
FT Region 103..114
FT /label= C2
FT /note= "Conserved region 2"
FT 115..124
FT /label= V2
FT /note= "Variable region 2"
FT 125..188
FT /label= C3
FT /note= "Conserved region 3"
FT 189..210
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..592
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09162.
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.

XX SQ Sequence 592 AA;
Query Match 93.0%; Score 2779; DB 22; Length 592;
Best Local Similarity 93.9%; Pred. No. 8.4e-154;
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVALTLATLFAVQANATDEDEEEL 60
DB 1 mnkiyriiwnlsalnawvavseltrnhtkrasatvktavlatlilfatvqanatedeeseel 60
QY 61 ESVQSVVSGSIQASMEGSGELETFISLMTNDSKEFVDPPIVVTILKAGDNLKIKQNTNENT 120
DB 61 esvqsvvsgsiqasmevsgseletisismtdnskefvdppivvvtlkgadnlkikqntn 120
QY 121 NASSTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nasstyslkkdltglinveteklsfgangkkvniisdtkglnfaketagngdttvhl 180
QY 181 GIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVKTGTGSGSENV 238
DB 181 gigstltdmlntgattndvntddekkrasvkdvlmagwnikgvkpgtta--sdnv 238
QY 239 DFVRTYDTEVFLSADTKTTTVNVVESKDNGKRTVEVKGAKTSVKEKDGKLVTKGKGENG 298
DB 239 dfvrtvteflsadtktttvnnveskdngkktevkgaktsvikekdgklvtgkkgeng 298
QY 299 SSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEVTSNTVTFASGKGTTA 358
DB 299 sstdegeglvtakevldavnkagwrmkttfngotgoadkfevtsntvtfasgngtta 358
QY 359 TVSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDE 418
DB 359 tvskddqgnitvkydvnvgdalnvnqlnsgwnldskavagsgkvisgnvspskgmde 418
QY 419 TVNINAGNTEISRNGKNIDTIATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSKDANK 478
DB 419 tvninagnnieitrngknidiatmtpqfssvslgagadaptlsvddegalnvsgskdank 478
QY 479 PVRTNVPAGVKEGDDVTNVAQLKGVAGQNLNRIDNVDGNARAGIAQAIATAGLVQAYLPG 538
DB 479 pvrtnvapgvgkegdvtnvaqlkgvagnlnrldhvnngnaraglaiaicaglvqaylpg 538
QY 539 KSMMAIGGGTYRGEAGYVAGYSSISDGGNWIIRKTASGNSRGRHFGASASVGYOW 592
DB 539 ksmmaigggtyleagyvagyssisaggwnwiktasgnsrgrhfgasasvgyow 592

RESULT 5

AAAY23745
ID AAY23745 standard; Protein; 589 AA.

XX AC AAY23745;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;

XX KW Immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-A1.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI: 1999-418754/35.
DR N-PSDB; AAX85797.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 122-124; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 589 AA;

Query Match 87.9%; Score 2626.5; DB 20; Length 589;
Best Local Similarity 89.1%; Pred. No. 6.1e-145;
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNALNAWVSEITRNHTKRASATVKTAVLATLFLFATVQANATDEDEEEL 60
DB 1 mnkiyriiwnsalnawvsselnrhtkrasatvatvlatlflsatvqanatdededel 60

QY 61 ESQRS-VVGSIQASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLKIQT 116
DB 61 esvarsalvlqmidekgnegestdglswsiyddhntlhg-atvtlkgadnlkikq-- 117

QY 117 NENTNASSFTYSLKDLDTGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGD 176
DB 118 ----sgkdfyslkkelkldtsveteklsfgangknvntsdtkglnfaketagtngdpt 173

QY 177 VHLNGTSLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIGVKTGSTTQOSE 236
DB 174 vhlngigtltldtlagssashvdagnqsthytraasikdvlhagwnikgvtgsttgqse 233

QY 237 NVDFVRYTYTVEFLSADTKTTTNNVESKNGKRTVEKIGAKTSVIKEKDKLVTKGKGE 296
DB 234 nvdfvrytytveflsadtktttvneskdngkrtevkigaktsvikekdglvtgkge 293

QY 297 NGSSSTDEGGLYTAKEVIDAVNKGWRMKTTTANGOTGOADKFETVTSCTNVTFASSKGT 356
DB 294 ngssstdegeglvtakevidavhagwrmttttangotgqadkfetvtsctkvtfasngt 353

QY 357 TATVSKDDGNTVMYDVNVGDALNVLQNSGWNLDKAVAGSSGKVISGNVSPSKGRM 416
DB 354 tatvskddgntvmydyvngdalnvnqlqnsqwnldskavagssgkvlsnvspksgrm 413

QY 417 DETVNIAGNNIEISRNKNIDIASTMAPOFSSVLGACADAPTLSDVEGALNVGSKDA 476
DB 414 detvniagnnieitrngnkidiastmtpqfssvslgacadtllsvddegalnvgskda 473

QY 477 NKPVRTTNVAPGVKEGDVNTVAQLKGAONLNNRIDNVGNRAGTAQATATAGLVQAYL 536
DB 474 nkpvrtnnvapgvkedvntvaqlkgavnlnrldnvnngnaraglaqataglaqayl 533

QY 537 PKSMMAIGGGYRGPAGYAIGYSSISDGNWIKTASGNSRGRHFGASVGYQW 592
DB 534 pksmmaigggtylgeagyaigyssisdgnwviktasgnsrgrhfgtsasgyqw 589

RESULT 6
AAU06173
ID AAU06173 standard; Protein; 589 AA.

XX AAU06173;
AC 24-OCT-2001 (first entry)
XX
DT N. meningitidis P20 surface antigen Nhha polypeptide sequence.
XX
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
KW Neisseria meningitidis strain P20.
XX
OS
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..105
FT /label= V1
FT /note= "Variable region 1"
FT Region 106..117
FT /label= C2
FT /note= "Conserved region 2"
FT Region 118..121
FT /label= V2
FT /note= "Variable region 2"
FT Region 122..185
FT /label= C3
FT /note= "Conserved region 3"
FT Region 186..205
FT /label= V3
FT /note= "Variable region 3"
FT Region 206..224
FT /label= C4
FT /note= "Conserved region 4"
FT Region 225..233
FT /label= V4
FT /note= "Variable region 4"
FT Region 234..589
FT /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI: 2001-488774/53.
DR N-PSDB; AAS09163.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain P20 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 589 AA;

Query Match 87.9%; Score 2626.5; DB 22; Length 589;
Best Local Similarity 89.1%; Pred. No. 6.1e-145;
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNALNANWAVASELNRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
DB 1 mnkiyriiwnalnawvvseltrnhtkrasatvatvatllisatvqanadtdeedeel 60
QY 61 ESQVRS--VWGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLIKQNT 116
DB 61 esvarsalvlqfmidkegnestdgiswyddhntlhg-atvclagdnlikq-- 117
QY 117 NENTNASSFTYSLKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTT 176
DB 117 ---sgkdfyslkkelditsveteklsfgangknvitsdtkglnfaketagngdpt 173
QY 177 VHLNGISTLDTLGLAGSSASHVDAGNOSTHYTRAASIKDVLNAGWNKGVKGTSGTQOSE 236
DB 174 vhlngistltdtlagssashvdagnsthytraasikdvlnagwnkvgkgtstgqse 233
QY 237 NVDFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIREKDKGLVTGKGGE 296
DB 234 nvdvrltydvtveflsadtktttvnveskdngkrtvekgigaktsvirekdkglvtgkgge 293
QY 297 NGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNVTTFASGKGT 356
DB 294 ngstdegeglvtakevidavnkgwrmtttangqtqgqadkfetvtsgtkvtfasngt 353
QY 357 TATVSKDDQGNITVMVDVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 416
DB 354 tatvskddqgnitvkvdyvngdalinvnqlnsgwnldskavagssgkvisgnvspkghm 413
QY 417 DETVNIAGNNEIETSRNGKNIDTATSMAPQSSVSLGAGADAPTLSVDDDEGALNVGSKDA 476
DB 414 detvniagnnieitrngknidatsmtpqfssvslgagadapltlsvdddegalnvgska 473
QY 477 NKPVRITNAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAAYL 536
DB 474 nkpvrinavpgvkegdvtnvaqlkgvaqnlrridnvngnaragiaqaiataglayl 533
QY 537 PGKSMMAIGGTYRGEAGYALGYSSISDGGNWIITKGTASGNSRGRHFGASASVGYQW 592
DB 534 pgksmmaigggtyrgeagyalgyssisdggnwiktgtasgnsrgrhfgtsasvgyqw 589

RESULT 7
AAU23743
ID AAY23743 standard; Protein; 599 AA.

XX
AC AAY23743;

XX
DT 08-SEP-1999 (first entry)

XX
DE A surface protein of Neisseria meningitidis.

XX
KW Surface protein; surface glycoprotein; infection; vaccine;

XX
KW Immunoreactive peptide.

XX
OS Neisseria meningitidis.

XX
PN W09931132-A1.

XX
PD 24-JUN-1999.

XX
PF 14-DEC-1998; 98WO-AU01031.

XX
PR 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.
PA (UYQU) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85795.
XX
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 114-115; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 599 AA;

Query Match 86.6%; Score 2587.5; DB 20; Length 599;
Best Local Similarity 88.0%; Pred. No. 1.2e-142;
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

QY 1 MNKIYRIIWNALNANWAVASELNRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
DB 1 mnkiyriiwnalnawvvseltrnhtkrasatvktavlatllfatvqanadtdeedeel 60
QY 61 ESQVRS--VWGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLIKQ-- 114
DB 61 epvvralsvlqfmidkegnestdgiswyddhntlhg-atvclagdnlikqnt 119
QY 115 --NTNENTNASSFTYSLKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172
DB 120 nktntentndssfyisllklditsveteklsfgangknvitsdtkglnfaketagn 179
QY 173 GDTTVHLNGISTLDTLGLAGSSASHVDAGNOST--HYTRAASIKDVLNAGWNKGVKGTGS 230
DB 180 gdtvhlngistltdtlntgattntndvntddkkrasvkdvinagwnkvgkpgt 239
QY 231 TTGQSENVDVVRTYDVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIREKDKGLVT 290
DB 240 ta--sdnvdvrtvtydvtveflsadtktttvnveskdngkrtvekgigaktsvirekdkglvt 297
QY 291 GKKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNVT 350
DB 298 gkgkengsstdegeglvtakevidavnkgwrmtttangqtqadkfetvtsgtntvf 357
QY 351 ASGKGTATVSKDDQGNITVMVDVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410
DB 358 asgkgtatvskddqgnitvkvdyvngdalinvnqlnsgwnldskavagssgkvisgnvs 417
QY 411 PSKGMDETVMNINAGNNEIETSRNGKNIDTATSMAPQSSVSLGAGADAPTLSVDDDEGALN 470
DB 418 pskgmdetvmninnagnnieitrngknidatsmtpqfssvslgagadapltlsvddkgaln 477
QY 471 VGSKDANKPVRITNAPGVKEGVDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAG 530
DB 478 vgskdankpvrinavpgvkegdvtnvaqlkgvaqnlrridnvgnaragiaqaiatag 537
QY 531 LVQAYLPKSKMMAITGGTYRGEAGYALGYSSISDGGNWIITKGTASGNSRGRHFGASASVGY 590
DB 538 lvqaylpkksmmaigggtyrgeagyalgyssisdggnwiktgtasgnsrgrhfgasasvgy 597
QY 591 QW 592
||

Db 598 qw 599

RESULT 8

AAU06176

ID AAU06176 standard; Protein: 599 AA.

XX

AC AAU06176;

XX

DT 24-OCT-2001 (first entry)

XX

DE N. meningitidis H38 surface antigen NhhA polypeptide sequence.

XX

KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX

OS Neisseria meningitidis strain H38.

XX

FH Key Location/Qualifiers

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..105

FT /label= V1

FT /note= "Variable region 1"

FT Region 106..117

FT /label= C2

FT /note= "Conserved region 2"

FT Region 118..131

FT /label= V2

FT /note= "Variable region 2"

FT Region 132..195

FT /label= C3

FT /note= "Conserved region 3"

FT Region 196..217

FT /label= V3

FT /note= "Variable region 3"

FT Region 218..236

FT /label= C4

FT /note= "Conserved region 4"

FT Region 237..243

FT /label= V4

FT /note= "Variable region 4"

FT Region 244..599

FT /label= C5

FT /note= "Conserved region 5"

XX

PN WO200155182-A1.

XX

PD 02-AUG-2001.

XX

XX 25-JAN-2001; 2001WO-AU00069.

XX

PR 25-JAN-2000; 2000US-0177917.

XX

PA (UYQU) UNIV QUEENSLAND.

XX

PI Peak IRA, Jennings MP;

XX

DR WPI; 2001-488774/53.

DR N-PSDB; AAS09166.

XX

XX New NhhA surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

XX

PS Claim 9; Fig 1; 9lpp; English.

XX

CC The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen NhhA

CC (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broad

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen NhhA

CC from N. meningitidis strain H38 is 1 of 10 NhhA polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX

SQ Sequence 599 AA;

Query Match 86.6%; Score 2587.5; DB 22; Length 599;

Best Local Similarity 88.0%; Pred. No. 1.2e-142;

Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

Qy 1 MNKYRIIWSALNNAWAVSELTRNHTKRASATVTVAVLATLLFATVQANATDEEBEL 60

Db 1 mnkyriiwsalnnaawavseltrnhtkrasatvtavlatllfatvqanatedeeel 60

Qy 61 ESVQRS-VVGSIQASMEGSGELET---ISLSMTNDSKEFVDPIYIVVTLKAGNLIKQ-- 114

Db 61 epvvrslvlfqmidkegenestgnfgwlyydnhtihg-atvtlkagdnlikkqnt 119

Qy 115 --NTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTN 172

Db 120 nkntnentndssftysllkldltltsveteklsfgangknvntsdtkglnfaketagn 179

Qy 173 GDTTVHLNGIGSTLDTLAGSASHVDAGNQST--HYTRAASIKDVLNAGWNKIKGVKGS 230

Db 180 gdttvhlngigstltdtllntgattntndnvtddkkrasvkdvltnagwnikgvkpgt 239

Qy 231 TTGOSENVDFVRTYDTVEFLSADTKTTVNVESKDKGRTEVKIGAKTSVKEKGKLVPT 290

Db 240 ta--sdnvdvfhvtydtveflsadtkttvnveskdkgrtevkigaktsvikekgklvt 297

Qy 291 GKKGSGSSTDEGEGLVTAKEVIDAVNAKAGWRMKT---TANGOTGOADKFPETVTSNTVF 350

Db 298 gkgksgsstsdegeglvtakevidavnaagwrmktttangtgqadkfetvtsntvtf 357

Qy 351 ASGKTTATVSKDOGNITVYDVNVGDALNVNQLONGWNLDSKAVAGSSGKVISGNVS 410

Db 358 asgkttatvskddggnitvdydvnvgdalnvnqlqngswnlidskavagssgkvisgnvs 417

Qy 411 PSKGMDETVNINAGNNTIEISRNKKNIDTATSMAPQSFSSVSGAGADAPTLSDDBEGALN 470

Db 418 pskgmdetvnnagnnietfrngknidiatmtppqsfsvslgagadaptlslvddkgaIn 477

Qy 471 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGAQNLRNDRIDNVDCNARAGIAQAIATAG 530

Db 478 vgskdankpvrntnvapgvkegdvtnvvaqlkgvaqnlrnnrldnvdgnaragiaaiatag 537

Qy 531 LVQAYLPKSKMMAIGGGTYRGAGYAIGYSSISDGGNWIKTAGSNGRHFGASVGY 590

Db 538 lvqaylpksgmmaigggtyrgeagyaigyssisdggnwiiktagsgnshgfhgasvgy 597

Qy 591 QW 592

Db 598 qw 599

RESULT 9

RAY23739

ID AAU23739 standard; Protein: 594 AA.

XX

AC AAU23739;

XX

DT 08-SEP-1999 (first entry)

XX

DE A surface protein of Neisseria meningitidis.

XX

KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

```
XX      Neisseria meningitidis.
OS      WO9931132-A1.
PN      24-JUN-1999.
PD      14-DEC-1998; 98WO-AU01031.
XX      12-DEC-1997; 97GB-0026398.
XX      (ISIS-) ISIS INNOVATION LTD.
PA      (UYQU ) UNIV QUEENSLAND.
XX      Jennings MP, Moxon ER, Peak IRA;
PI      WPI; 1999-418754/35.
XX      DR      N-PSDB; AAX85791.
XX      Neisseria meningitidis surface proteins useful for treating N.
PT      meningitidis infections
XX      Claim 1; Page 95-97; 132pp; English.
XX      The present sequence represents a surface protein of Neisseria
CC      meningitidis which is approximately 62 kDa. The N. meningitidis
CC      surface glycoproteins, nucleic acids, the primers and optionally
CC      a thermostable polymerase, or antibodies are useful in a kit for
CC      the detection or diagnosis of N. meningitidis infection in humans.
CC      The N. meningitidis surface glycoproteins can also be used to
CC      prevent or treat N. meningitidis infection in humans, especially
CC      in the form of vaccines. The proteins and antibodies can also
CC      be used to identify immunoreactive peptides.
XX      Sequence 594 AA;
SQ

Query Match      85.4%; Score 2552; DB 20; Length 594;
Best Local Similarity 86.8%; Pred. No. 1.3e-140;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

QY      1 MNKIYRIWNSALNANVAVSELFRNHTKRASATVKTAVLATLFTATVQANATDEDEEEL 60
DB      1 mnkiyriwnsalnawvvselltrnhtkrasatvatavlatlftatvqanatd-dddyl 59
QY      61 ESQOR-SWVGSIQASMEGSELETISLSMTNDSKEFVDPVI-----VVTLKAGDNL 110
DB      60 epvqrtavlvlsfrsdkegtgekeg-----tedsnwv--yfdkvrklkagaitikagdnl 112
QY      111 KIKONTNENTNASSFTYSLKKDITGLINVETELKLSFGANGKKNIIISDTKGLNFAKETAG 170
DB      113 kikontnentndsfyslkkdildtveteklsfgangkkniiisdtkglnfaketag 172
QY      171 TNGDTPVHLNGIGSTLDTLAGSSASHVDAGNST--HYTRAASIKDVLNAGWNKIGVKT 228
DB      173 tngdtpvhlngigstltdtlngattntvndnvtdekkraasvkdvlnaagwnikgvkp 232
QY      229 GSTGGOSENVDFRTYDTVEFLSADTKTTNVVNESKDNKRTVEKTCARTSVIKEDGKL 288
DB      233 gttc--sdnvdfvrtvdtveflsadtktttvnnveskdnkrtvektvktvikekdgkl 290
QY      289 VTGKGKENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGTGOADRFETVTSCTNV 348
DB      291 vtgkgkdengsstdegeglvtakevidavnnkagwrmtttangtgoadrfetvtsctnv 350
QY      349 TFASGGKTATVSKDDOGNTVYVDVNVGDALNVQNLQNSGWNLDSKAVAGSSGKVIISGN 408
DB      351 tfasgkgtatvskddognitvdyvnnvgdnlvnglqnsqwnldskavagssgkvlisgn 410
QY      409 VSPSKGMDFTVINAGNNTEISRNGKNIDTATSMAPQFSSVSLGAGADAPTLSVDDEGA 468
DB      411 vspskgmdftvinagnnleitrngknidiatcmappqfssvslgagadaptilsvddegga 470
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```
QY      469 LNVGSKDANKPVRTITNVAPGVKEGDVNTNVAOLKGVANLNRRIDNVGNARAGIAQAIAT 528
DB      471 lnvgskdtnkpvritnvpagvkegdvntnvaqlkgvaqlnlnridnvdgnaraglaqaiat 530
QY      529 AGLVQAYLPCKSMWAICGGTYRGEGYAGYGSYSTSDGGNWIILKGTASGNSRGHFGASASV 588
DB      531 aglvqaylpgksmma199dtyrgeagyagysysldsgnwlilkgtasgnsrghfgasav 590
QY      589 GYQW 592
DB      591 gyqw 594

RESULT 10.
AAU06179
ID      AAU06179 standard; Protein; 594 AA.
XX      AC      AAU06179;
XX      24-OCT-2001 (first entry)
XX      N. meningitidis BZ198 surface antigen NhhA polypeptide sequence.
XX      Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX      Neisseria meningitidis strain BZ198.
XX      Key      Location/Qualifiers
FT      Region      1..50      /label= C1
FT      /note= "Conserved region 1"
FT      Region      51..104     /label= V1
FT      /note= "Variable region 1"
FT      Region      105..116    /label= C2
FT      /note= "Conserved region 2"
FT      Region      117..126    /label= V2
FT      /note= "Variable region 2"
FT      Region      127..190    /label= C3
FT      /note= "Conserved region 3"
FT      Region      191..212    /label= V3
FT      /note= "Variable region 3"
FT      Region      213..231    /label= C4
FT      /note= "Conserved region 4"
FT      Region      232..238    /label= V4
FT      /note= "Variable region 4"
FT      Region      239..594    /label= C5
FT      /note= "Conserved region 5"
XX      WO200155182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UYQU ) UNIV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI; 2001-488774/53.
XX      DR      N-PSDB; AAS09169.
XX      New NhhA surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
```


PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 9lpp; English.

XX The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha

CC from N. meningitidis strain B2198 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX

SQ Sequence 594 AA;

Query Match 85.4%; Score 2552; DB 22; Length 594;
Best Local Similarity 86.8%; Pred. No. 1.3e-140;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 mnkiyriiwnlsalnawvseltrnhtkrasatvatavlatllfatvqanadtd-dddlyl 59
Qy 61 ESVQR-SVVGSTQASMEGSGELETISLSMTNDSKEFVDPYI-----VVTLAGDNIL 110
Db 60 epvqrtavvlsfrsdegekeg-----tedsnawv--yfdkvrkagaitlkagdnl 112
Qy 111 KIKQNTNENTNASSFTYSLKDLTGLINVEFKLSFGANGKKNVNIISDTKGLNFAKETAG 170
Db 113 kikqntentndssftyslkkdltltsveteklsfgangknvnitsdtkglnfaketag 172
Qy 171 TNGDPTVHLNGISLTTLTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKLGKVT 228
Db 173 tngdptvhlngislttlintgattntvndvntddekkrasvkdvlnagwnkvgkp 232
Qy 229 GSTTQGSNDVDFVRYDTVEFLSADTKTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKL 288
Db 233 gttta--sdnvdfvrydtveflsadtktttvnveskdngkktvekgigaktsvirekdgkl 290
Qy 289 VTGKKGKNGSSTDEGGLVTAKEVIDAVNKGWRMKTMTTANGQTQADKPFETVTSQNV 348
Db 291 vtgkkgkngsgstdeglvtakevidavnkagwrmtktmttangqgtgqadkpfetvtsqnv 350
Qy 349 TFASCKGTTATVSKDDQGNITVMYDNNVGDALNVQLNSGWNLDKAVAGSSGKVISGN 408
Db 351 tfasckgkttatvskddqgnitvmydnnvgdalnvnqlngsgwnldskavagssgkvisgn 410
Qy 409 VSPSKGKMDETVINAGNIEISRNGKIDTATSMAPOFSSVSLGAGADAPTLSDVDDGGA 468
Db 411 vpskkgkmdetvinagnieitrngknidatsmapfssvslgagadaptlsvddgga 470
Qy 469 LNVGSKDANKPVRIINAPGVKEGQVTVNAQLKGVQAQLNNRIDNVDGNARAGIAQAIAT 528
Db 471 lnvgskdankpvriinavgvkegdvtnvaqlkgvaqnlnnridnvdgnaragiaqaiat 530
Qy 529 AGLVQAYLPKGSMAIGGTGVRGEAGYAGYSSISDGGNWIITKGTASGNSRHFICASV 588
Db 531 aglvqaylpkgsmaiggtgvrgeagyaigyssisdggnwiitkggtasgnsrhfgicasav 590
Qy 589 GYQW 592
Db 591 gyqw 594

RESULT 11
AAU23740

ID AAY23740 standard; Protein; 594 AA.
XX
AC AAY23740;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.

OS Neisseria meningitidis.

PN WO9931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYQU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-FSDB; AAX85792.

PT Neisseria meningitidis surface proteins useful for treating N.
XX meningitidis infections

PS Claim 1; Page 100-101; 132pp; English.

CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.

SQ Sequence 594 AA;

Query Match 84.8%; Score 2533; DB 20; Length 594;
Best Local Similarity 86.4%; Pred. No. 1.7e-139;
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

Qy 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 mnkiyriiwnlsalnawvseltrnhtkrasatvatavlatllfatvqasttd-dddlyl 59
Qy 61 ESVQR-SVVGSTQASMEGSGELETISLSMTNDS-----KEFVDPYIIVVTLKAGDNLKI 112
Db 60 epvqrtavvlsfrsdegekeg-----vtedsnvgvyfdkkgvitagtitikagdnlki 114
Qy 113 KQNTNENTNASSFTYSLKDLTGLINVEFKLSFGANGKKNVNIISDTKGLNFAKETAGTN 172
Db 115 kqntentnassftyslkkdltltsvgteklsfsansknvnitsdtkglnfakktactn 174
Qy 173 GDTTVHLNGISLTTLTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKGVKTCG 230
Db 175 gdttvhlngislttlintgattntvntddekkrasvkdvlnagwnkvgkpt 234
Qy 231 TTGQSENVDVRYDTVEFLSADTKTTVNVESKDKNGKRTVEKIGAKTSVIREKDGKLV 290
Db 235 ta--sdnvdfvrydtveflsadtktttvnveskdngkrtvekgigaktsvirekdgkltv 292
Qy 291 GKGKNGSSTDEGGLVTAKEVIDAVNKGWRMKTMTTANGQTQADKPFETVTSQNVTF 350
XX

Db 293 gkdkgendstkdgeglvtakevidavnkagwrmktttangtqgdkfetytsntvtf 352
QY 351 ASGKGTATVSKDDOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410
Db 353 asgkgtatvskddgdnitvmYdvNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 412
QY 411 PSKGMDETVMNINAGNIEISRNKKNIDATSMAPQFSSVSLGAGADAPTSLVDDGALN 470
Db 413 pskgmdetvniagnnieitrngknidiatmtpqfssvslgagadaptslsvddgaln 472
QY 471 VGSKDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDVGNARAGIAQATATAG 530
Db 473 vgskdankpvrItnvapgvkegdvtnvaqlkgvaqnlhndvgnaraglaqatag 532
QY 531 LVQAYLPKGSMAIGGTYRGAGYAIGYSSISDGGNWIIGKTASNSRGHFGASASVGY 590
Db 533 lvqaylpkgmmaiggytyrgeagyaigyssisdggnwiikgtasnsrghfgasasvgy 592
QY 591 QW 592
Db 593 qw 594

RESULT 12
AAV57044
ID AAV57044 standard; Protein; 594 AA.
AC AAV57044;
XX
XX
DT 21-FEB-2000 (first entry)
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;
KW infection; treatment; prevent; antibacterial drug.
OS Neisseria meningitidis.
FH Key Location/Qualifiers
FT Misc-difference 104 /note= "Encoded by AATC"
FT
XX WO9558683-A2.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-EP03255.
XX
XX 13-MAY-1998; 98GB-0010276.
XX
XX (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Ruelle J;
XX
XX WPI; 2000-053103/04.
DR N-PSDB; AA239864.
XX
XX New polypeptide from neisseria meningitidis useful for diagnosis,
PT treatment or prevention of bacterial infections in mammal
XX
XX Claim 4; Fig 2; 74pp; English.

XX This is the Neisseria meningitidis BASB029 amino acid sequence from
XX serogroup B strain ATCC13090. The BASB029 protein is homologous to the
XX Haemophilus influenzae surface fibril (HSF) protein. The invention
XX relates to BASB029 polynucleotide sequences (AA239864-239865) and
XX polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.
XX BASB029 polypeptides are useful in a method of diagnosing a Neisseria
XX meningitidis infection in a mammal. Compositions containing an immune
XX polynucleotides and polypeptides are useful for generating an immune
XX response in an animal. A therapeutic composition comprising an antibody
XX directed against BASB029 is useful in treating humans with Neisseria
XX meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an
CC infection which results from increased or decreased expression of the
CC polynucleotide, and for therapeutic or prophylactic purposes,
CC particularly genetic immunisation. Antibodies against BASB029
CC polynucleotides and polypeptides are also useful for treating infections
CC particularly bacterial infections. The protein is useful in the
CC screening and development of antibacterial drugs. Fused recombinant
CC protein is useful for the stimulation of the immune system of an organism
XX receiving the protein.

SQ Sequence 594 AA;

Query Match 84.8%; Score 2533; DB 21; Length 594;
Best Local Similarity 86.4%; Pred. NO. 1.7e-139;
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

QY 1 MNKIYRIWNSALNARVAVSELTRNHTKRASATVKTAVLATLILFATVOANATDEDEEEL 60

Db 1 mnkiyriwnsalnawavseltrnhtkrasatvktavlatlilfatvqastld-ddlyl 59

QY 61 ESVQR-SVVGSIQASMEGSELETISLSMTNDS-----KEFVDPYIVYTLKAGDNLKI 112

Db 60 epvqrtavvlsfrskdgtgeke-----vtedsnvgvyfdkkgvltagtitlkagdnki 114

QY 113 KONTNENTNASSFTYSLKKDLTLCLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172

Db 115 kqntnentnassftyssllkdltslsvgteksfsansknvitsdtkglnfakktactn 174

QY 173 GDTTVHLNGIGSTLTDLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKGVKTS 230

Db 175 gdttvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnikgvkpgt 234

QY 231 TFGQSENVDVFTYDTPVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVIKEKDKLVT 290

Db 235 ta--sdnvdfvtydteflsadtktttvnveskdngkrtvkgigaktsvikekdglvt 292

QY 291 GKGKGENSGSTDEGEGLVTAKEVIDAVNAGWRMKTTTANGTGQADKFTVTSCTNVTF 350

Db 293 gkdkgendstkdgeglvtakevidavnkagwrmktttangtqgdkfetytsntvtf 352

QY 351 ASGKGTATVSKDDOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410

Db 353 asgkgtatvskddgdnitvmYdvNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 412

QY 411 PSKGMDETVMNINAGNIEISRNKKNIDATSMAPQFSSVSLGAGADAPTSLVDDGALN 470

Db 413 pskgmdetvniagnnieitrngknidiatmtpqfssvslgagadaptslsvddgaln 472

QY 471 VGSKDANKPVRITNVAPGVKEGDTNVQALKGVAQNLRNIDVGNARAGIAQATATAG 530

Db 473 vgskdankpvrItnvapgvkegdvtnvaqlkgvaqnlhndvgnaraglaqatag 532

QY 531 LVQAYLPKGSMAIGGTYRGAGYAIGYSSISDGGNWIIGKTASNSRGHFGASASVGY 590

Db 533 lvqaylpkgmmaiggytyrgeagyaigyssisdggnwiikgtasnsrghfgasasvgy 592

QY 591 QW 592

Db 593 qw 594

RESULT 13
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
XX AC AAU06174;
XX
XX DT 24-OCT-2001 (first entry)
XX
XX DE N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain EG327.
XX PH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT 51..104
FT /label= V1
FT /note= "Variable region 1"
FT 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT 117..126
FT /label= V2
FT /note= "Variable region 2"
FT 127..190
FT /label= C3
FT /note= "Conserved region 3"
FT 191..212
FT /label= V3
FT /note= "Variable region 3"
FT 213..231
FT /label= C4
FT /note= "Conserved region 4"
FT 232..238
FT /label= V4
FT /note= "Variable region 4"
FT 239..594
FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
PN 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU) UNIV QUEENSLAND.
PI Peak IRA, Jennings MP;
XX WPI: 2001-488774/53.
DR N-PSDB; AAS09164.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 594 AA;
Query Match 84.8%; Score 2533; DB 22; Length 594;
Best Local Similarity 86.4%; Pred. No. 1.7e-139;

Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;
QY 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEBEL 60
DB 1 mnkiyriiwnlsalnawavseltrnhtkrasatvatlatllfatvqastcd-dddlyl 59
QY 61 ESVQR-SVYGSIOASMEGSELETISLSMTNDS-----KEFVDPYIYVITKAGDNLKI 112
DB 60 epvqrtavslfrskdkegtgeke-----vtedsnwgvvyfdkkgvltagtitikagdnlki 114
QY 113 KONTNENTNASSFTYSLKKDLTGLINVEKTEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172
DB 115 kqntnentnassftysllkkdltltsvgteklsfsansknvntsdtkglnfakktactn 174
QY 173 GDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNTKGVKTCG 230
DB 175 gdttvhlngigstltdtllntgattntvndvtddekkraasvkdvinagwnikgvkpgt 234
QY 231 TTGQSENVDFVRTYDTVEFLSADTKTTTVNVESKONGKRTKVEKIGAKTSVKEKDGKLYT 290
DB 235 ta--sdnvdfvrtvdtveflsadtktttvneskdngkrtevkigaktsvikekgklyt 292
QY 291 GKKGKNGSSDTDEGGLYTAKEVIDAVNAGWRMKTTFANGOTGQADKFETVTSNTVTF 350
DB 293 gkdkgendsstdkgeglvtakevidavnkagwrmttttangtggadkfetvtsgtnvtf 352
QY 351 ASGKGTATTATVSKDDOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGVISGNVS 410
DB 353 asgkgtattatvskddognitvmydvnvvgdnlvngnqlnsgwnldskavagssgvvisgnvs 412
QY 411 PSKGKMDETVINAGNNIEISRNKGNIDTATSMAPOFSSVSLGAGADAPTLSDYDDEGALN 470
DB 413 pskgkmdetvinagnnieitrngknidiatmtpfssvslgagadaptlsvddegaln 472
QY 471 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAG 530
DB 473 vgskdankpvrntnvapgvkegdvtnvaqlkgvaqnlrnhidnvdgnaraglaqalatag 532
QY 531 LYQAVLPKSKMMAIGGGTYRGEAGYAGYSSISDGNWLIKGTASGNSRGHCASASVGY 590
DB 533 lvqaylpgksmmaigggtyrgeagyalgysissdgnwnlikgtaagnsrghigasasvgy 592
QY 591 QW 592
DB 593 QW 594
RESULT 14
AA23742
ID AA23742 standard; Protein; 598 AA.
XX AC AA23742;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
XX (UYQU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;
XX WPI; 1999-418754/35.
DR N-PSDB; AAX85794.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 108-110; 132pp; English.
XX
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 84.5%; Score 2524; DB 20; Length 598;
Best Local Similarity 85.5%; Pred. No. 5.7e-139;
Matches 520; Conservative 17; Mismatches 45; Indels 26; Gaps 8;

QY 1 MNKYRIWNSALNAWAVASELNRHNRKASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mnkyriwnsalnawavaseltrnhkrasatvatavlatllfatvqanat-dddlyl 59

QY 61 ESVOR-SVSGSIQASMEGSGELETISLMTNDSKEFVDPYI-----VVTLKAGDNL 110
DB 61 esvor-svsgsiqasmegegletislmtndskefvdpyi-----vvtlkagdnl 110

QY 111 KIQONTNENTNA-----SSFYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAK 166
DB 111 kiqontnentna-----ssfyslkkdltglinvtetklsfgangkkvniisdtkglnfak 166

QY 167 ETAGTNGDTTVHLNGIGSTLTDLAGSSASHVDAGNGST--HYTRAASIKDVLNAGWNK 224
DB 167 etagtngdttvhlngigstltdlagssashvdragngst--hytraasikdvlnagwnk 224

QY 225 GVKTGTGSGSENVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEK 284
DB 225 gvkgtgtsgsenvdfvrytdtveflsadtktttvnnveskdnkrtevkigaktsvikek 284

QY 285 DGKLVTKGKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTS 344
DB 285 dgklvtkgkgsgsstdegglvtakevidavnkgawrmktttangtqgdkfetvts 344

QY 345 GTNVTAFASGKGTATVSKDQGNITVMYDYNVDALNVNOLQSGWNLDSKAVAGSSGKV 404
DB 345 gtnvtafasgkgtatvskdqgnitvmtydvnvdalnvnlqsgwnldskavagssgkv 404

QY 405 ISGNVSPSKGMDETVINAGNIEIRNGKNIDIAFMSAPQSSVSLGAGADAPTLSDV 464
DB 405 isgnvpskkgmdetvinagnieirngknidiatfmsapqssvslgagadaptlsvd 464

QY 465 DEGALNVGSKDANKPVRTITWVAGVKEGDTNVNQAQLKGVAQNLRNIDVNDGNARAGIAQ 524
DB 465 degalnvgskdankpvritwvagvkegdtnvnqaqlkgvaqnlrnidvndgnaragiaq 524

QY 525 AIATAGLVQAYLPCKSMATGGTYRGEAGYATGYSSISDPGGNWIKGTASGNSRHFGA 584
DB 525 aiataglvqaylpcksmatggtyrgeagyaigyssisdgtgnwilkgtasgnsrhfga 584

QY 585 SASVGYQW 592
DB 585 sasvgyqw 598

RESULT 15

AAU06177
ID AAU06177 standard; Protein; 598 AA.
XX
AC AAU06177;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H15 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H15.
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..130 /label= V2
FT /note= "Variable region 2"
FT Region 131..194 /label= C3
FT /note= "Conserved region 3"
FT Region 195..216 /label= V3
FT /note= "Variable region 3"
FT Region 217..235 /label= C4
FT /note= "Conserved region 4"
FT Region 236..242 /label= V4
FT /note= "Variable region 4"
FT Region 243..598 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PE 25-JAN-2001; 2001WO-AU000069.
XX
PR 25-JAN-2000; 2000US-0177917.
XX
PA (UYQU) UNIV QUEENSLAND.
XX
PI Peak IRA, Jennings MP;
XX
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09167.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
PS Claim 9; Fig 1; 91pp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX

SQ	Sequence	598	AA;
Query Match			
Best Local Similarity		84.5%;	Score 2524; DB 22; Length 598;
Matches		520; Conservative	17; Mismatches 45; Indels 26; Gaps 8;
Qy	1	MNKYRIIWSALNAWAVSELTRNHRKASATVKTAVLATLLFATVQANATDEDEEEL	60
Db	1	mnkiyriiwnsalnawvvseltlrnhrkrasatvatatllfatvqanatd-dddlyl	59
Qy	61	ESVQR-SVVGSIQASMEGSELETISLWNTSDSKFVDPYI-----VVTLKAGDNL	110
Db	60	epvqrtavvlfrsdkegtgekg-----tedsnwav--yfdkxrvlkagaitlkkagdn	112
Qy	111	KIKQNTNENTNA----SSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAK	166
Db	113	kikqntnntentndsfstysllkdlldlcsveteklsfgangknvnitsdtkglnfak	172
Qy	167	ETAGTNGDPTVHLNGIGSTLDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIK	224
Db	173	etagtngdptvhlngigstltdtllntgattntvntdtddekkraasvkvlnagwnik	232
Qy	225	GVKGTSTGQSENVDFTVTEPLSADTKTTTVNVESKONGKTEVKIGAKTSVIREK	284
Db	233	gvkpgtta--sdnvdfrvtydtveflsadtktttvnveskdngkktevkigaktsvikek	290
Qy	285	DGKLVTKGKGKENGSTDEGEGLVTAKEVIDAVNKAGHRMKTTTTANGOTGOADKEETVTS	344
Db	291	dgklvfgkgdeengsstdegeglvtakevidavnkagwrmkttttangtqgqadkfetvts	350
Qy	345	GTNVTFFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKV	404
Db	351	gtkvtfasngtattatvskddggnitvkydvnvgdalnvqlnqsgwnldskavagssgkv	410
Qy	405	ISGNVSPSKGMDETVNTINAGNNIEISRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVD	464
Db	411	isgnvpsksgmdetvnnagnnieitrngknidiatsmtpqfssvslgagadaptsld	470
Qy	465	DEGALNVGSKDANKPVRTNVPAGVKEGDVTNVAQLKGAQNLLNNRIDNVDCNARAGIAQ	524
Db	471	degalnvsgskdankpvrntnvpagvkegdvtnvagqlkgvaqnlnnridnvdgnaraglaq	530
Qy	525	AIATAGLVQAYLPGKSMMAIGGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGA	584
Db	531	aiataglaqaylpqksmmaigggtyrgeagyaigyssisdgnwiiikgtasgnsrghfga	590
Qy	585	SASVGYQW 592	
Db	591	sasvgyqw 598	

Search completed: July 3, 2002, 08:36:27
Job time: 323 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:11 ; Search time 39.66 seconds
(without alignments)
364.598 Million cell updates/sec

Title: US-09-771-382-10

Perfect score: 2988

Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGSRGFGASVGYQW 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2779	93.0	592	4	US-09-377-155-17
2	2779	93.0	592	4	US-09-669-974-17
3	2626.5	87.9	589	4	US-09-377-155-19
4	2626.5	87.9	589	4	US-09-669-974-19
5	2587.5	86.6	599	4	US-09-377-155-15
6	2587.5	86.6	599	4	US-09-669-974-15
7	2552	85.4	594	4	US-09-377-155-7
8	2552	85.4	594	4	US-09-669-974-7
9	2533	84.8	594	4	US-09-377-155-9
10	2533	84.8	594	4	US-09-669-974-9
11	2524	84.5	598	4	US-09-377-155-13
12	2524	84.5	598	4	US-09-669-974-13
13	2521	84.4	598	4	US-09-377-155-5
14	2521	84.4	598	4	US-09-669-974-5
15	2464.5	82.5	591	4	US-09-377-155-21
16	2464.5	82.5	591	4	US-09-669-974-21
17	2445.5	81.8	591	4	US-09-377-155-11
18	2445.5	81.8	591	4	US-09-669-974-11
19	2443	81.8	592	4	US-09-377-155-2
20	2443	81.8	592	4	US-09-669-974-2
21	1135	38.0	1098	1	US-08-409-995-2
22	1135	38.0	1098	3	US-08-685-467-2
23	1135	38.0	1098	4	US-09-377-155-32
24	1135	38.0	1098	4	US-08-913-942-2
25	1135	38.0	1098	4	US-09-669-974-32
26	1135	38.0	1098	4	US-09-268-347-44
27	1132.5	37.9	2353	4	US-09-377-155-33

28	1132.5	37.9	2353	4	US-08-913-942-4	Sequence 4, Appl
29	1132.5	37.9	2353	4	US-09-669-974-33	Sequence 33, Appl
30	1131.5	37.9	2354	4	US-09-268-347-47	Sequence 47, Appl
31	1121	37.5	658	1	US-08-409-995-5	Sequence 5, Appl
32	1121	37.5	658	3	US-08-685-467-5	Sequence 5, Appl
33	1121	37.5	658	4	US-08-913-942-5	Sequence 36, Appl
34	1102.5	36.9	2411	4	US-09-268-347-36	Sequence 6, Appl
35	1061	35.5	607	1	US-08-409-995-6	Sequence 6, Appl
36	1061	35.5	607	3	US-08-685-467-6	Sequence 6, Appl
37	1061	35.5	607	4	US-08-913-942-6	Sequence 6, Appl
38	1061	35.5	1912	1	US-08-409-995-4	Sequence 4, Appl
39	1061	35.5	1912	3	US-08-685-467-4	Sequence 4, Appl
40	1000.5	33.5	679	4	US-08-913-942-15	Sequence 15, Appl
41	1000.5	33.5	679	4	US-09-268-347-26	Sequence 26, Appl
42	975	32.6	1094	4	US-09-268-347-32	Sequence 32, Appl
43	730	24.4	1002	4	US-09-268-347-24	Sequence 24, Appl
44	721	24.1	1004	4	US-09-268-347-30	Sequence 30, Appl
45	666	22.3	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-377-155-17

; Sequence 17, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 592

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

; US-09-377-155-17

Query Match 93.0%; Score 2779; DB 4; Length 592;

Best Local Similarity 93.9%; Pred No. 2,4e-207;

Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

Db 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

QY 61 ESQVRSVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTIKAGDNLIKQNTNEPT 120

Db 61 ESQVRSVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTIKAGDNLIKQNTNEPT 120

QY 121 NASSTYSLKDLTGILINYTEKLSFGANGKVNIIISDTKGLNFAKETAGTNGDTTVHLN 180

Db 121 NASSTYSLKDLTGILINYTEKLSFGANGKVNIIISDTKGLNFAKETAGTNGDTTVHLN 180

QY 181 GIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIKGVKTGTTGQSENV 238

Db 181 GIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIKGVKTGTTGQSENV 238

QY 239 DFRVRYDVEFLSADTKTTTVNVESKDNGKREVIKIGAKTSVIKEDGKLVTKGKGNG 298

Db 239 DFRVRYDVEFLSADTKTTTVNVESKDNGKREVIKIGAKTSVIKEDGKLVTKGKGNG 298

QY 299 SSTDEGELVTAKEVIDAVNKGWRMKTITANGQTQADKFEVTSGTNTVTFASGKGTTA 358

Db 299 SSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGTTA 358
QY 359 TVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418
Db 359 TVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418
QY 419 TVNINAGNNIEISRNGKNIDIIATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 478
Db 419 TVNINAGNNIEISRNGKNIDIIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 478
QY 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAIATAGLVQAYLPG 538
Db 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAIATAGLVQAYLPG 538
QY 539 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592
Db 539 KSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGRHFGASASVGYOW 592

RESULT 2

US-09-669-974-17
; Sequence 17, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-17

Query Match 93.0%; Score 2779; DB 4; Length 592;
Best Local Similarity 93.9%; Pred. No. 2.4e-207;
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
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Db 61 ESVQSVVGSIQASMEGSGELETISLMTNDSKEFDVPIVVTLKAGDNLKIKONTNENT 120
QY 121 NASFTYSLKKDLTGLINVTETELKSPGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLN 180
Db 121 NASFTYSLKKDLTGLINVTETELKSPGANGKKNVNIISDTKGLNFAKETAGTNGDPTVHLN 180
QY 181 GIGSTLDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNWKIKVKTGSTTQSENV 238
Db 181 GIGSTLDMNLNTGATNTVNDNVNTDDEKKRAASVSKDVLNAGNWKIKVKGPTTA--SDNV 238
QY 239 DFVRTYDVEFLSADTKTTTVNVESKDKRTEVKIGAKTSVKEKDKGLVTGKKGENG 298
Db 239 DFVRTYDVEFLSADTKTTTVNVESKDKRTEVKIGAKTSVKEKDKGLVTGKKGENG 298
QY 299 SSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGTTA 358
Db 299 SSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGTTA 358

Db 299 SSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGTTA 358
QY 359 TVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418
Db 359 TVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418
QY 419 TVNINAGNNIEISRNGKNIDIIATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 478
Db 419 TVNINAGNNIEISRNGKNIDIIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSKDANK 478
QY 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAIATAGLVQAYLPG 538
Db 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIAIATAGLVQAYLPG 538
QY 539 KSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592
Db 539 KSMMAIGGGTYLGEAGYAGYSSISAGGNWIIKGTASGNSRGRHFGASASVGYOW 592

RESULT 3

US-09-377-155-19
; Sequence 19, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-19

Query Match 87.9%; Score 2626.5; DB 4; Length 589;
Best Local Similarity 89.1%; Pred. No. 1.6e-195;
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
QY 61 ESVQSVVGSIQASMEGSGELET--ISLMTNDSKEFDVPIVVTLKAGDNLKIKONT 116
Db 61 ESVQSVVGSIQASMEGSGELETISLMTNDSKEFDVPIVVTLKAGDNLKIKONT 116
QY 117 NENTNASSFTYSLKKDLTGLINVTETELKSPGANGKKNVNIISDTKGLNFAKETAGTNGDPT 176
Db 117 NENTNASSFTYSLKKDLTGLINVTETELKSPGANGKKNVNIISDTKGLNFAKETAGTNGDPT 176
QY 177 VHLNGIGSTLDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGNWKIKVKTGSTTQSE 236
Db 177 VHLNGIGSTLDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGNWKIKVKTGSTTQSE 236
QY 237 NVDFVRTYDVEFLSADTKTTTVNVESKDKRTEVKIGAKTSVKEKDKGLVTGKKG 296
Db 237 NVDFVRTYDVEFLSADTKTTTVNVESKDKRTEVKIGAKTSVKEKDKGLVTGKKG 296
QY 297 NGSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGT 356
Db 297 NGSTDEGELVTAKEVIDAVNKGWRMKTTTTTANGOTGOADKFETVTSCTKVTTFASGNGT 356
QY 357 TATVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKM 416
Db 357 TATVSKDDOQGNITVYDYNVGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKM 416

Db 354 TATVSKDQGNITVYKVDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 413
QY 417 DETVINAGNNEIISRNKNDIATSMAPQFSSVSLGAGADAPTLSVDDGALNVGSKDA 476
Db 414 DETVINAGNNEIISRNKNDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDA 473
QY 477 NKPRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 536
Db 474 NKPRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 533
QY 537 PKGSMAIAGGGTYLGEAGYAIGYSSISDGTNNVIKGTASGNSRHFSGASVGYQW 592
Db 534 PKGSMAIAGGGTYLGEAGYAIGYSSISDGTNNVIKGTASGNSRHFSGASVGYQW 589

RESULT 4

US-09-669-974-19
; Sequence 19, Application us/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 589
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-19

Query Match 87.9%; Score 2626.5; DB 4; Length 589;
Best Local Similarity 89.1%; Pred. No. 1.6e-195;
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60
QY 61 ESVQRS-VVGSIQASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 116
Db 61 ESVARSALVLPQMDIKEGNESTGNGWSTYYDDHNTLHG-ATVTLKAGDNLKIKQ-- 117
QY 117 NENTNASSFTYSLKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTNGDT 176
Db 118 ----SGKFTYSLKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTNGDPT 173
QY 177 VHLNGTGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGNWKIKVKTGSTTGOSE 236
Db 174 VHLNGTGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGNWKIKVKTGSTTGOSE 233
QY 237 NVDFVRYTYDVEFLSADTKTTTVNYESKNGKRTVEIKGAKTSVIKEKDKLVTKGKGE 296
Db 234 NVDFVRYTYDVEFLSADTKTTTVNYESKNGKRTVEIKGAKTSVIKEKDKLVTKGKGE 293
QY 297 NGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFEVTSNTVTFASGKT 356
Db 294 NGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFEVTSNTVTFASGKT 353
QY 357 TATVSKDQGNITVYKVDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 416

Db 354 TATVSKDQGNITVYKVDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 413
QY 417 DETVINAGNNEIISRNKNDIATSMAPQFSSVSLGAGADAPTLSVDDGALNVGSKDA 476
Db 414 DETVINAGNNEIISRNKNDIATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSKDA 473
QY 477 NKPRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 536
Db 474 NKPRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 533
QY 537 PKGSMAIAGGGTYLGEAGYAIGYSSISDGTNNVIKGTASGNSRHFSGASVGYQW 592
Db 534 PKGSMAIAGGGTYLGEAGYAIGYSSISDGTNNVIKGTASGNSRHFSGASVGYQW 589

RESULT 5

US-09-377-155-15
; Sequence 15, Application us/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-15

Query Match 86.6%; Score 2587.5; DB 4; Length 599;
Best Local Similarity 88.0%; Pred. No. 1.7e-192;
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
QY 61 ESVQRS-VVGSIQASMEGSELET---ISLMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 114
Db 61 EPVARSALVLPQMDIKEGNESTGNGWSTYYDDHNTLHG-ATVTLKAGDNLKIKQ-- 119
QY 115 --NTNENTNASSFTYSLKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTN 172
Db 120 NKTNTNENTNASSFTYSLKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTN 179
QY 173 GDTTVHLNGTGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNWKIKVKTGS 230
Db 180 GDTTVHLNGTGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNWKIKVKTGS 239
QY 231 TTGQSENVDFVRYTYDVEFLSADTKTTTVNYESKNGKRTVEIKGAKTSVIKEKDKLV 290
Db 240 TA--SDNVDFVRYTYDVEFLSADTKTTTVNYESKNGKRTVEIKGAKTSVIKEKDKLV 297
QY 291 GKKGKNGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFEVTSNTVTF 350
Db 298 GKKGKNGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKFEVTSNTVTF 357
QY 351 ASGKGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV 410
Db 358 ASGKGTATVSKDDQGNITVYKVDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV 417
QY 411 PSKGRMDETVNINAGNNEIISRNKNDIATSMAPQFSSVSLGAGADAPTLSVDDGALN 470

Db 418 PSKGMDETVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTSLVDDRGALN 477
QY 471 VGSKDANKPVRITNAPGVKEGDTNVAOLKGYAQNLRNDRIDNVDGNARAGIAQAATAG 530
Db 478 VGSKDANKPVRITNAPGVKEGDTNVAOLKGYAQNLRNDRIDNVDGNARAGIAQAATAG 537
QY 531 LVQAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASNSRGRHFGFASASVGY 590
Db 538 LVQAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASNSRGRHFGFASASVGY 597
QY 591 QW 592
Db 598 QW 599

RESULT 6
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 86.6%; Score 2587.5; DB 4; Length 599;
Best Local Similarity 88.0%; Pred. No. 1.7e-192;
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

QY 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
QY 61 ESVORS-VVGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIQ-- 114
Db 61 EPVVRSLVLOFMIDREGENGESTNGHSIYYDHNHTLHG-ATVTLKAGDNLKIQNT 119
QY 115 --NTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTN 172
Db 120 NKNTNENTNDSFTYSLKKDLTGLTSLVETKLSFGANGKVNITSDTKGLNFAKETAGTN 179
QY 173 GDTTVHLNGIGSLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKTS 230
Db 180 GDTTVHLNGIGSLTDTLLNTGATTNVDNNTDDKKRAASVKDVLNAGWNKIGVKPGT 239
QY 231 TTGOSENVDFVRTYDVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGKLV 290
Db 240 TA--SDNVDFVHTYDVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGKLV 297
QY 291 GKKGKENGSSDTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKPFETVTSCTNV 350
Db 298 GKKGKENGSSDTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKPFETVTSCTNV 357
QY 351 ASGKGTATVSKDDOGNITVMYDVGDLNVLQNSGNLDSKAVAGSSGKVISGNV 410

Db 358 ASGKGTATVSKDDOGNITVMYDVGDLNVLQNSGNLDSKAVAGSSGKVISGNV 417
QY 411 PSKGMDETVNINAGNIEISRNKNIDTATSMAPQFSSVSLGAGADAPTSLVDDRGALN 470
Db 418 PSKGMDETVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTSLVDDRGALN 477
QY 471 VGSKDANKPVRITNAPGVKEGDTNVAOLKGYAQNLRNDRIDNVDGNARAGIAQAATAG 530
Db 478 VGSKDANKPVRITNAPGVKEGDTNVAOLKGYAQNLRNDRIDNVDGNARAGIAQAATAG 537
QY 531 LVQAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASNSRGRHFGFASASVGY 590
Db 538 LVQAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASNSRGRHFGFASASVGY 597
QY 591 QW 592
Db 598 QW 599

RESULT 7
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6157312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

Query Match 85.4%; Score 2552; DB 4; Length 594;
Best Local Similarity 86.8%; Pred. No. 9.5e-190;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

QY 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 ESVOR--SVVGSIOASMEGSGELETISLSMTNDSKEFVDPYI-----VVTLKAGDNL 110
Db 60 EPVQRTAVVLFSRDKEGEGEKEG-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL 112
QY 111 KIKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAG 170
Db 113 KIKONTNENTNDSFTYSLKKDLTGLTSLVETKLSFGANGKVNITSDTKGLNFAKETAG 172
QY 171 TNGDPTVHLNGIGSLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVK 228
Db 173 TNGDPTVHLNGIGSLTDTLLNTGATTNVDNNTDDKKRAASVKDVLNAGWNKIGVKP 232
QY 229 GSTGOSENVDFVRTYDVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGK 288
Db 233 GITA--SDNVDFVRTYDVEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGK 290
QY 289 VTGKGKENGSSDTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKPFETVTSCTNV 348
Db 291 VTGKGKENGSSDTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTQADKPFETVTSCTNV 350
QY 349 TFASGKGTATVSKDDOGNITVMYDVGDLNVLQNSGNLDSKAVAGSSGKVISGN 408

Db 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 352
QY 351 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 410
Db 353 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 412
QY 411 PSKGKDETVNINAGNIEISRNGKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALN 470
Db 413 PSKGKDETVNINAGNIEISRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDDDEGALN 472
QY 471 VGSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNAGNARAGIAQATATAG 530
Db 473 VGSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNAGNARAGIAQATATAG 532
QY 531 LVOAYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 590
Db 533 LVOAYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 592
QY 591 QW 592
Db 593 QW 594

RESULT 10
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

Query Match 84.8%; Score 2533; DB 4; Length 594;
Best Local Similarity 86.4%; Pred. No. 2.8e-188;
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;
QY 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQASTD-DDDLYL 59
QY 61 ESVQR-SVSGIQASMEGSELETISLSMTNDS-----KEFVDPYIVVTLKAGDNLKI 112
Db 60 EPVQRTAVLSFRSDKEGTEKE-----VTEDSNWGVYFDKKGVLTAGTITLAKAGDNLKI 114
QY 113 KONTNENTNASSFYSLKKDLTGLINVTETKLSFGANGKKNVNIISDTKGLNFAKETAGTN 172
Db 115 KONTNENTNASSFYSLKKDLTGLTSTVTEKLSFGANSKNVNIISDTKGLNFAKKTAEIN 174
QY 173 GDTTVHLNGIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIKGVKTGS 230
Db 175 GDTTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVKDVLNAGNINIKGVKPGT 234
QY 231 TTGOSENVDVRYTDTVEFLSADTKTTTNNVESKDNKRTVEKIGAKTSVKEKDGKLVY 290

Db 235 TA--SDNVDFVRYTDTVEFLSADTKTTTNNVESKDNKRTVEKIGAKTSVKEKDGKLVY 292
QY 291 GRKGENGSSSTDEGGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 350
Db 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 352
QY 351 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 410
Db 353 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 412
QY 411 PSKGKDETVNINAGNIEISRNGKNIDTATSMAPQFSSVSLGAGADAPTLSVDDDEGALN 470
Db 413 PSKGKDETVNINAGNIEISRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDDDEGALN 472
QY 471 VGSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNAGNARAGIAQATATAG 530
Db 473 VGSKDANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNVNAGNARAGIAQATATAG 532
QY 531 LVOAYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 590
Db 533 LVOAYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASNSRGRHFGASASVGY 592
QY 591 QW 592
Db 593 QW 594

RESULT 11
US-09-377-155-13
; Sequence 13, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-13

Query Match 84.5%; Score 2524; DB 4; Length 598;
Best Local Similarity 85.5%; Pred. No. 1.4e-187;
Matches 520; Conservative 17; Mismatches 45; Indels 26; Gaps 8;
QY 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59
QY 61 ESVQR-SVSGIQASMEGSELETISLSMTNDSKEFVDPYI-----VVTLLKAGDNL 110
Db 60 EPVQRTAVLSFRSDKEGTEKE-----VTEDSNWAV--YFDEKRVLLKAGATLKAGDNL 112
QY 111 KONTNENTNASSFYSLKKDLTGLINVTETKLSFGANGKKNVNIISDTKGLNFAK 166
Db 113 KONTNENTNASSFYSLKKDLTGLTSTVTEKLSFGANGKKNVNIISDTKGLNFAK 172
QY 167 ETAGTNGDPTVHLNGIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNINIK 224
Db 173 ETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVKDVLNAGNINIK 232
QY 225 GVTGSTTGOSENVDVRYTDTVEFLSADTKTTTNNVESKDNKRTVEKIGAKTSVKEK 284

Db 173 ETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGNNIK 232
QY 225 GVKTSSTTGOSENVDVRYDTVEFLSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 284
Db 233 GVKPGGTTA--SDNVDFVRYDTVEFLSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 290
QY 285 DGKLVTKGKGGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 344
Db 291 DGKLVTKGKGGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 350
QY 345 GTWVTASGKGTTATVSKDDQGNITVMYDVGDLNVLNQLNSGWNLDKSKAVAGSSGV 404
Db 351 GTRVTEASGNGTTATVSKDDQGNITVKYDVGDLNVLNQLNSGWNLDKSKAVAGSSGV 410
QY 405 ISGNVSPSKGMDETVNIAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDV 464
Db 411 ISGNVSPSKGMDETVNIAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDV 470
QY 465 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNNRIDNVGNARAGIAQ 524
Db 471 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNNRIDNVGNARAGIAQ 530
QY 525 AIATAGLVAQYLPKGSMAITGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRHFGEA 584
Db 531 AIATAGLVAQYLPKGSMAITGGTYRGEAGYAGYSSISDGTGNWVIKGTASGNSRHFGE 590
QY 585 SASVGYOW 592
Db 591 SASVGYOW 598

RESULT 14

US-09-669-974-5
; Sequence 5, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-5

Query Match 84.4%; Score 2521; DB 4; Length 598;
Best Local Similarity 85.5%; Pred. No. 2.4e-187;
Matches 520; Conservative 16; Mismatches 46; Indels 26; Gaps 8;

QY 1 MNKIYRIIWNLSALNNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKISRIIWNLSALNNAVWVSELTRNHTKRASATVATATLLFATVQANATD-DDDLYL 59
QY 61 ESVOR-SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI-----VTLKAGDNL 110
Db 60 EPQVORTAVLFSRDKSGTGEKEG-----TEDSNWAV--YFDEKRVLLKAGAILKAGDNL 112
QY 111 KIKONTNENTNA-----SSFTYSLKDLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAK 166

Db 113 KIKONTNENTNENTNDSSFTYSLKDLTGLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAK 172
QY 167 ETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGNNIK 224
Db 173 ETAGTNGDPTVHLNGIGSTLTDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGNNIK 232
QY 225 GVKTSSTTGOSENVDVRYDTVEFLSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 284
Db 233 GVKPGGTTA--SDNVDFVRYDTVEFLSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 290
QY 285 DGKLVTKGKGGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 344
Db 291 DGKLVTKGKGGSGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQOADKFETVTS 350
QY 345 GTWVTASGKGTTATVSKDDQGNITVMYDVGDLNVLNQLNSGWNLDKSKAVAGSSGV 404
Db 351 GTRVTEASGNGTTATVSKDDQGNITVKYDVGDLNVLNQLNSGWNLDKSKAVAGSSGV 410
QY 405 ISGNVSPSKGMDETVNIAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDV 464
Db 411 ISGNVSPSKGMDETVNIAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDV 470
QY 465 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNNRIDNVGNARAGIAQ 524
Db 471 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNNRIDNVGNARAGIAQ 530
QY 525 AIATAGLVAQYLPKGSMAITGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRHFGEA 584
Db 531 AIATAGLVAQYLPKGSMAITGGTYRGEAGYAGYSSISDGTGNWVIKGTASGNSRHFGE 590
QY 585 SASVGYOW 592
Db 591 SASVGYOW 598

RESULT 15

US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 82.5%; Score 2464.5; DB 4; Length 591;
Best Local Similarity 84.2%; Pred. No. 5.7e-183;
Matches 506; Conservative 30; Mismatches 46; Indels 19; Gaps 8;

QY 1 MNKIYRIIWNLSALNNAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 59
Db 1 MNKIYRIIWNLSALNNAVWVSELTRNHTKRASATVKTAVLATLLFATVQANANNEEEDL 60
QY 60 -LESVORSV-VGSIQASMEGSGELETISLSMTNDSKEFVDPYIV----VTLKAGDNLKIK 113
Db 61 YLDPVORTAVLVNSDKSGTGEKEKVE-ENSDWAVYFNEKGVLTAREITLAKAGDNLKIK 119
QY 114 QNTNENTNASSFTYSLKDLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAKETAGTNG 173

Db 120 Q-----NGTFTYSLKKDLTDLTSVGTSEKLSFANGKNVNITSDTKGLNFAKETAGTNG 173
QY 174 DFTVHLNGIGSLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKTGST 231
Db 174 DFTVHLNGIGSLTDTLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNKIGVKPGTT 233
QY 232 TQGSNVDFVRTYDVEFLSADTKTTTNNVESKDKGRTEVKIGAKTSVIREKDGKLVGT 291
Db 234 A--SDNVDFVRTYDVEFLSADTKTTTNNVESKDKGRTEVKIGAKTSVIREKDGKLVGT 291
QY 292 KGKGENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNNVTFA 351
Db 292 KDKGENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTTANGQTQADKFETVTSGTNNVTFA 351
QY 352 SKGKTATVSKDDOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411
Db 352 SKGKTATVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 411
QY 412 SKGKMDETVNNAGNNIEISRNGKNIDATSMAPQFSSVSLGAGADAPTLSVDDEGALNV 471
Db 412 SKGKMDETVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDGD-ALNV 470
QY 472 GSKDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLNNRIDNVDCGNARAGIAQAIATAGL 531
Db 471 GSKDKNKPRIITNAPGVKEGDTVNVQALKGVAQNLNNRIDNVDCGNARAGIAQAIATAGL 530
QY 532 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVGQ 591
Db 531 VQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIICKGTASGNSRGHFGASASVGQ 590
QY 592 W 592
Db 591 W 591

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Job time: 339 sec

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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:32 ; Search time 58.79 Seconds
(without alignments)
967.595 Million cell updates/sec

Title: US-09-771-382-10
Perfect score: 2988
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHPGASASVGYOW 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2988	100.0	592	2 A81888	probable surface f
2	2464.5	82.5	591	2 G81133	adhesin NMB0992 (i
3	561	18.8	298	2 H64138	adhesin homolog Hi
4	410.5	13.7	2059	2 D82671	surface protein XF
5	394.5	13.2	1190	2 A82615	surface protein XF
6	375.5	12.6	1107	2 AC0976	probable autotrans
7	373.5	12.5	1588	2 A86036	probable adhesin Z
8	373.5	12.5	1588	2 H91188	probable adhesin E
9	341.5	11.4	658	2 AH0110	probable surface p
10	252	8.4	1004	2 C82672	surface-exposed ou
11	248.5	8.3	1325	2 A64905	ydek protein - Esc
12	231.5	7.7	1343	2 E90893	hypothetical prote
13	227.5	7.6	1343	2 D85724	hypothetical prote
14	220.5	7.4	1238	2 AH0038	probable exported
15	219.5	7.3	949	2 D90803	Aida-1 adhesin-lik
16	219.5	7.3	1005	2 H85611	probable adhesin Z
17	219.5	7.3	1910	2 AF0394	probable adhesin h
18	219	7.3	1018	2 H83135	probable adhesin P
19	212	7.1	1417	2 A83080	hypothetical prote
20	210.5	7.0	1275	2 T33369	hypothetical prote
21	210.5	7.0	4919	2 T31105	hypothetical prote
22	210	7.0	1286	2 S28634	adhesin AIDA-1 pre
23	209.5	7.0	5188	2 B85547	probable RTX famil
24	209	7.0	1428	2 AC2224	hypothetical prote
25	209	7.0	4936	2 AH2515	hypothetical prote
26	208.5	7.0	936	2 I40711	sapB protein - Cam
27	207.5	6.9	1477	2 B43855	high-molecular-we
28	207.5	6.9	5291	2 F90696	hypothetical prote
29	205	6.9	1109	2 A56143	surface-array prot

ALIGNMENTS

RESULT 1

A:1888
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: A81888
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491
A:Reference number: A81775; MUID:20222556
A:Accession: A81888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-592 <PAR>
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: NMA1200

Query Match	Score	DB 2	Length	592;
Best Local Similarity	100.0%;	Pred. No. 6.7e-146;		
Matches	592;	Conservative	0;	Mismatches
Indels	0;	Gaps	0;	
Qy	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL	60	
Db	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEEL	60	
Qy	61	ESVQSVSGSIOASMEGSELETISLSMTNDSKEFVDPYIVTVLKAGDNLKIKQNTNENT	120	
Db	61	ESVQSVSGSIOASMEGSELETISLSMTNDSKEFVDPYIVTVLKAGDNLKIKQNTNENT	120	
Qy	121	NASSFTYSLKDLTGLINVEETKLSFGANGKKNIIISDTKGLNFAKETAGTGTTVHLN	180	
Db	121	NASSFTYSLKDLTGLINVEETKLSFGANGKKNIIISDTKGLNFAKETAGTGTTVHLN	180	
Qy	181	GGSTLTDLTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKTGTTGQSENVD	240	
Db	181	GGSTLTDLTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKTGTTGQSENVD	240	
Qy	241	VRDYDFEFLSADTKTTTVNVEKDKGKTEVKIGARTSVIKEDGKLVTKGKGENGSS	300	
Db	241	VRDYDFEFLSADTKTTTVNVEKDKGKTEVKIGARTSVIKEDGKLVTKGKGENGSS	300	
Qy	301	TDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFTVTSNTVTFASGKGTATV	360	
Db	301	TDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFTVTSNTVTFASGKGTATV	360	
Qy	361	SKDDQGNITVMDVNVGDALNVNQLNSKAVAGSSGKVISGNVSPSKGMDTV	420	
Db	361	SKDDQGNITVMDVNVGDALNVNQLNSKAVAGSSGKVISGNVSPSKGMDTV	420	

QY 421 NINAGNNIEISRNKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPV 480
DB 421 NINAGNNIEISRNKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPV 480
QY 481 RTTNVAPGVKEGDTNVAOLKGVQALNNRINDVGNARAGIAQAATATAGLVAQYLPGRS 540
DB 481 RTTNVAPGVKEGDTNVAOLKGVQALNNRINDVGNARAGIAQAATATAGLVAQYLPGRS 540
QY 541 MMAIGGTYRGEAGYAIGYSSISDGGNWLIIKGTASGNSRGHFGASASVGYOW 592
DB 541 MMAIGGTYRGEAGYAIGYSSISDGGNWLIIKGTASGNSRGHFGASASVGYOW 592

RESULT 2
G81133
adhesin homology [imported] - Neisseria meningitidis (strain MC58 serogroup B)
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Kettellin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Suh, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <FET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722623
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

Query Match 82.5%; Score 2464.5; DB 2; Length 591;
Best Local Similarity 84.2%; Pred. No. 4.4e-119;
Matches 506; Conservative 30; Mismatches 46; Indels 19; Gaps 8;
QY 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVKTAVLATLILFATVQANATDEDEEE- 59
DB 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVKTAVLATLILFATVQANATDEDEE 60
QY 60 -LESVQSV-VGSIQASMEGSGELETISLMTNDSKFEVDPIV---VTLKAGDNLKIK 113
DB 61 YLPVQRTAVLIVNSDKEGTGEKVE-ENSDWAVYFNKGVLTAREITLTKAGDNLKIK 119
QY 114 QNTNENTNASSFTYSLKDLTLINIVETKLSFGANGKKNIIISDTKGLNFAKETAGTNG 173
DB 120 Q-----NGNTFTYSLAKDLTLTSVGTSEKLSFANGKNVNIITSDTKGLNFAKETAGTNG 173
QY 174 DTTVHLNGIGSTLTDTLTLAGSASHVDAGNOST--HYTRAASIKDVLNAGNNIKGVKTGST 231
DB 174 DTTVHLNGIGSTLTDTLTLAGSASHVDAGNOST--HYTRAASIKDVLNAGNNIKGVKTGST 233
QY 232 TGOSENVDVRYTDTVEFLSADTKTTTVNYESKNGKRTVEKIGAKTSVIKEKDKLVGT 291
DB 234 A--SDNVDFVRYTDTVEFLSADTKTTTVNYESKNGKRTVEKIGAKTSVIKEKDKLVGT 291
QY 292 KKGKNGSSDDEGELVTAKEVIDAVNKGWRMKTITTTANGQTQADKFETVTSCTNVTFA 351
DB 292 KDKGNGSSDDEGELVTAKEVIDAVNKGWRMKTITTTANGQTQADKFETVTSCTNVTFA 351
QY 352 SGKTTATVSKDDGNTVMTVDVNVGALNVQNLQNSGNWLDKSAVAGSSGKVISGNVSP 411
DB 352 SGKTTATVSKDDGNTVMTVDVNVGALNVQNLQNSGNWLDKSAVAGSSGKVISGNVSP 411
QY 412 SKGKMDVTNINAGNNIEISRNKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNV 471
DB 412 SKGKMDVTNINAGNNIEISRNKNIDIATSMAPQFSSVSLGAGADAPTLSDVDEGALNV 470

QY 472 GSKDANKPVRIITNAPGVKEGDTNVAOLKGVQALNNRINDVGNARAGIAQAATATAGL 531
DB 471 GSKDANKPVRIITNAPGVKEGDTNVAOLKGVQALNNRINDVGNARAGIAQAATATAGL 530
QY 532 VOAYLPGKSMAIIGGTYRGEAGYAIGYSSISDGGNWLIIKGTASGNSRGHFGASASVGYO 591
DB 531 VOAYLPGKSMAIIGGTYRGEAGYAIGYSSISDGGNWLIIKGTASGNSRGHFGASASVGYO 590
QY 592 W 592
DB 591 W 591

RESULT 3
I64138
adhesin homology H11732 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C:Accession: I64138
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630
A:Accession: I64138
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-298 <TIGR>
A:Cross-references: GB:U32846; GB:L42023; NID:gl574588; PID:gl574589; TIGR:H11732

Query Match 18.8%; Score 561; DB 2; Length 298;
Best Local Similarity 43.1%; Pred. No. 6e-22;
Matches 144; Conservative 34; Mismatches 86; Indels 70; Gaps 11;
QY 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVKTAVLATLILFATVQA-----N 50
DB 1 MNKIYRIIWSALNANVAVSELTRNHTKRASATVKTAVLATLILFATVQA-----N 50
QY 51 ATDEDEEELESVQSVVSGSIQASMEGSGELETISLMTNDSK-EFVDPIVTVTLKAGDN 109
DB 61 STEDDIED-----SAATKDNKNQALKAGDTLTKAGKN 94
QY 110 LKIKONTNENTNASSFTYSLKDLTLINIVETKLS-----FGANGKKNVNIISD 158
DB 95 LKAKL----DQGGKSVTFALAKDL---DVKTAQVSDTLTIGGNTPAAGGATPKVSIIT 146
QY 159 TKGLNFAKETAGTNGDTTVHLNGIGSTLTDLAGSSAS-HVDAGNQSTHYTRAASIKDVL 217
DB 147 ADGLKLAK---GTNGDPAVHLNGLASTLPDVTNTGASTSVTFSPSIEKTRAATIKDVL 203
QY 218 NAGNNIKGVKTGSTTGOSENVDVRYTDTVEFLSADTKTTTVNYESKNGKRTVEKIGAK 277
DB 204 NAGNNIKGVKTGSTTGOSENVDVRYTDTVEFLSADTKTTTVNYESKNGKRTVEKIGAK 261
QY 278 TSVIKERKDKLVTK-----GKGENGS-STDE 303
DB 262 TSVIKERKDKLVTK-----GKGENGS-STDE 295

RESULT 4
D82671
surface protein Xf1529 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82671
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below

Db 1004 --VKVNSLNN-----SATPTAAGVDATAIGAIGATASGADSIAMGNKASASADNA 1050
QY 467 GAL-----NVGSKDANKPRVITNVAPGVKEGVDVTVNAQLKGVQAQLNNRIDNV 514
Db 1051 VAIGNHVADRANTVSVGSAGSER--QVTNVAAGTADTDVAVNSQLNOGLITAKQYTDGV 1108
QY 515 DGNAR-----AGIAQAIATAGLVQVAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWII 570
Db 1109 VGSRLRDTDGVAAATATANLPQAYIPGRGMTSVGVSSYRGQSAIAVGVSSVESGRWVF 1168
QY 571 KGTASGNSRHFCSASVGVQW 592
Db 1169 KFGSANTRSQVGIGAGVGVQW 1190

RESULT 6
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.;
S.; Moulé, S.; O'Gaora, P.
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.;
S.; Moulé, S.; O'Gaora, P.
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 12.6%; Score 375.5; DB 2; Length 1107;
Best Local Similarity 22.0%; Pred. No. 1.1e-11;
Matches 184; Conservative 103; Mismatches 232; Indels 317; Gaps 36;

QY 9 WNSALNANW-----VAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 51
Db 337 WNETTSFSASHGSSITNKITNVAAGLSSEST-----DAVNSQLPETFNEKVDQNT 388

QY 52 TD-----EDEEELESVQSV-----VGSIOASMEGS-GELE 82
Db 389 TDIAANTNTQNSTAINTSNTSVDINTSITGLTDNALLWDEDTGAFSANHGGSTSKIT 448

QY 83 TISL-SMTNDSKEFVDPYIVVTLKAGDNL-KIKQNTNENTNASSFTYSLKKDL-TGLINV 139
Db 449 NVAAGALSEDSTAVN-----GSQLEYTNQKVDQNTSAIA-----DINTSITNL 492

QY 140 ETEKLSFGANGKKNIIISDTKGLNFAKE-TAGTNGDPTVHLNGIGSLTDLTLAGSSASHV 198
Db 493 GTDALSW-----DDEGAFSASHGTSCTNKITNVAAGETASDSTDAINGSQLYET 542

QY 199 D-----ACNQSHYTRAAIKDVLNAGNKNIGKVTGSGTQSENVDVFTYD 245
Db 543 NMLISQYNESISOLAGTSETYI-----TENGTG-----VKYIRIND 579

QY 246 T-----VEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDKGLVTKGKGEN----- 297
Db 580 NGLEGODAYATGATGAVGDYAVASGAC-LALQNSL-----SSIEGSLALGSGTSNRAIT 636

QY 298 -----GSSTDEGEGL-----VTAKEVIDAVNKA-----GWRMKTITANGOTQ----- 335
Db 637 TGIRETSATSDGVVIGYNTDRELGLALSGLTGDSESYRQITNVADGSEAQDAVTVROLQN 696

QY 336 -----ADKFEVTSCTNVTASGKTTA-----TVSKDDOG-----NITVMYDVNVGD 378
Db 697 AIGAVTTPTTKYHANSTEEDSLAVGDTSLAMGAKTIIVNADAGIGLGLNTLVNADAINGI 756

QY 379 ALNVN-----OLQNSGWNLDK-----AVAGSSGKVISGNVS 410
Db 757 AIGSNARANHANSIAMNGNSQTTTRGAQTDYATYMDTTPNSVGEFSVSGEDGQRIQTNVA 816
QY 411 PSKGMDETVTNAG-----NNIEISRNGNI-----DIATSM 444
Db 817 AGSADTDA-----VNVGOLKVTDAQVSRNTOSITNLNTQVSNLDTRVTNIENIGDITVTS 873
QY 445 PQF-----SSVSLGAGADAP-----TSLVDDE-CALNVGSKDANKPV 480
Db 874 TKYFKTNTDGDADANAAGADSAIGSGSIAAENSVALGTNSVADEANTVSVGSSTOOR-- 931
QY 481 RITNVAPGVKEGVDVTVNAQLK----- 501
Db 932 RITNVAAGVNTDVA NVAQLKASEAGSVRYETNADGSVNYSVLNLGDGSGTTRIGNVSA 991
QY 502 -----GVAQ----- 536
Db 992 AVNDTDAVNYAQLKRSVEEANTYTDQKMGEMNSKIRKIEKNKMGSGGIASANMAGLPOAYA 1051
QY 537 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFCSASVGVQW 592
Db 1052 PGANMISIAGGTNGESAVAGVMSVSESGWYKLGTSNSOGDYSAAIGAGFQW 1107

RESULT 7
A86036
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11208551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UNGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: Z5029

Query Match 12.5%; Score 373.5; DB 2; Length 1588;
Best Local Similarity 23.1%; Pred. No. 2.2e-11;
Matches 176; Conservative 95; Mismatches 261; Indels 231; Gaps 30;

QY 7 IIV-----NSALNANWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 880 LMDADAGENGAFSA-----AHGKKTASVITNVAN-----GAISAASSDAINGSOL 926

QY 61 ESYQSVSVGSI--QASMEGSGELETISLSMTN-----DSKEFVDPYIVVTLKAGDNLK 111
Db 927 YTTNKYIADALGDAEVNADGTITAPTYTIANAEYNNVNGDALDLD-----DNAL 976

QY 112 IKONTNENTNASSFTYSLKKD-----LTGLINVE-TEKLSFGANGKKNV-----IISDTK 160
Db 977 L--WDETANGGAGAYNASHDGRASITNVANGSISDSDTDAVNGSQLNATNMNMEQNTQ 1033

QY 161 GLNFAKETACTNGDITVHLNGIG-----STLUTDTLAGSSASHVDAGNQSHYTRAAISKDV 216
Db 1034 IIN-----OLAGNTDATTIQENGAGINIVRTNDDGLAFNDASAQGVGATAGYNSVAKGDSS 1090

QY 217 LNAG-WNKGKVTGSGTQSENVDVFTYDVEFLSADTKTTTVNVESKDNKRTEYKIG 275
Db 1091 VAIGQGSYSDVDTGIALGSSSVSRV-----IAKGRDTSIT-----ENG-----VVIG 1134

QY 276 AKTSVKEKDKGLVTKGKGEN-----SSTDEGEGLVTAKEVIDAVNKAQWRM--- 324

Db 1135 YDIT-----DGLLGLSISDGGKYRIINVADGSEAHDAVTVROLNAIGAVATPTKY 1189
Qy 325 -----KTTTANGOTG-----QADKFTVTSNTV----- 348
Db 1190 PHANSTEEDSLAVGTDLSAMGAKTIVNGDKGIGIGYAYVDANALNGAIGNAQVIHVN 1249
Qy 349 TFASGKGTAT-----VSXDDQGNITVMYDVNVG-----DAL 380
Db 1250 STAIANGSTTTTGAQNTYNTAYNMDAPQNSVGEFSVGSADGQRQIT--NVAAGSADTDAV 1306
Qy 381 NVNQLQ-----NSGWNLSK----- 395
Db 1307 NVGOLKVTDAQVQNTQSTITNLDNRVTNLDNRVTNIENGIGDIVTGTSTKFTKTDGVD 1366
Qy 396 -----AVAGSSGKVISGNVSPSKG-----KMDFTVINAGNNEISRN---GKNIDIA 440
Db 1367 ASAQKDSVAIGSGSIAAADSVALGTGVSATEENTISVGSSTNORRTITNVAAGKNATDA 1426
Qy 441 TSMAPOFSSVSLGAGADAPTLISVDDDEGALNVGSKDANKPVRITINVPAGVYKGDVTNVAQL 500
Db 1427 VNVAKLSSEAGGVRYDTKADGSIDYNTLGGGNG--TTRISNVASGVNNNDVVNYAQL 1485
Qy 501 KQVQA-----NLNRRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGTY 549
Db 1486 KQSVQETQYTDORMVENDNKLSTESKLSGSIASAMAMTGLPQAYTPCASMASIGGTY 1545
Qy 550 RGEAGYATGYSISDGGNWIILKGTASGNSRHFAGASASVGYOW 592
Db 1546 NGEAVALGVSVSANGRWYKLGSTNSQGEYSALGAGIOW 1588

RESULT 8

H91188
Probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD)
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001
C:Accession: H91188
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic
A:Reference number: A99629; PMID:21156231; PMID:11258796
A:Accession: H91188
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA837903.1; PID:g1363955; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs4480

Query Match 12.5%; Score 373.5; DB 2; Length 1588;
Best Local Similarity 23.1%; Pred. No. 2.2e-11;
Matches 176; Conservative 95; Mismatches 261; Indels 231; Gaps 30;

Qy 7 LIW-----NSALNAWAVSELTRNHTKRASATVAVTAVLATLLFATVOANATDEDEESEL 60
Db 880 LLDWADAGENGAFSA-----AHGKDKTASVITNVAN-----GAISAASDAITNGSQL 926
Qy 61 ESVQSVVVGSI--QASMEGSGELETISLSMTN-----DSKEFVDPIVTVTLKAGDNLK 111
Db 927 YTNKYIADALGGDAEVNADGTITAPTITIANAEYNNVGDALD-----DNAL 976
Qy 112 IKONTNENTNASSFTYSLKKD-----LGLINVE--TEKLSFGANGKYN-----IISDTK 160
Db 977 L---WDETANGAGAYNASHDKCSIIITNVANGSISEDSTDAVNGSQLNATNMIEQNTQ 1033
Qy 161 GLNFAKETAGTNGDITVHLNGIG-----STLDTTLGSSASHVDAGNQSTHYTHRAASIKDV 216
Db 1034 IIN---QLAGNTDARTYIENGAGINVTNRDNDGLAFNDASQGVGATAGYNSVAKGDS 1090
Qy 217 LNAG-WNIKGVKTGTTGSENVDFVRYDITVEFLSADTKITTVNVESKDNKRTVEKIG 275

Db 1091 VAIGGYSYSDVDTGIALGSSSVSSRV-----IAKSRDTSIT-----ENG---VVIG 1134
Qy 276 AKTSVIKEDKGLVTKGKGENG-----SSTDEGELVTAKEVIDAVNKAQHRM--- 324
Db 1135 YDIT-----DGLLGLSISDGGKYRIINVADGSEAHDAVTVROLNAIGAVATPTKY 1189
Qy 325 -----KTTTANGOTG-----QADKFTVTSNTV----- 348
Db 1190 PHANSTEEDSLAVGTDLSAMGAKTIVNGDKGIGIGYAYVDANALNGAIGNAQVIHVN 1249
Qy 349 TFASGKGTAT-----VSXDDQGNITVMYDVNVG-----DAL 380
Db 1250 STAIANGSTTTTGAQNTYNTAYNMDAPQNSVGEFSVGSADGQRQIT--NVAAGSADTDAV 1306
Qy 381 NVNQLQ-----NSGWNLSK----- 395
Db 1307 NVGOLKVTDAQVQNTQSTITNLDNRVTNLDNRVTNIENGIGDIVTGTSTKFTKTDGVD 1366
Qy 396 -----AVAGSSGKVISGNVSPSKG-----KMDFTVINAGNNEISRN---GKNIDIA 440
Db 1367 ASAQKDSVAIGSGSIAAADSVALGTGVSATEENTISVGSSTNORRTITNVAAGKNATDA 1426
Qy 441 TSMAPOFSSVSLGAGADAPTLISVDDDEGALNVGSKDANKPVRITINVPAGVYKGDVTNVAQL 500
Db 1427 VNVAKLSSEAGGVRYDTKADGSIDYNTLGGGNG--TTRISNVASGVNNNDVVNYAQL 1485
Qy 501 KQVQA-----NLNRRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGTY 549
Db 1486 KQSVQETQYTDORMVENDNKLSTESKLSGSIASAMAMTGLPQAYTPCASMASIGGTY 1545
Qy 550 RGEAGYATGYSISDGGNWIILKGTASGNSRHFAGASASVGYOW 592
Db 1546 NGEAVALGVSVSANGRWYKLGSTNSQGEYSALGAGIOW 1588

RESULT 9

AH0110
Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0110
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; PMID:21470413; PMID:11586360
A:Accession: AH0110
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-658 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0902

Query Match 11.4%; Score 341.5; DB 2; Length 658;
Best Local Similarity 24.5%; Pred. No. 3e-10;
Matches 155; Conservative 74; Mismatches 235; Indels 169; Gaps 24;

Qy 45 ATVOANATDEDEEELSVQSVVGS--IQASMEGSGELETISLSMTNDSKEFVDPIV- 101
Db 110 ATISSTSD-----AVGSQLYNVQDGTFRPHANSVNPDTSLASGLETIAGV 157
Qy 102 -VTLKAGDNKLTQNTNENTNASSFTYSLKKDLTGLINIVETEKLSFG-----ANGKKVNI 155
Db 158 PATVVSGDNGVIGNT-----ALVGAATGGTGAIGTGQVTAAGATAIGS 202
Qy 156 ISDTKGLNFAKETAGTNGDITVHLNGIGSTLDTTLGSSASHVDAGNQSTHYTHRAASIKD 215
Db 203 AAQAQG---AQSLALGAGAVTTSQANSI-----ALCAASINTVGAQSSSAYALTAPQAS 253

QY 216 VLNAG-----WNIGVKGTGGTGGSENV-----DFVRYDVTVEFLSADTKTTV-- 259.
Db 254 VGEIGTGTALGNRKITGVAAQSASSDAVNVAQLTAYGDQVQ-QONTANITSLGGRVTTIEG 312
QY 260 NVESKDNQ-----KRTEVKIGAKT-----SVIK 282
Db 313 SMASIANGGVKFYFHANSVTPQDPSVASTGTSVALGPASLASGNAALASGAGAVAGCAAA 372
QY 283 EKDGLKVTGKKGKENGSSSTDEGELGYTAKEVIDAVNKAQWRMKTTTANGOTGQADKFETV 342
Db 373 SADGSAVIGQSGDNGRGENYIG-----KYNSASNTSSG-----TV 409
QY 343 TSGTNTVFASGKGTATTATVSKDDOGNITVMYDVNVGDAVNQNLQNSGWNLDKSAVAGSSG 402
Db 410 SVGNAT-----GETRYSNVADG-----LQATDAVNLRLDG-----TAASI 447
QY 403 KVISGNSVPSKGMDETVTNINAGNNI-EISRNGKNIDI--ATSMAPQFSSVSLGACADAP 459
Db 448 VVVENNVSGIQLQNTDGMFQVNNSSGLAKPSATCANSATGGAGSVASGNNSTAFGSGAKAT 507
QY 460 TLS-----VDDEGALNVGSKDANKPVRIITNPAPGVKEGVDVTVAQLKGVAQN----- 506
Db 508 AANSAALGANSVADRANSVSGVGNR--QITNVAPATQGTDAVNFQDLKLSISNOTNAY 565
QY 507 LNNRIDNVDCNAR-----AGTAAQTATAGLQVQALPYLPGKSMMAIGGTVRGEGAGYAIG 559
Db 566 TNQYSELKQDLRKQNSVLSAGIASAMSASLTPQYTSGSSMTTIGAASVYRGQSALSLGV 625
QY 560 SSTSDGNGNIIKGTASNSRGHFGASASVGYQW 592
Db 626 SSTSDGRWYSKLGQASSNTQDGFIGVGVGYQW 658

RESULT 10
C82672
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: C82672
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences
Nature 406, 151-157, 2000
A:title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: C82672
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1004 <SIN>
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001
A:Experimental source: strain 9aSc
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canarigo, L.E.A.; Carraro, D.M.; Carner, H
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Klicajina, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mencia, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshukano, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1516

[illegible]

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1343 <STO>
A:Cross-references: GB:AE005174; NID:g12515159; PIDN:AAG56256.1; GSPDB:GN00145; UWGP:Z21
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ydek

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Query Match          7.6%; Score 227.5; DB 2; Length 1343;
Best Local Similarity 22.7%; Pred. No. 0.00053;
Matches 147; Conservative 86; Mismatches 252; Indels 163; Gaps 27;

QY 1 MNKIYRIINWALNNAVAVSELTRNHTKRASATVKTAVLATLFAATVQANATDEDEEEL 60
   ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MNRIYRVINWCTLQVFAQSELTRRVGKTSTVNLKSSGLTKTFS----- 45

QY 61 ESQVRSVGSIQASMEGSGELETISLSMTNDSKEFDVPIVIVTLKAGDNLKIKONTNEMT 120
   | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 46 -----RLTLGVLAL-----SGSVGASLEVDNG-----QITNIDT 76

QY 121 NASFTYSLKDLTLGLINVEKLSFGANGKKNVNIISDTKGLNFAKETAGT----- 171
   : : : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 77 DVAYDALVGVWYGTGVNLILA-----GGNASLTITTSVIGGN--EDSEGTNNVLGTWR 129

QY 172 ---NGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHY-----TRAASIKDVLNAGWNK 224
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 130 LYDSGNARPLN-VQSGGTGLNIKQKHGVDG-----YRLGTQAAGVGTV-----NVE 178

QY 225 GVKGTSTGQSENVDFRYDYVEFLSADTKTTTVNV-----ESKDNKRTVEKIGAKT 278
   | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 GEDSVLTTELFE-----IGSYGTGLNITDKGYVTSSIVAILGYQANSKVVYKERGG--E 232

QY 279 SVIKEKDGKLVTKGKGENGSSDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTGOADK 338
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 233 WLKNDSSIEFOIGNOQGTGEATIREGGLITAENTLIIGNATG-----VGLNVQ--DQDS 286

QY 339 FETVSGTNNVTFASG-----KGTATVSKDDQGNITVMYD----- 373
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 287 VIVRRLYNGYFCGAVNISNNGLINNKEYSLVGVDGSHGVNVVTDKGHWNFLGTGEAF 346

QY 374 --VNVGDA----LVNQQLQSNWNLDSKAVAGSSGKVISGNVSPSKGMDETVNIAGN 427
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 347 RYIYIGDAGXELNVSR-----EGKVDSGIITAGMKETGTGNLTV---KDKNSVITLGTN 399

QY 428 IEISRNKG-NIDIATSMAPOFSSVSLCAGADAPTLSDDEGALNV-----GSKDANKPVR 481
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 400 LGYDGHGEMNI-----SNEGLVSVNGSSSLGYGETGVKVSITTTGGIWEVKNVY 449

QY 482 ITNVAPGVKEGDTNVNAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP--GK 539
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 450 TTIGVAGVGNLNSDGG--KFVSONITFLGDKASGIGTGLNMDATSSFDVGINVGNFGS 507

QY 540 SMAIAGGTYRGAGYAI-----GYSSISDGGWIKGTASGNSR 579
   : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 508 GIVNVSGATLNTGTGFGFIGNGASGRGIVNISTDSLWNLK-TSSTNAQ 554
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RESULT 14
AH0038
Probable exported protein YPO0309 [imported] - Yersinia pestis (strain C092)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0038
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0038
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1238 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89171.1; PID:g15978410; GSPDB:GN00175
C:Genetics:
A:Gene: YPO0309

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Query Match          7.4%; Score 220.5; DB 2; Length 1238;
Best Local Similarity 20.7%; Pred. No. 0.0011;
Matches 142; Conservative 123; Mismatches 239; Indels 183; Gaps 37;

QY 19 VSELTRNHT-----KRASATVKTAVLATLFAAT--VQANAT-----DEDEEELESVOR 65
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 78 ISYLTNSALDTSRYSLYIKNDTLITEQSASINVQSGSISSGVYIDNQSSDDSTIRV 137

QY 66 SVVGSIQASMEGSGELETISLSMTNDSKEFDVPIVIVTLKAGDNLKIKONTNEMTNASSF 125
   | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 138 DLSGILLSLSLAPALSIFS--SAGNDST-----IILNTHAISGVTGIGQSDNNSQNGATI 190

QY 126 TYSLKDLTLGLINVEKLSF--GANGKKNVNIISDTKGLNFAKETAGT--NGDTTVHLNG 181
   | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 TH---VDVTDGINVENSQSVIRNAANG-----GTSIINFNSKSIINTEYNSFYIQNTNY 240

QY 182 IGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKGTSTG----- 233
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 241 VGVIIIDI-----NID--GDISSANSQAARIYNYNGLASLRFPRANNVGTGLYIDN 292

QY 234 QSEN---VDFVRYDTPVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIK-----E 283
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 293 SSQNGAVTDIILTGD---LTATSGSALQANASDEGNIETAIKLNNVSYSLDALNISDYT 349

QY 284 KQGL-----VTGKKGKENGSSD-----EGEGLVTAKEVIDAVNKAGWRMKTITANGQTG 334
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 350 RSGNILLDLDISGTITAENGTKIKVMAAGEGST---MLINVNNITSSQSLDINNYP 406

QY 335 QADKEFTVSGTNVTFASGKGTATVSKDDQGNITVMYDVNVGDA---LVNQL--QNSG 389
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 407 LGSFAISATATGHLTAENGQGMQLQTHS-----SLGDAYTLHFNDITAMSSG 454

QY 390 WNLDSKAVAGSSGK--VISGNVSPSKGMDETVNIAGNIEISRNKG---NIDIATSM 444
   : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 455 ISLINEANGTSTADITVTGQINVSHG---EGITLNA-----LTTDGRTLNVNDV--NNIA 505

QY 445 POFSSVSL-----GACADAPTLSVD--DEGAL-----NVGSKDANKP 479
   : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 506 SEYDAIRLYNRYNDNYATGVDDGTGADNGTSTIDITRGALVSOQGYGINIETNTADTY 565

QY 480 VRTTNVAPGVKEGDTNVNAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYL--- 536
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 566 VTVGGLVHG---GNGTAI---GI-----HRLDNIQTSATLELSQGVALEGVTVQALVFTG 613

QY 537 -----PKSMAIAGGTYRGAGYAI-----GYSSISDGG 566
   : : : | | | | | | | | | | | | | | | | | | | | | | | |
Db 614 SYAEINDAALDLANSHLVLLGA---GDAAFDLTRIDNREAILDGPNRITGFTLTNKTN 670

QY 567 N--WIITKGT--ASGNSRGHFASASVG 589
   | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 671 NSIWTTLTGANMADGDANAFLSANIAGG 697
```

RESULT 15
D90803
Aida-I adhesin-like protein [imported] - Escherichia coli (strain O157:H7, substrain C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:Accession: D90803
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90803
A>Status: preliminary
A:Molecule type: DNA

A:Residues: 1-949 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA34819.1; PID:ql3360856; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECs1396

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Query Match          7.3%; Score 219.5; DB 2; Length 949;
Best Local Similarity 21.4%; Pred. No. 0.00087;
Matches 179; Conservative 97; Mismatches 253; Indels 307; Gaps 42;

QY 1 MNKIYRIIWNALNVAWVSELTRNHTKRASATVK-----TAVLATLLFATVQANATDE 54
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 5 LNTSYRLVWNHITGTLVASELARSGRKAGVAVALSAAVTSVPALAAADKVVQAGETVN 64
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 55 D-----EEEELESVORSVVVGS1-----QASM 75
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 65 DGTLTNHDNQIVFGTANGMTISTGLELGPDSSENTGGQWQIONGGIAGNTVTTNQRQVYL 124
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 76 EGSGELET-----ISLSMTNDSKEFVDPIYIVT-----LRAGDNL 110
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 125 EGGTASDVTIRDDGGOSLNGLAVENTLNNRGEQWHEGCVATCTIINRDGYQSVKSGG-- 182
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 111 KIKQNTNENTNA-----SFTYSLKDKDLTGLINVEFKLSFGANGKKVNIISDTKGLNFA 165
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 183 -LATGTIINTGAEGGPDSDNSVTGQK-----VQGTAEASTTINKNGRQIILFS-----GLA 231
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 166 KET---AGTNGDTTVHLNGIGSTLTDTLTLAGSSASHVDAGNQSTHYTHRAASIKDVLN-AGW 221
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 232 ROTLIYAG--GDOSVH---GRALNTTLNG-----GYQVHRDGLA-LNTVINNEGOW 276
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 222 NIKGVKGTSTTGOSENVDFVRTYDVEFLSADTKTTNVNVESKDNGKTEVKIGAKTSVI 281
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 277 QV--VKAGGAAG-----NTTIN-----QNGELRVHAGGEATV 308
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 282 KEKDKGLVT-----GKGKG-----ENGSTDEGEGLVTAKEVID----- 315
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 309 QNTGGALVTSTAATVIGTNRLGNFTVENGKADGVVLESGGRDLVLESHSAQNTLVDDGGT 368
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 316 -AVNKAGWRMKTTTANGQTQADKPFETVTSCTNVTFASCK-----GTT 357
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 369 LAVSAGGRKATSVITSGGALIADSGATV-EGTN---ASGKFSIDGTSQASGLLLENGGS 424
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 358 ATVSKDDQ-GNITVMYD-----VNVGDALNVNOLQN 387
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 425 FTVNAGGQAGNTVGHRTGLTLAAGGSLSGRTQLSKGASWVLNGDVVSTGDIVNAGEIRF 484
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 388 SGWNLD-----SKAVAGSSG-----KVISGNVSPSKGMDETVNI----- 422
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 485 DNQTTNPAALSRAVAKSNSPVTFKLTTNLTGQGGTINMRVRLDGSNASDQDLVINGGQA 544
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 423 -----NAGN-NIEISRNGKNNDI-----ATSMAPQFS-SVSLGACADAPILSVDD 465
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 545 TGTWLAFTNVGNSNLGVATGQGIKRVVDAQNGATEEGAFALSRPLQAFNYTLNRDS 604
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 466 EGALNVGSKDANK---PVRITNVAPG-----VKEGDVTNVAOLKGVAAOHLNNRI----- 511
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 605 DEDWILRSENAYRAEVPLTYSMLTQMDYDRILAGSRSHQTVNGENNVRLSIQGGHLG 664
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 512 -DNVDGNARAGIAQAIATAG-----LVQAYLPKSKMM-----AIG----- 545
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 665 HDNNGGIARGATPESGSGYGFVRLEGDLRLTEVAGMSLTGTVYGAAGHSSVDVKDDGSR 724
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 546 GGTYRGEAGYATGYSSI---SDGGNW---IIKGT-----ASGNSRGHFGASASVGYOW 592
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 725 ACTVRDDAGSLGGYLLNVLHTSSGLWADIVAQGRHSMKASSDNDNDFRAR---GWGW 777
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
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Job time: 309 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:49:07 ; Search time 29.79 Seconds
(without alignments)
769.452 Million cell updates/sec

Title: US-09-771-382-10
Perfect score: 2988
Sequence: 1 MNKIYRIWNSALNAWAVS.....TASGNSRGHGASASGVQW 592

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	248.5	8.3	1325	1 YDEK_ECOLI	P32051 escherichia
2	210	7.0	1286	1 AIDA_ECOLI	Q03155 escherichia
3	197	6.6	1608	1 HLYA_SERMA	P15320 serratia ma
4	197	6.6	1655	1 OMPB_RICCN	Q9kka3 r outer mem
5	196.5	6.6	1039	1 AG43_ECOLI	P39180 escherichia
6	194.5	6.5	1654	1 OMPB_RICRI	Q53047 r outer mem
7	189	6.3	1567	1 ICEN_XANCT	P18127 xanthomonas
8	189	6.3	1953	1 BIGA_SALTY	P25927 salmonella
9	188.5	6.3	2249	1 OMPA_RICRI	P15921 rickettsia
10	187	6.3	1025	1 SLAP_CAUCR	P35828 caulobacter
11	186	6.2	1645	1 OMPB_RICVY	P96989 r outer mem
12	185.5	6.2	1656	1 OMPB_RICJA	Q06653 r outer mem
13	181.5	6.1	1861	1 APU_THETU	P38536 t amylopull
14	180	6.0	2003	1 YDBA_ECOLI	P33666 escherichia
15	180	6.0	2021	1 OMPA_RICCN	Q52657 rickettsia
16	179	6.0	933	1 SLAP_CAMFE	P35827 campylobact
17	179	6.0	1577	1 HLYA_PROMI	P16466 proteus mir
18	173	5.8	2329	1 YS99_CAEEL	Q02624 caenorhabdi
19	172.5	5.8	959	1 N100_YEAST	Q06229 saccharomyc
20	172	5.8	918	1 YMBJ_CAEEL	P34487 caenorhabdi
21	171.5	5.7	1196	1 ICEN_PSESX	Q33479 pseudomonas
22	170.5	5.7	2334	1 WAPA_BACSU	O07833 bacillus su
23	168	5.6	1300	1 120K_RICRI	P14914 rickettsia
24	167.5	5.6	1034	1 ICEN_PANAN	Q47879 pantoea ana
25	167.5	5.6	1322	1 ICBA_PANAN	P20469 pantoea ana
26	167	5.6	1569	1 YPJA_ECOLI	P52143 escherichia
27	165.5	5.5	1210	1 ICEN_PSEFL	P09815 pseudomonas
28	164.5	5.5	1258	1 ICEN_ERWHE	P16239 erwinia her
29	164	5.5	814	1 SLAI_BACAN	P49051 bacillus an
30	164	5.5	1200	1 ICEN_FSESY	P06620 pseudomonas
31	164	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
32	163.5	5.5	574	1 FLA3_CAMJE	Q46113 campylobact
33	162	5.4	1694	1 IGA0_HAEIN	P44969 haemophilus

34	162	5.4	1702	1 IGA2_HAEIN	P45384 haemophilus
35	161	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
36	161	5.4	575	1 FLA2_CAMJE	P22251 campylobact
37	161	5.4	1770	1 PMPC_CHLFR	O84419 chlamydia t
38	160	5.4	1148	1 ICBK_PSESX	O30611 pseudomonas
39	159.5	5.3	574	1 FLB3_CAMJE	Q46114 campylobact
40	159	5.3	1150	1 APNU_PIG	P12021 sus scrofa
41	158	5.3	575	1 FLB2_CAMJE	P22252 campylobact
42	157.5	5.3	1153	1 PVDB_PLAKN	P50493 plasmodium
43	156	5.2	497	1 FLIC_ECOLI	P04949 escherichia
44	156	5.2	1228	1 SLAP_BACST	P35825 bacillus st
45	155	5.2	1723	1 PM20_CHLPN	Q9z812 chlamydia p

ALIGNMENTS

RESULT 1
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051: P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORET).
GN YDEK OR ORET OR B1510.
OS Escherichia coli
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Oshio Y., Oshima N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
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RESULT

HLYA_SERMA	STANDARD;	PRT;	1608	AA.
ID	HLYA_SERMA			
AC	PI5320;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	01-NOV-1990 (Rel. 16, Last annotation update)			
DE	Hemolysin precursor.			
GN	SHLA.			
OS	Serratia marcescens.			
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;			
OC	Serratia.			
OX	NCBI_TaxID=615;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.			
RC	STRAIN=SN8;			
RX	MEDLINE=88257037; PubMed=3290200;			
RA	Poole K., Schiebel E., Braun V.;			
RT	"Molecular characterization of the hemolysin determinant of Serratia marcescens";			
RL	J. Bacteriol. 170:3177-3188(1988).			
CC	-1- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.			
CC	-1- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.			
CC	-1- SUBCELLULAR LOCATION: Outer membrane.			
CC	-1- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).			

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CC	EMBL; M22618; AAA50323.1; -.
DR	PIR; A28182; A28182.
DR	Hemolysis; Toxin; Outer membrane; Signal.
KW	
FT	SIGNAL 1 30
FT	CHAIN 31 1608
FT	HEMOLYSIN.
SQ	SEQUENCE 1608 AA; I165078 MW; D669B476FE7DAD51 CRC64;

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RESULT 4
OMPB_RICCN STANDARD; PRT; 1655 AA.
ID OMPB_RICCN
AC Q9KKA3; Q9KK98; Q9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (SCA5) (rOmpB)
DE (rOmp B) (Contains: 120 kDa surface-exposed protein [Surface protein
DE antigen] (120 kDa outer membrane protein ompB); 32 kDa beta peptid[
GN OMPB OR RCI085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Odata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,

```


DNA Res. 3:379-392(1996).
[3]
SEQUENCE FROM N.A.
RN STRAIN-ML 308-225;
RC Henderson I.R., Owen P.;
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
[4]
PRELIMINARY SEQUENCE OF 53-78.
RN STRAIN-ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN
RP SEQUENCE OF 53-63.
RX STRAIN-K12 / EMG2;
RA MEDLINE=97443975; PubMed=92986646;
RL Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN
RP GENE NAME.
RX MEDLINE=97257509; PubMed=9103983;
RA Henderson I.R., Meehan M., Owen P.;
RT "Antigen 43, a phase-variable bipartite outer membrane protein,
determines colony morphology and autoaggregation in Escherichia coli
K-12.";
FT K-12.";
CC FEMS Microbiol. Lett. 149:115-120(1997).
CC -!- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY
CC FUNCTION AS AN ADHESIN.
CC -!- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA
CC CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA
CC CHAIN).
CC -!- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.
CC -!- SIMILARITY: TO ADHESIN AIDI-I AND TO BORDETTELLA PERTACTIN.
CC
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DR EMBL; AE000291; AAC75061.1; ALT_INIT.
DR EMBL; D90838; BAA15825.1; ALT_INIT.
DR EMBL; D90839; BAA15832.1; ALT_INIT.
DR EMBL; U24429; AAB47869.1; -
DR Ecogene; EGI2686; flu.
KW Outer membrane; Signal; Complete proteome.
FT SIGNAL 1 52
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).

FT	VARIANT	829	835	LNLVHTS -> MNLIYNA (IN STRAIN ML 308-225).
FT	VARIANT	845	847	OGT -> LGA (IN STRAIN ML 308-225).
FT	VARIANT	855	855	S -> T (IN STRAIN ML 308-225).
FT	VARIANT	888	888	O -> L (IN STRAIN ML 308-225).
FT	VARIANT	1025	1025	S -> I (IN STRAIN ML 308-225).
FT	CONFLICT	61	63	ETV -> TTT (IN REF. 5).
SQ	SEQUENCE	1039 AA;	106841 MW;	5170D647C8DEEB0 CRC64;

Query Match 6.68; Score 196.5; DB 1; Length 1039;
Best Local Similarity 20.18; Pred. No. 0.0083;
Matches 134; Conservative 79; Mismatches 268; Indels 185; Gaps 27;

Qy	1	MNKIVRIIWSALNAWAVASEL	TRNHTKRASATVKTAVLATL	LLFATVLAQANATDEDEEEL	60
Db	5	LNTCYRLVWNTGAFVASELA	RARGKGVAVALSAAVTSLPV	LAADIVVHPGE---	61
Qy	61	ESVQSVVSGSIQASMEGSELE	TISLSMTNDSKEFVDPYIVV	TLKAGDNLIKIKONTNENT	120
Db	62	---	---	---	---
Qy	121	NASFTYSLKKDLTGLINVE	TEKLSFGANGKKVNIISDTK	GLNFAKETAGTNGDTTVHLN	180
Db	85	ISTGLEYPDNEA	---	---	---
Qy	181	GI	---	---	---
Db	119	GLQVNP	CGSVSDVISAGGOSQGR	AVNTTLNGGEQWHEGATATG	VINDKQWQV--
Qy	226	VKTGS	---	---	---
Db	177	VKPGT	VATDVVNTGAE	GGPD-AENGDTGQFVRGDA	VRTTINKNGRQIVRAEGTANTTW
Qy	273	KIGAKTSV	---	---	---
Db	236	YAGGDQTVHGH	ALDTTLNGGYQYVHNGT	ASDTVYNSDGMQIVKNG-G	VAGNTTVYNQGR
Qy	308	VTAKEVIDAVN	---	---	---
Db	295	LQVDAGGTAT	NWTLKQGGALVTSTAATV	GINLGAFSVEKGADNVLENG	RDLVLTG
Qy	356	TTATSKDDQGNIT	WYDVNVGDALNVQLNSG	NLDSKAVAGSSGKVISGNV	SPSK---
Db	355	HTATNTRVDDG	---	---	---
Qy	414	---	---	---	---
Db	406	SIGGGQADAL	MLEKGSFTLNAG	---	---
Qy	471	VGSKDANKP	VRITNVAPGVKEG	DTNVNVAQLKGVAQNLR	INDVGNARAGIAQAIATAG
Db	462	LSGRKTVN	---	---	---
Qy	531	LVQAYLP	PGSKMMAIGGGT	---	---
Db	511	AVNL	---	---	---
Qy	573	TASGNS	578	---	---
Db	568	NATVQS	573	---	---

RESULT 6
ID OMPB_RICRI STANDARD; PRT: 1654 AA.
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein

Db	469	VQLSGTHAELRLGNAGSIFKLDGTVVINGKVQNTALVGGALAAAGTITLDDSGATITGD---	526
QY	314	IDAVNAGWRMKTTTANGQTGQADKPEYTV-SGTNNVTFASG-----KGTATVSKDDQ	365
Db	527	IGNAGGAALQRIITLAN-----DAKKTTLGCAIIGAGGGTIDLOANGGTIKLT-STQ	579
QY	366	GNITVMYDV-----NVGDALNVNOLQNSGWN-----LDSKAVA-----GSSGKVIS-	406
Db	580	NNIWDVDFDLAIAIDQTVGVVDASSLTNAQTLLTNGIKTIGANNKTLQCFNIGSSKTVLSN	639
QY	407	GNVSPSKGWDFTVNNAGNNIISLRNGKNIDATSWAPQ----FSSV-----SLGAGAD	457
Db	640	GNVA-----INELVIGNDG-AVOFAHDTYLLITRTTNAAGOGKTIENPVPVNGTTLAAGTN	693
QY	458	APTLSVDDEGALNVGSKDANKPVRIITNVAPVKGEDVTNVNAQLKGVNAOLNNRINDVDG-	516
Db	694	LGS-ANPLAEINFGSGKVNVDT-VLNVGGEVNL-YATNITTTDA---NVGSFVNAGGT	747
QY	517	NARAGIAQAIAATAGLVQ-----AYLPKGSMAIGGTYRGAGYAIGYSSISDGGNWI	569
Db	748	NIYSG-----TVGGQGNKFNVALENGTIVTKFLGNATENGNTTIAAN-STLIQIGSNT	800
QY	570	IKGTASNSRG 580	
Db	801	ADCVASADGTG 811	

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RESULT 7
ICEN_XANCT
ID ICEN_XANCT STANDARD; PRT: 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OX Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
  Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -! FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
  CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -! SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -! DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
  OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
  REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -! MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
  NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -! SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
  FAMILY.
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CC -----
CC EMBL; X52970; CAA37140.1; -.
CC PIR; S11672; S11672.
CC HSSP; P06620; IINA.
CC InterPro; IPR000258; Ice_nucleatn.
CC Pfam; PF00818; Ice_nucleatn; 81.
  
```


Query Match 6.3%; Score 189; DB 1; Length 1567;
Best Local Similarity 21.6%; Pred. No. 0.032;
Matches 128; Conservative 83; Mismatches 265; Indels 116; Gaps 25;

QY 20 SELTRNHTKASATVKTAVLATLLFATVOANATDEDEEELESVORSVVGSIQAAMEGSG 79
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 760 SDVTAGYGSTGTAGADSLTIAG--YGSTQTSGD-----SSLTAGYSTGTARKGS- 808
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 80 ELETISLMTNDSKEFDVPYIVVTLTKAGDNLIKIKONTNENTNASSFTYSLKRLDLGLNLNV 139
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 809 --DITAGYSGTGTAGADS---TLIAGYG----STQTSQSDSSLT-----AGYGST 849
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 140 ETEKLSPGANGKKVNIISDTKGUNFAKETAGNGDDTVHNLINGISTLTDTLTAGSASHVD 199
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 850 QTAR-----EGSDV-----TAGYG----STGTAGADSLTIAGYSTGT-----AGSDSS-LT 891
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 200 AGNQSTHYTRAASIKIDVLNAGWIKGVKTSITGOSENVDFVRTDYTFEFLSADRTKTTVV 259
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 892 AGYGSTOTARKGS--DV-TAGY-----GSGTGAGADSLTIAGYSGTGTSGDSSLTAG 941
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 260 NVESKDNGKRTEVKIGAKTSVIKEDCKLVTKGKGENGSSDDEGLEVLTAKEVIDAVNK 319
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 942 YGSTOTARKGSDVTAGYSGTGTAGADSLTIAGYSGTGTSGS-----DSSLT 987
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 320 AGWRMKTTTANGOTGQADKFETVTSNTVTFASGGKTTATVSKDDQGNTVMYDYNVGDA 379
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 988 AGYGSTOTAREGSDVTAGYSGTGTACADSLTIAGYSGTGTAGSD--SSLTAGY-----GST 1041
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 380 LNVNQLONSWNLDKXAVGSSCKVISGNVSPSKGMDEFVNINAGNIEISRKNNDI 439
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1042 QTAQSGSDVTAGYSGTGTAGADSLTIAGYSGTGTAGSDSSLTAGY----- 1087
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 440 ATSMAPQFSVSLG-----AGADAPTLSVDDEGALNVGSKDKPKVRITNVAPGVKRGD 493
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1088 STQTAROGSDITAGYSGTGTAGADSLIA--GYGSTQTAGYDSLNTAGYSGTGTAREDS 1145
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 494 VTNVAQLKVQVNNRINDVGNARAGTAQAIATA-GLVQAYLPKSNMAITGGGTGRGE 552
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1146 LTAGYSGTSTAGHDSSLIAGYSGTGTAGYNSILTTGYGSGTQTAQESSSLTAGYSGT--ST 1203
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 553 AGY----AICYSSISDGG--NWIIKTASCNSRGH-----FGASASVGYY 591
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 1204 AGYDSTLTAGYSGTGTAGYKSTLTAGYSGNSTAGHESLIAGYSGTGTAGYE 1255
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

RESULT 8
BIGA_SALT
ID BIGA_SALT STANDARD; PRT; 1953 AA.
AC P25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein biga precursor.
DN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rhs homolog."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;

DR PRINTS: PR00327; ICENUCLEATN.
DR PROSITE: PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
Nature 413:852-856(2001).
[3]
SEQUENCE OF 1-765 FROM N.A.
STRAIN=LT2;
MEDLINE=G1100301; PubMed=1987123;
Wu J.Y., Siegel L.M., Kredich N.M.;
"High-level expression of Escherichia coli NADPH-sulfite reductase: requirement for a cloned cysG plasmid to overcome limiting shiroheme cofactor.";
J. Bacteriol. 173:325-333(1991).
CC -! CAUTION: Ref.3 sequence differs from that shown due to frameshifts in positions 414 and 732.
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EMBL; AF133696; AAD39458.1; .
EMBL; AE008859; AAL22340.1; .
EMBL; M64606; AAA27042.1; ALT_FRAME.
EMBL; M64606; AAA27043.1; ALT_FRAME.
PIR; C39200; C39200.
PIR; C39200; C39200.
DR StyGene; SG10437; bigA.
KW Virulence; Repeat; Signal; Complete proteome.
FT SIGNAL 1 27
FT CHAIN 28 1953
FT PUTATIVE SURFACE-EXPOSED VIRULENCE
FT PROTEIN BIGA.
FT 101 252
FT REPEAT 101 103
FT REPEAT 104 113
FT REPEAT 114 122
FT REPEAT 123 133
FT REPEAT 134 144
FT REPEAT 145 155
FT REPEAT 167 177
FT REPEAT 178 188
FT REPEAT 189 199
FT REPEAT 200 210
FT REPEAT 211 221
FT REPEAT 222 232
FT REPEAT 233 243
FT REPEAT 244 252
FT CONFLICT 207 207
FT CONFLICT 514 514
FT CONFLICT 1698 1698
FT CONFLICT 1795 1798
FT CONFLICT 1836 1837
SQ SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;
D -> DRGDVVTPDD (IN REF. 1).
A -> R (IN REF. 3).
D -> N (IN REF. 1).
QYLE -> ITLQ (IN REF. 1).
SA -> T (IN REF. 1).

Query Match 6.3%; Score 189; DB 1; Length 1563;
Best Local Similarity 21.9%; Pred. No. 0.042;
Matches 145; Conservative 93; Mismatches 253; Indels 170; Gaps 32;

QY 50 NATDEDEEELESVQR-----SVVSGIQASMCGSGELETTISLMTNDSKEFDVPYIV 101
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db 288 NYSEQDNQWLTTADGKTLNVTGWDMVDANAIAVIEGTQE---NGLYWKYDR---GYLI 340
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY 102 VTLAGDNLIKIKONTNENTNASSFTYSLKRLDLTGLI--NVET----EKLSFGANGKK 152
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||

```
Db 341 I---ADNTTIVISGDQAHNSDRGMDISGDRTGVIIISGDRVTNTLTGSSVTDGATGMV 397
QY 153 V-----NIISD-----TKGL-----NEAKETAGTNGTTHVLNAGIGSTLIDT-- 199
Db 398 ISGDTNTISGHSTVDNATGALISGNGTTFNAGDIAGVSGGTATIIDGDNATIKTGT 457
QY 190 ----LAGSSASHVDAGNQSTHYTRAASIKDVLNAGW-----NIKGVTGSTTQSGSENVDF 241
Db 458 SDISGAGSTGVIDGNARNVNDGDMITDGGTGCHITGDNVDNAGSTTVSGADA--- 514
QY 242 RTYDTVEFLSADTKYTTVVNVESKDNKRTVEKTKTAKTSVIEKDKGLVTKG-----KG 295
Db 515 ----TALYIEGDNALVINEGNTQISGAVGTRIDGDDAHTTNTGDIADVAGAGAAVING 570
QY 296 ENGSSDDEGLVY--AKEVI--DAVNKAGWRMKTITANGOTGOADKFETVTSNTVF- 350
Db 571 DNGSLTQAGDLLVTDGAMGIIYTGNEA-----KNTGNATVRDADSVDGFGVAGEKNTFK 625
QY 351 -----ASRGKTTATYSKDDQGNITVMDVNVGDALNVNQLONGWNLDSKAVAGSSGV 404
Db 626 NKGDIDVSLNGTCALVSGD-----MSQVTLGDGINVSVQ-----DSEGVFSSATGV 672
QY 405 ISGNVSPSKGMDETVINAGNIEISRNKNIDIAFMSAPQSSVSLGAGADAPTLVSD 464
Db 673 ---SVSGDSNAVDITGNV-----ISADYGQDDLAAG-APPLTGVVGGNGTNTLN-- 720
QY 465 DEGALNVGSKD---ANKPVRTITNAPGVKEGV-----TNV-----AQLKGVA 504
Db 721 --GALNIDDDLSATGQGYLDVVGLSVGTGDDNDVDGGINITHSEDPDGTADITGIS 778
QY 505 QNLNNRI-----DNVDCGNARAG---IAQAIATAGLV-----QAYLP-----GK 539
Db 779 VSGNSTVTLNGHSTIDNTVVGHVLRVYNGGSLILGDDSDVDVNVVSIPTGYTYNA 838
QY 540 SMAIGGTVYRGEAG-----YAI-----GYSSISDGGNWIIRKGTASGNRGRHFGASV 588
Db 839 LLMADGEGTSIENKGDITSHGVSVIRADNGSEVNSGDLIVATSSNSEDRAAITRAS 898
QY 589 G 589
Db 899 G 899

RESULT 9
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT; 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
DE antigen) (rOmpA) (rOmpA).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiidae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
RT repeated, near-identical sequences."
RL Infect. Immun. 58:2760-2769(1990).
CC -I- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -I- PTM: GLYCOSYLATED (PROBABLE).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC -----
DR EMBL; M31227; AAA26380.1; -.
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 2249
FT DOMAIN 212 1180
FT REPEAT 212 286
FT REPEAT 287 358
FT REPEAT 359 430
FT REPEAT 431 505
FT REPEAT 506 577
FT REPEAT 578 652
FT REPEAT 653 724
FT REPEAT 725 799
FT REPEAT 800 874
FT REPEAT 875 949
FT REPEAT 950 1021
FT REPEAT 1022 1093
FT REPEAT 1094 1165
FT REPEAT 1166 1180
FT TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.3%; Score 188.5; DB 1; Length 2249;
Best Local Similarity 22.5%; Pred No 0.052;
Matches 155; Conservative 79; Mismatches 273; Indels 181; Gaps 38;

QY 10 NSALNANWAVAVSELTRNHT-----KRASATVKT-AVLATLFLATVOANATDEDEEE-- 59
Db 703 DSTGNANGIVTFTGNTVGTGDTGNTNATLVNAGTAGTATLGAVIKATTTKLTNAASVL 762
QY 60 -LESQVSVVGSIOASMEG-----SCELETISLSMTNDSKEFVDPIVTVLTKAG--- 107
Db 763 TLTNANAVLTGAIDNTTGGDNVGLNGLSQTVDIGNTS-----LATISVGAGT 815
QY 108 ---DNLKIKONTNENTNASSFTYSKKD--LTGLINVEKLSFGANGKKVNIISDTKGL 162
Db 816 ATLGGAIVKATTTKLTNAASVLTLTNANAVLTGAVDNTT-----GGDNVGLNGL 868
QY 163 N-FAKETAGTNGTTHVLNAGIGSTLIDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGW 221
Db 869 SQVTGDTGNTSLATISV-GAG--TATLGGAIVKAT-----TTKLTNAASVLTLTNA-- 917
QY 222 NIKGVKVG---STTGOSENVDFVRYTDTVEFLSADTKTT---TVNVEKSD---NG--K 268
Db 918 --NAVLTGAIDNTTG--GDNVGLNGLNGLSQTVDIGNTSLATISVGAGTATLGGAIVK 974
QY 269 RTEVKIGAKTSVIEKDKGLVGTG---KRGENGSSSTDEGEGLVTAK---EVIDAVNKA 320
Db 975 ATTTLKLTDAASAVKFTNPVVVTVGAIDNTGNANGIVFTGNSVTGNVGNVGNLATVNVG 1034
QY 321 -----GWRMKTITAN-----GOTGOADKFETVTSNTVTFASGKGTAT 359
Db 1035 AGLLQVQGVVKKANTINLTNDASAVTFNPPVVTGIDNTGNANGI-VFTFTGNTSTGN 1093
QY 360 VSKDDOGNITVMDVNVGDAL-----NVN-----QLONGSW 390
Db 1094 V-----GNTNATLVNAGLLOVQGVGVKKANTINLTNDASAVTFNPPVVTGAIDNTG- 1147
QY 391 NLDSKAVAGSGKGVISGNVSPSKGMDETVINAGNIEISRNK-----KNIDIASMAPQ 446
Db 1148 NANGIVTFTGNTSTVTDI-----GNTNATLVNAGITLQAGSSLAANNIDFGASTLE 1203
QY 447 FSSVSLGAGADAP-----TLSDVDEGALNVGSKDANK-----PVRTNVAPG-----V 489
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Db 1204 FNGPLDGGKALPYFKGAINGNAILNVTNKLITASHLTGTVAEINIGAGNLTIDA 1263
QY 490 KEGDVTNVAQLKGVQNLNNR-----IDNVGNARAGIAQAIATAGLVQVAYLPG--KS 540
Db 1264 SVGDVTILN-----AQINFRARDSVLVLSNLTG---VGVNNILLAADLV---AFGADEG 1312
QY 541 MNAIGGTVRGEGAGYAGYS--SISDGG 566
Db 1313 TVVFNGVGNGLNVSNACTARNIGDGG 1340
RESULT 10
ID SLAP_CAUCR STANDARD; PRT; 1025 AA.
AC P35828; Q46015;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE S-layer protein (Paracrystalline surface layer protein).
GN RSAA OR CC1007.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=69394;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.
RC STRAIN=ATCC 19089 / CB15; PubMed=1393820;
RX MEDLINE=93007489; PubMed=1393820;
RA Gilchrist A., Fisher J.A., Smit J.K.;
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter
RT crescentus paracrystalline surface layer protein.";
RL Can. J. Microbiol. 38:193-202(1992).
RN [2]
RP REVISIONS TO 376; 636 AND 842-843.
RA Awram P.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
RA Atterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
RN [4]
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=89008089; PubMed=3049545;
RA Fisher J.A., Smit J.K., Agabian N.;
RT "Transcriptional analysis of the major surface array gene of
RT Caulobacter crescentus.";
RL J. Bacteriol. 170:4706-4713(1988).
RN [5]
RP CHARACTERIZATION.
RC STRAIN=CB15;
RX MEDLINE=98292737; PubMed=9620954;
RA Awram P., Smit J.K.;
RT "The Caulobacter crescentus paracrystalline S-layer protein is
RT secreted by an ABC transporter (type I) secretion apparatus.";
RL J. Bacteriol. 180:3052-3069(1998).
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A
CC PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER
CC (TYPE I) SECRETION APPARATUS.
CC -!- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE

CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.
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CC -----
DR EMBL; AF062345; AAC38665.2; -;
DR EMBL; AE005779; AAK22991.1; ALT_INIT.
DR HSSP; P01549; 2MCM.
DR TIGR; CC1007; -;
DR InterPro; IPR001343; Hemlysn_Ca_bind.
DR Pfam; PF00353; hemolysinCbind; 1.
DR PRINTS; PR00313; CABNDNGRPT.
KW Cell wall; S-layer; Calcium-binding; Complete proteome.
FT INIT_MET 0
SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;
Query Match 6.3%; Score 187; DB 1; Length 1025;
Best Local Similarity 24.1%; Pred. No. 0.024;
Matches 160; Conservative 73; Mismatches 274; Indels 156; Gaps 29;
QY 18 AVSELRNHTKRSATVTKAVLATL-----LFAVQAN-----ATDEDEEEELSVQ 64
Db 138 AYDKIGNAVATAAGVDVAAVAFSLRQANIDYLTAFVRAVNTFFTAADID-----LAVK 192
QY 65 RSVVSGI--QASMEGSELETISLSMTNDSKEFVDPIYVVTLKAGDNKLKIKONTNNTNA 122
Db 193 AALIGTILNAATVSGIGGYATATAAMIND---LSDGALSTDNAAGVNL---FTAYSSGV 246
QY 123 SSFTYSL---KKDLTGLINVT-----EKLSPGANGKKVNIISDTKGLNF 164
Db 247 SGTLSLTGTDLTGTANNDTFVAGEVAGATLTGVDTLGGAG-----TDVLNW 297
QY 165 AKETAGTNGDTVHLNGI-----GSTLDTLAGSSASHVDAG-NQ 203
Db 298 VQAAAVTALPTGVTISGIIETNMVTSAAITLNTSSGVTGLTALTNTSGAAQVTTAGAG 357
QY 204 STHYTRAAAIKD--VLNAGNKGKVTGTTGSGENVDVFTVDFEFLSADTKTTTVNV 261
Db 358 NLTATTAQAANNAVVDGGANTVASTGVTGTTTVCANSAASCTVSVSVANSSTTTTGA 417
QY 262 ESKDNGKRTVEKIGAKTSVIKEKDKLVTKGKKGNGSSTDEGEGLVTA-KEYIDAVNKA 320
Db 418 IAVTGGTAVTVAQTAGNAVNNTLTQADVTVTGNSSTTAVTQTAAATAGATVAGRVNGA 477
QY 321 GHRMKTTTANGOTGOADKFETVTS-----TNVTFASGKGTTATVSKDDQGN 368
Db 478 VTITDSAAAAT--AGKIATVTLGSGFGAATIDSSALTIVNL-SGTGTSLGIR---GAL 531
QY 369 TVMYDVNVGDALNVNOLQNSWNLDKAVAGS-----SGKVISQNVSPSKMDVTYN 421
Db 532 TATPANT-LTLNVNGLTTTGAITDSEAAADGFTTINAGSTASSTIASLVAADATTLN 590
QY 422 INAGNNIEISRN-----GKNI--DIATSMAPQFSSVSLGAGADAPTIVSD 465
Db 591 ISGDARVTITSHATAALTGTTVNSVGATLGAELATGLV--FTG---GAGADSLIGATT 645
QY 466 EGALNVGSKDANKPVRIITNVAPG--VKEGDVTVNAOLKGAQNLLNRIDNVD----- 515
Db 646 K-AIVMGAGDVTVTSSATLGGGSYNGDGTDV-----LVANVNGSSFSADPAFGFFT 699
QY 516 ----GNARAG-----IAQATATAGLVQ-----AVLPCKSMMAIGGGYRGEAGYAG 559
Db 700 LRVAGAAAGSHNANGFTALQLGATAGATFTTNVAVNVGLTVLAAPTGTITVTLANATGT 759
QY 560 SSI 562
| :

Db 760 SDV 762

RESULT 11

```
OMPBRICTY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOMP)
DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
[1]
SEQUENCE FROM N.A.
RP STRAIN=WILMINGTON;
RX MEDLINE=94040787; PubMed=8224896;
RA Hahn W.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
[2]
PARTIAL SEQUENCE.
RP STRAIN=WILMINGTON;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNBR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
[3]
IDENTIFICATION OF CLEAVAGE SITE.
RP MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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Query Match 6.2%; Score 186; DB 1; Length 1645;

Best Local Similarity 21.1%; Pred. No. 0.046; Mismatches 251; Indels 266; Gaps 37;

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QY 28 KRASATVKTAVLATL-----LFATVQANATDEDEEELESVQRVSVGSIQASMEGSG 79
DB 10 KIISAGLVTAATVIVAGFSGVAMGAVMQYNRT-----TNAATTVDDGAG 54
QY 80 ELET-----ISLSMTNDSKEFVDPYIVVTLKAGDNKLTQKNTNENTNASSFTYSUKDLTGL 136
DB 55 FDOTGAGVNLPVATNS-----VIT--ANSNNAITFT-PNGNLNLSFLDTANTLAVT 103
QY 137 INVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGS--TLTDTLAGSS 194
DB 104 IN-ENTTLGF-----VTNVTKGNFFFTIGACKSLTITGHGTAQAAATKSAQNV 154
QY 195 ASHVDAGNQ-----STHVTRAASIKDV-----LNAGWNK----- 224
DB 155 VSKVNAAGAINNDLSGVGSIDFTAAPSVEFLNINPTTQEAPLTGLDNAKIVNGANGIL 214
QY 225 -----GVKTGSTTGQSENVDFVRYTDFEFLSADTKTTTVNVEKD----- 265
DB 215 NITNGFVKVSKDTFAGIKT-INIGDNQGLMFTTTPDAANALNLQGGNTINFNRDGTGK 273
QY 266 -----NGKRTVEKI-----GAKTSVIKED-----GKLVTKGKG-----ENG 299
DB 274 LVLVSKNGNATEFNVTSGLGNLKGVIETDTTAAAGKLIANGAANAIVGTNDNGAAG 333
QY 300 ---STDEG-----EGLVTAKEVIDAVNKAGWRMKTITANGOT-----GOADKFET 341
DB 334 FIVSDVNGNAATISGQVYAKDIV-----IQSANAGQVTFEHLVDVGLGGKTNFKT 384
QY 342 VTSCTNVTASGKGTATVSKDDQGNITVMYDVN-----VGDALNVNQLNSGNWL 392
DB 385 ADSKVIITENASFGST-----DFGNLAVQIVVPNNKILTNFGIDA-----KNNG-NT 431
QY 393 DSKAVAGSGKVISGNVSPS-----KGKMDETVNI-----NAGNNIEISR 432
DB 432 AGVITFNANGTLVSGNTDPNIVVNIKAIEVGAGIVOLSGIHGAELRLGNAGSIFKLA- 490
QY 433 NGKNIDIATSWAPQFSVSLGAGA---DAPTLSDVD--EGALNVGSKD---ANKPVRI 484
DB 491 DGVINGPVNQNLPLVNNALAAAGSIQDGSAAITGIDIGNAVNAALQDITLANDASKILT 550
QY 485 VAP-----GVKEG-----DVTNVAQLKGAQN--- 506
DB 551 LSGANIIGANAGGAIHFQANGGTIQLTSTONNILLVDFDLDTTDTQGVVDASSLTNNQTL 610
QY 507 -LNNRIDNVGNAR-----AGTAQAIATAGLV-----QAILPGKSM 542
DB 611 TINGSIGTIGANTKTLGRFVWGSSKTLINAGDVAINELVMENDGSHVLTHTYLTITNTIN 670
QY 543 AIGGTYRGEAGYAGYSSISDGGNLIKTASGNSRGHFGASVSG 589
DB 671 AANOGKIIVAADPINTDIALDGTN--LGSAESPLSNIHFAATRAANG 715
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RESULT 12

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OMPBRICJA STANDARD; PRT; 1656 AA.
ID OMPB_RICJA
AC O06653;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOMP)
DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
```

```
OX NCBI_TaxID=35790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH;
RA Uchiyama T.;
RT "Sequencing of the gene encoding the protein rOmp B of Rickettsia japonica.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC
DR EMBL: AB003681; BAA20138.1; -.
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1338 120 KDA SURFACE-EXPOSED PROTEIN.
FT STRAND 1339 1656 32 KDA BETA PEPTIDE.
FT DOMAIN 528 533 POLY-GLY.
FT SEQUENCE 1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
SQ
Query Match 6.2%; Score 185.5; DB 1; Length 1656;
Best Local Similarity 22.0%; Pred. No. 0.051;
Matches 140; Conservative 81; Mismatches 229; Indels 187; Gaps 34;
QY 46 TVQANATDEDEEELS-----VQRVVGSIQASMEGSELETSISMTNDSKEFVDPYI 100
DB 262 TIFNGTGTGRVLVLLSKNGAATDFNVTSGLGNLKGIIELNVAINGQ----- 310
QY 101 VYTLKAGDNLKIQNTNENTNASSFTYSLKDLTGLINVETELKSLFGANGKKNVLIISDTK 160
DB 311 -LIANAGPANAVGTWNGAGRAAGFVVSD-----NGKAATIDGQVY 351
QY 161 GLNFAKETAGTNDTTV--HLNGIGSTLTDTLAGSSASHVDAGNQSTHY-----TRAA 211
DB 352 AKDMVIOANANGQVNFRIHVDVG--IDGTTAFKTAASIVAITQNSNFGTTDFGNLAAQV 409
QY 212 SKDVLNAGNWKGVGTGTGTGQSEN-----VDFVRVYDVVEFLSADTKTTTVN---- 260
DB 410 TVPDTMTL-----TGNFTGDANNPGNTAGVITPAAN--GTLASASADANAVTNNITA 460
QY 261 VESKNG-----KTEVKIGAKTSVKEKDKLVTKG-----GKGNGSSSTDEGE 305
DB 461 IEASGVGVOLSTGTHAEURLGNAGSVFKLADGTGVINGKVNQTVLVGGVLAAGAITLDSG 520
QY 306 GLVTAKEVIDAVNKAGWR--MKTTTANGQTGQADKPEVT-----SGTNVTFASGK 354
DB 521 ATITG---DINGNGGGAALQSITLAN-----DATKTLTLGGANIISANGGTINQANG 570
QY 355 GTTATVSKDDQGNITVYDV-----NVGDALNVNOLQNSGNLDSKAVSGSGKVIG 407
DB 571 GTIKLTS--TQNNIVVDCDLAIATDQTGVVDASSLT-----NAQTLTISGTIGIIGAN 621
QY 408 NVSPSK---GKMDVTN-----IN--AGNN--IETSRNGKNIDIATSNAPQ-----FSSV 450
DB 622 NTLTGQFNIGSSKTTLNGGNVAINELVIGNNGSVQFAHTYLTITRTNAGQGKIIFNPV 681
QY 451 -----SILGAGADPTLSVDDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAG 505
```

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DB 682 VNNNTTLAAGT-----:||| || | :||| || | :||| || | :||| || |
QY 506 NLNRRIDNVGNARAGIAQAIATAGLVQAYLPKGSNMAIGGTYGRCAGYATGYSSISDG 565
DB 726 YATN-ITTTDAN-----VGSFVFNAG-----GKNIVS---GTVGGQOQGNKFNVTALDNG 770
QY 566 -----GNWIIKGT-----SGNSRGHFGASA 586
DB 771 TTVKFLGNATFNNGTIAANSTLOISGNTADFIASA 807
RESULT 13
APU_THETU STANDARD; PRT; 1861 AA.
AC P38536;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-pullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase
DE type II) [includes: Alpha-amylase (EC 3.2.1.1) (1.4-alpha-D-glucan
DE glucanohydrolase); Pullulanase (EC 3.2.1.41) (1.4-alpha-D-glucan
DE glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].
GN AMYB.
OS Thermoanaerobacter thermosulfurogenes (Clostridium
OS thermosulfurogenes).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacterium.
OX NCBI_TaxID=33950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3896 / EM1;
RX MEDLINE=94252998; PubMed=8195085;
RA Matuschek M., Burchardt G., Sahm K., Bahl H.;
RT "Pullulanase of Thermoanaerobacterium thermosulfurogenes EM1
RT (Clostridium thermosulfurogenes): molecular analysis of the gene,
RT composite structure of the enzyme, and a common model for its
RT attachment to the cell surface.";
RL J. Bacteriol. 176:3295-3302(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in pullulan and in amylopectin and glycogen, and the
CC alpha- and beta-limit dextrins of amylopectin and glycogen.
CC -!- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
CC S-LAYER ANCHOR.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 S-LAYER HOMOLGY (SLH) DOMAINS.
CC
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CC
DR EMBL: M57692; AAB00841.1; -.
DR HSP: Q08751; 1BVZ.
DR InterPro: IPR000461; Alpha.amylase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR001119; SLH.
DR InterPro: IPR004185; alpha-amylase_N.
DR InterPro: IPR004193; isoamylase_N.
DR Pfam: PF00128; alpha-amylase; 1.
DR Pfam: PF02806; alpha-amylase_C; 1.
DR Pfam: PF02903; alpha-amylase_N; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF02922; isoamylase_N; 1.
DR Pfam: PF00395; SLH; 3.
```

DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01072; SLH_DOMAIN; 3.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;
KW Multifunctional enzyme; Glycoprotein.
FT SIGNAL 1 35 POTENTIAL.
FT CHAIN 36 1861 AMYLOPULLULANASE.
FT DOMAIN 928 1018 FIBRONECTIN TYPE-III 1.
FT DOMAIN 1157 1248 FIBRONECTIN TYPE-III 2.
FT ACT_SITE 628 628 BY SIMILARITY.
FT ACT_SITE 657 657 BY SIMILARITY.
FT ACT_SITE 734 734 BY SIMILARITY.
FT DOMAIN 1681 1739 SLH 1.
FT DOMAIN 1740 1803 SLH 2.
FT DOMAIN 1804 1861 SLH 3.
FT CONFLICT 1734 1734 D -> E (IN REF. 1; AAB00841).
SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;

Query Match 6.1%; Score 181.5; DB 1; Length 1861;
Best Local Similarity 19.5%; Pred. No. 0.093;
Matches 128; Conservative 98; Mismatches 226; Indels 205; Gaps 29;

QY 2 NKIVRIIWSALNA---WVAVSELTNRHTKRASATVKTAVLATLLFATVQA----- 49
DB 1208 NEVINYIDTSVINGVTYNYKVAVDLSFNRTESNVVTKIPDVPIKVFNVTPDPTPDA 1267
QY 50 -----NATDEEBELESVQSVVSGSIQASMEGSELE-----TISLMTNDSKE 94
DB 1268 VNLGATPNTATPSAQOMTKIDNTY-SITLTLDEGTQIEYKVGWDBKVEKDEYGN 1326
QY 95 FVDPYIVVTLKAGDN-LIKIKQNTNENTNASSFTYSLKKDLTGLINVTETKLSFGA-NGKK 152
DB 1327 FASNRKVTIVNOGNEMTINDTVYRWRDIPFIYSPSNNTVDSNTSMVEVKNYTKGAK 1386
QY 153 VNI-----ISDTGLNFAKETA---GPN-----GDTTVHLNGIG--STLT-----DT 189
DB 1387 VTINGDSFVQDKGV-FTKDSLVNYGVNKKIKHVEPNDGSGVYNDQGRITELTKDIEDV 1445
QY 190 LAGSASHVDAGNQSTHYTRAASIKDVLNAGNIKVGKSTTGQSNVDVFRTYDFVEF 249
DB 1446 IQENNSGSGTGNNNTS-----TSGNSSTSGSGTSGTSTISNTSNTSNT 1494
QY 250 LSADTKTTTVNVEKNGKRTVEKIGAKTSVIEKDGKLV---TGKKGNGSGSTDEGEG 306
DB 1495 IGVITKNGNITITLDAGK-----AKDLIVNSKDKKVVFDITIGEGQQ-----KV 1540
QY 307 LVTAKEVIDAVNAGWRMKTITANGOTGQADKPTVTSNTVTFASGKGTATVSKDDQG 366
DB 1541 VQISKDILD-----TSAANGKD-----IVIKSDNA 1565
QY 367 NITVMYDVNVGDALVNLQNSGNLDSKAVAGSGKVISGNVSPKGMDETVNINAGN 426
DB 1566 SIAL-----TKDALNQIQN-GVNSIK-----DNGKPNVINYVSLSN 1603
QY 427 NIELSRGNKIDITASMAPOFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRI----- 482
DB 1604 VWDITISGISGNV-----TLAKPVEVTLNISK--ANDPKRVAVY 1641
QY 483 -----TNVAPGVKEGDTVNAQLKGVAQNLRNIDVGNARAGIAQAIAT 528
DB 1642 YNPITNWEVYVGGKVDASSGTITFNATHFSQY--AAFEYDKTFNDIKDNKAKDIEVLAS 1699
QY 529 AGLVQA-----YLPKGS-----MMAIGGGTYRGEAGYAGYSSISDGGNW 568
DB 1700 RHIVEGMDTQYEPNKTVTTRAFTAMILRLLNLIKDETYSGE-----FSDVK-SGDW 1749

RESULT 14
YDAA_ECOLI STANDARD; PRT; 2003 AA.
AC P33666; P76087; P76088; P76856; P76857; P76859;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ydbA.
GN YDAA OR B1401/B1405.
OC Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 464-2003 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92190338; PubMed=1665988;
RA Moszer I., Glaser P., Danchin A.;
RT "Multiple IS insertion sequences near the replication terminus in
Escherichia coli K-12.";
RL Biochimie 73:1361-1374(1991).
CC -!- SIMILARITY: TO S-TYPHIMURIUM ORF NEAR CYSG (AC P25928).
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT
BETWEEN AMINO ACIDS 839 AND 840.
CC -----
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CC -----
CC EMBL; AE000237; AAC74483.1; ALT_SEQ.
DR EMBL; AE000237; AAC74487.1; ALT_SEQ.
DR EMBL; D90778; BAA15009.1; ALT_SEQ.
DR EMBL; D90778; BAA18880.1; ALT_SEQ.
DR EMBL; D90779; BAA18881.1; ALT_SEQ.
DR EMBL; X62680; -; NOT_ANNOTATED_CDS.
DR EcoGene; EGI1307; ydbA.
KW Hypothetical protein; Complete proteome.
FT CONFLICT 489 489 I -> V (IN REF. 2).
FT CONFLICT 495 495 I -> V (IN REF. 2).
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 6.0%; Score 180; DB 1; Length 2003;
Best Local Similarity 23.0%; Pred. No. 0.12;
Matches 160; Conservative 89; Mismatches 224; Indels 222; Gaps 43;

QY 55 DEEELESVQSVV-----GSTQASMEGSELETSLMTNDSKEFV----- 96
DB 149 DKTEKTLTIRDSVFTYENADGTI-SLQDSNGRKATINLQIDENNTVALEGSADGAT 207
QY 97 -----DPYIVVTLKAGDNLKIKQNTNENTNASSFTYSLKKDLTGL-IN-----VETEK 143

Search completed: July 3, 2002, 08:49:15
Job time: 721 sec

FT	CONFLICT	809	823	LLRQGGVKSNTIN -> KATLGGAIIKATTK (IN REF. 1).
FT	CONFLICT	898	898	D -> Y (IN REF. 1).
FT	CONFLICT	908	908	P -> N (IN REF. 1).
FT	CONFLICT	985	985	N -> K (IN REF. 1).
FT	CONFLICT	1009	1009	L -> S (IN REF. 1).
FT	CONFLICT	1013	1013	Y -> S (IN REF. 1).
FT	CONFLICT	1182	1182	K -> Q (IN REF. 1).
FT	CONFLICT	1314	1314	N -> Y (IN REF. 1).
FT	CONFLICT	1451	1451	H -> N (IN REF. 1).
FT	CONFLICT	1624	1624	G -> D (IN REF. 1).
FT	CONFLICT	1628	1628	E -> G (IN REF. 1).
FT	CONFLICT	1872	1872	A -> V (IN REF. 1).
FT	CONFLICT	1875	1875	T -> P (IN REF. 1).
FT	CONFLICT	1878	1879	MS -> LP (IN REF. 1).
FT	CONFLICT	1936	1936	E -> A (IN REF. 1).
FT	CONFLICT	1965	1970	MTAPLP -> ITPPLS (IN REF. 1).
FT	CONFLICT	1997	1997	G -> R (IN REF. 1).
SQ	SEQUENCE	2021 AA;	203328 MW;	327FC42D7CB24668 CRC64;
Query Match 6.0%; Score 180; DB 1; Length 2021;				
Best Local Similarity 20.5%; Pred. No. 0.12;				
Matches 138; Conservative 94; Mismatches 277; Indels 164; Gaps 30;				
Qy	13	LNAWVAYSELTRN-HTKRASATYKT-AVLATLLFATVQANATDEDEEELESVQSVVGS	70	
Db	274	LNLGALSQVTGNIGNTNALATISVGAGKATLGGAIVKATTTKLTNDASAVTFNPNV--	331	
Qy	71	IQASMEGSSELETISLSMTNDSK---EFVDPYIVVTLKAG-----DNLKIKONTNENT-	120	
Db	332	VTGAIDNTGNANNIGVTFGTGDSVTGTGNTGNALATISVGAGKATLGGAIIKATTTKLT	391	
Qy	121	NASFTYSLKDLTGLINVTETKLSFCGANGKYNIIISDTKGLNFAKETAGTNGDTTVHLN	180	
Db	392	NASAVTFNPNVVTGAI-----DNTGNANG-----IVTFGTGDSVTGTGNTGNALATISVG	443	
Qy	181	GIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDVL-NAGWNIKGVKT---GSTTQS	235	
Db	444	AGKATLGGAIIKATTTKLTNDASAVTFNPNVVTGAI DNTGNANGIVTFGTGDSVTGTGNI	503	
Qy	236	ENVDFTYDTVEFLSADTKTTTVNESKONG---KTEVKIGAKTSVIREKDGKLVG-	291	
Db	504	GNTNALAT-----ISVGAGKATL-----GGAIKATTTKLTNDASAVTFNPNVVTGA	551	
Qy	292	---KGCGENGSTDEGELVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEVTSCTNV	348	
Db	552	IDNTGNANGIVTFGTGDSVT-----GNIGNTNALATISVGAGK	590	
Qy	349	TFASGKGTATVSK--DDOGNITVMYDVNVGDALNVNLQNSGNWNLDSKAVAGSSGKVIS	406	
Db	591	ATLGGAIIKATTTKLTNDASAVTFNPNVVTGAI-----NTG-NANGIVTFGTGNSVT	644	
Qy	407	GNVSPSKGKMDETVMNAGNNEISRNKNIDITATSMAPOFSSV-----SLGAGADAP	459	
Db	645	GNIGNTNAL--ATVNVGAG---IATLEGAVIKATTTKLTNAASVLTNTNNAVLGTGAIN	699	
Qy	460	TLSDVDEGAL-----NYGSKDANKPVRI-----TNVAPGVKEG	492	
Db	700	TTGVDNVGVNLNGLALSQVTGNTGNALATISVGAGKATLGGAIVKATTTKLTNDASAV	759	
Qy	493	DVTNVAQLKGAQNLRNNDVNDGNARAGIA-----QAIATAGLVQAYLP	537	
Db	760	TFTNPNVVTGA-----IDNT-GNANGIATFTGDSVTGTGNTGNALATVNV-----	805	
Qy	538	GKSMMAIGGTYRG-----EAGYATGYS-----SISDGGNWIKGTAGSNGSRGH	581	
Db	806	GAGLLRVQGGVKSNTINLTNDASAVTFNPNVVTGAI DNTGNANGIVTFGTGDSVTGN	865	
Qy	582	FG-----ASASVG	589	
Db	866	IGNTNALATISVG	878	

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